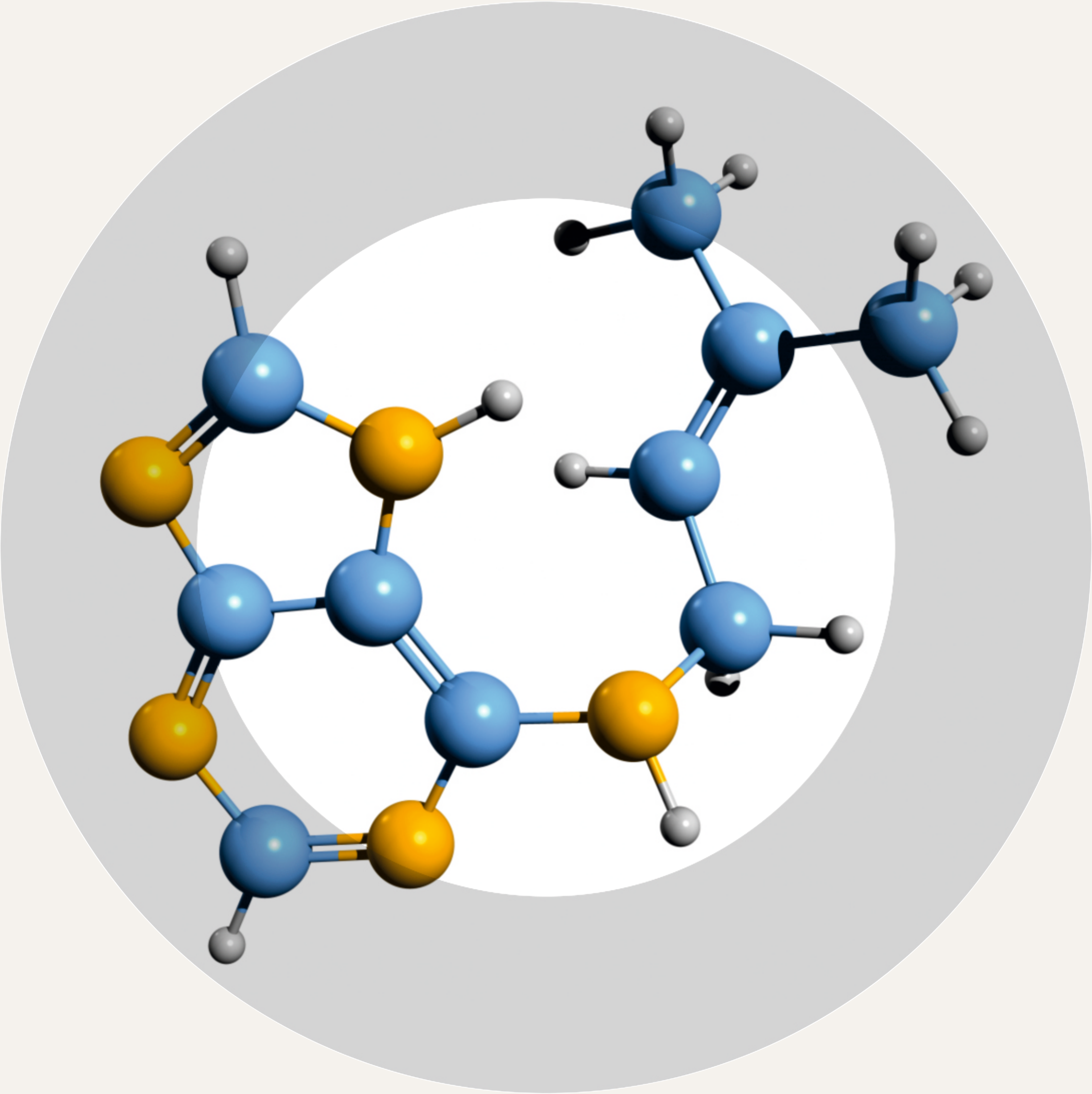

PHYTOHORMONES

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CONTENTS

CHAPTER1

HISTORY, NATURAL OCCURRENCE, AND THE CHARACTER OF THE PHYTOHORMONES

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ABSTRACT:

Phytohormones are a class of tiny chemicals that control plant formation and growth. Phytohormones are organic substances that exist in small amounts at various locations throughout plants. Auxin was the first of the identified phytohormones. Plant hormones served a variety of functions in the plant, including maintaining the structure of the plant and controlling the development of seeds, flowers' sex division, leaf withering, fruit ripening, and fruit development. Lacking phytohormones causes plants to stay as an indeterminate collection of cells because they are unable to distinguish. This part covered the short background of phytohormones as well as their biochemical characteristics.

KEYWORDS:

Auxin Hormones, Growth Regulators, Plant Hormones, Plant Growth, Plant Cells.

INTRODUCTION

Plant hormones are organic substances that have an impact on a plant's growth and evolution. They are frequently referred to as "plant growth regulators" to differentiate them from "animal hormones," but they both serve as molecular mediators. Plant hormones can be divided into three main categories and two additional categories that do not apply to them. Plants created plant hormones as a means of ensuring their longevity. Since a plant cannot escape a dangerous situation, it is crucial for it to have an internal communication system that enables the plant as a whole to respond appropriately to its surroundings. The transport of plant hormones play this part.

Plant hormones regulate a plant's reaction to its surroundings in addition to its rate of development. Similar to their animal equivalents, plant hormones function best in tiny doses and are typically produced in one location within the plant before being moved to another location where they are needed. However, they differ from animal hormones in that neither their production nor their action is restricted to a specific subset of target cells. Instead, any area of the plant that generates them can be affected by plant hormones. The first plant hormone, which he named "auxin," was identified in 1926 by Dutch scientist Frits W. Went (1903–1990), who was a specialist in the study of plants. Since the Latin term for "to increase" characterizes the outcome, he selected that word as the moniker. This hormone, which is now known as indoleacetic acid (IAA), is carried to the stems of immature plants where it promotes development. Other auxins that stimulate development in addition to IAA have been discovered, and auxins are now regarded as one of the three main hormone families[1]–[3].

Two other significant hormone subgroups exist in addition to auxins: cytokinins and gibberellins. The set of plant proteins known as cytokinins is significant because it promotes cell proliferation and slows the aging process in mature tissues. According to theory, cytokinins are made at the ends of roots, where they move upward through the plant and encourage budding as opposed to the long development auxins encourage. Gibberellins are a group of hormonal substances found in plants that promote the development of stems. (that part of a beginning plant that first pops out of a seed and reaches for the light). Gibberellins promote the first stages of root development, which is crucial for plant fetuses and plants. The first insights into the knowledge of GAs were discoveries from the plant pathology area, with research on the bakanae, or "foolish seedling" disease in rice. Rice stalks and foliage are severely elongated as a result of foolish seedling disease, ultimately toppling over. The fungi Gibberella fujikuroi was responsible for that stupid plant illness, according to Japanese chemist Eiichi Kurosawa, who discovered this in 1926. Later research at the University of Tokyo demonstrated that this fungus generated a chemical they called "gibberellin" that caused the signs of stupid seedling disease[1]. After World War II, contact between the West and Japan improved, which raised interest in gibberellin in the United States and the United Kingdom (UK).(US). Employees at the Department of Agriculture in the US and Imperial Chemical Industries in the UK separately separated gibberellic acid[1]. (with the Americans originally referring to the chemical as "gibberellin-X", before adopting the British name–the chemical is known as gibberellin A3 or GA3 in Japan)

Gibberellins gained popularity as their potential for use on a variety of economically significant species became more clear. For instance, a study on Thompson seedless table grapes that began at the University of California, Davis in the middle of the 1960s led to its widespread use throughout California by 1962. Paclobutrazol (PBZ), a recognized regulator of gibberellin biosynthesis, slows development and promotes early fruitset and seedset. A class of steroidal plant chemicals known as brassinosteroids (BRs). Brassins, also known as growth hormones, were partly isolated from rape pollen by Mitchell et al. in 1970, and they significantly accelerated the development of pinto bean (*P. vulgaris* cv. Pinto) plants. They discovered that auxin and GA biochemical functions are different from those of brassins. However, this discovery received little notice. The first BR, known as brassinolide, was identified in 1979, and it was found to be a distinct steroidal molecule. Before these findings, Marumo et al. partly isolated three physiologically active compounds from *Distylium racemosum* leaves in 1968; these compounds were subsequently identified as BRs.

These compounds show robust activity in the rice lamina leaning test. Castasterone was identified in 1982 by Yokota et al. from the insect galls of chestnut, and they theorized that it was a metabolic predecessor to brassinolide. Since then, Japan has effectively separated the majority of novel BRs from a variety of plant sources. It has been challenging to pinpoint the metabolic role of BRs because they exhibit a wide range of cellular activity. However, it has been discovered that *A. thaliana* and *P. sativum* (garden pea) BR biosynthesis and sensitivity mutations exhibit dwarfism. These results, along with biosynthesis research, proved that BRs are crucial factors for plants' typical development. Numerous studies have been written about the chemistry, metabolism, molecular biology, and use of BRs in natural products .In extending the work of Haberlandt, Jablonski, and Skoog (1954) discovered that the pith cells' ability to divide cells was caused by a material found in the arterial tissue From autoclaved herring fish sperm DNA, Miller and his colleagues (1954) extracted and refined the cell division component in crystallized form. Because of its capacity to encourage cell proliferation, this active substance was given the moniker "Kinetin" and became known as the first cytokinin. Later research revealed kinetin to be 6-furfuryl-amino purine.

Later, it was proposed to use the generic term kinin to refer to kinetin and other compounds with comparable characteristics. Miller and D.S. Lethum (1963–1955) concurrently separated and crystallized the first naturally occurring cytokinin from the watery endosperm of maize (Zea mays), which they called Zeatin. Cytokinins was the name Lethem ((1963) suggested for such substances .Jasmine is one of many plants that contain the chemical substance known as jasmonic acid (JA). The substance belongs to the family of plant proteins known as jasmonates. The octadecanoid pathway uses linolenic acid as a starting point for its biosynthesis. The Swiss scientist Edouard Demole and his coworkers first separated it in 1957 as the methyl derivative of jasmonic acid.

Greek origins of the term hormone translate it as being put in action. Cellular proliferation, development, gene translation, and transcription are all impacted by plant hormones. Although very identical compounds are created by fungus and microbes and can also have an impact on plant development, they are organically generated within plants. Humans can create a wide range of linked molecular substances. Plant growth regulators are artificial substances that are used to control the development of domesticated plants, pests, in vitro-grown plants, and plant cells. (PGRs). The word "phytohormone" was frequently used in the early stages of the research on plant hormones, but it is now less frequently used.

It's possible that substances that function as IAA intermediates also have auxin action. (e.g., indoleacetaldehyde). Other substances found in some plants have limited auxin action. (e.g., phenylacetic acid). Indoleacetyl aspartate, for example, is one of the conjugates of IAA that can exist. There have also been reports of 4-chloro-IAA in several taxa, but it is unclear how much of the natural auxin action in plants can be attributed to 4-Cl-IAA. Several manufactured auxins are also employed in industrial settings. Young cells of the growing seed and stalk make GAs from glyceraldehyde-3-phosphate via isopentenyl diphosphate. Their production begins in the plastid and progresses through cytosolic and membrane processes. Adenine undergoes metabolic change during CK production. It appears in growing seeds and root ends. Most organs respond to stress by producing ethylene. It is specifically produced in tissues going through senescence or aging. Ethylene diffuses from its location of production because it is a vapor. An essential step in its manufacturing, However, 1-aminocyclopropane-1-carboxylic acid (ACC) can be moved and may be responsible for the impacts of ethylene that occur away from the causative trigger. Both leaves and stems in the xylem and phloem release ABA. There is some proof that ABA may move from the stems in the xylem to the roots in the phloem (Figure.1).

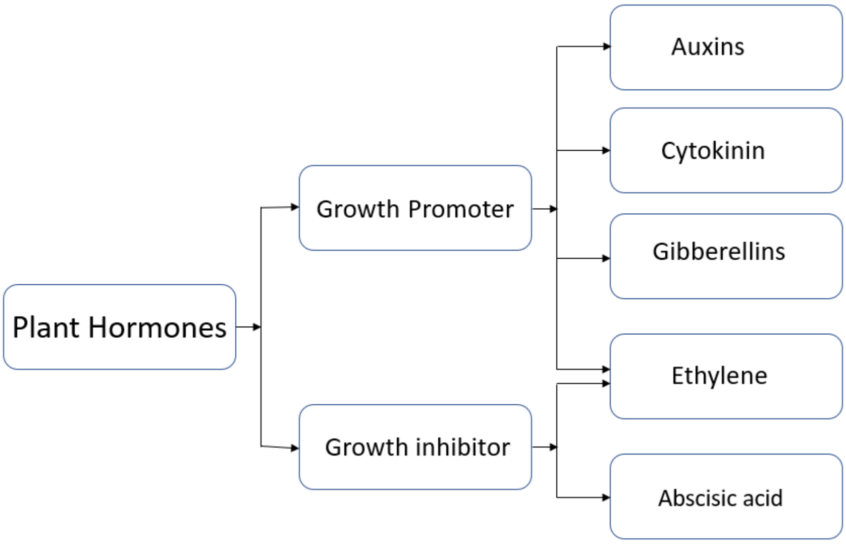

Figure 1: Phytohormones: Diagramed showing the different phytohormones and their function (Proton talk).

In very small amounts, plant hormones which are chemicals, not foods encourage and affect the development, division, and growth of cells and tissues. The following is a list of the most common questions we get asked about our products. Plants lack structures that produce and store hormones because they use more passive ways to transport substances throughout their bodies than do animals, which have two circulatory systems (cardiovascular and lymphatic) powered by a heart that transfers fluids throughout the body. Plants use simple substances as hormones because they can more easily pass through their cells. They are frequently produced and used locally, within the confines of the facility. Plant cells generate hormones that affect different cell components.

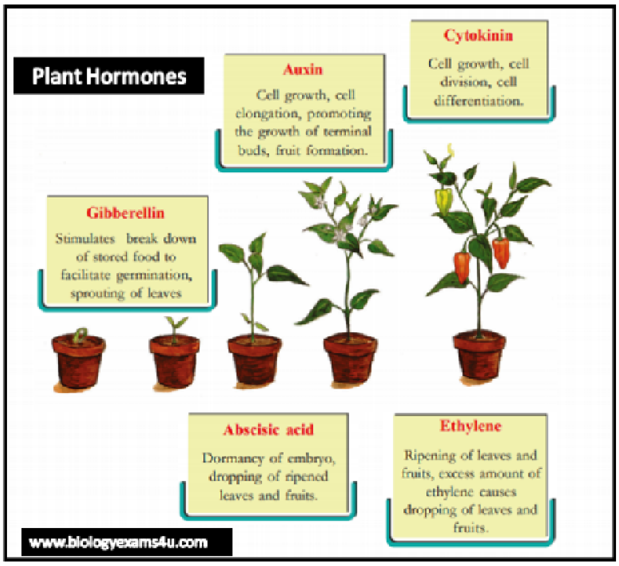

Figure 2: Phytohormones: Diagramed the role of the different phytohormones in the plants (Biology exam 4U).

There are four different motions that the plant uses to transfer hormones. Cytoplasmic streaming within cells and sluggish ion and molecular diffusion between cells are both used for limited mobility. Vascular structures, such as sieve tubes or phloem, which transport carbohydrates from the leaves to the roots and blossoms, and xylem, which transports water and mineral solutes from the bases to the vegetation, are used to transport hormones from one area of the plant to another. Hormones don't affect all plant cells, but those that do are designed to react at particular times during their development cycle (Figure.2). The most significant effects happen at particular times during the cell's existence, and the least significant effects happen before or after these times. At the end of the day, the only thing that matters is that you have a good time. Additionally, they must stop the negative impacts that hormones have when they are no longer required.

At locations of active development within the meristems, hormone synthesis frequently takes place before cells have completely differentiated (Figure. 2). They may be transferred from the manufacturing area to another area of the factory, where they have an instant impact, or they may be kept in cells and discharged at a later period. Plants can control the quantity of compounds used to biosynthesize hormones, which allows them to control the amounts of intracellular hormones and moderate their effects.

By conjugating them with sugars, amino acids, or peptides, they can be stored in cells, rendered inactive, or used to cannibalize already-formed hormones. Hormones can also be biologically broken down by plants, which destroys them. Other plant hormone amounts are commonly regulated by plant hormones .

LITERATURE REVIEW

Auxins are a class of naturally produced phytohormones with many roles in the growth and evolution of plants. It has a lengthy and diverse past to identify and measure these hormones in plant cells, going back to the middle of the 19th century. Analytical chemistry's development closely parallels that of auxin analysis. However, few of the approaches created over the years have been entirely abandoned, and many of them are still used in regular auxin studies today. This is true even though the methodologies for auxin determination have changed since the original bioassays.

The study of gibberellin began in Japan in the 19th century, when it was discovered that a rice illness was brought on by a fungus infestation. Later research revealed that the disease's signs, such as plant proliferation and infertility, were caused by the fungus Fusarium fujikuroi, from which the term "gibberellin" for the active ingredient was obtained. The profound effect of gibberellins on plant growth and development, particularly growth recovery in dwarf mutants and induction of bolting and flowering in some rosette species, prompted speculation that these fungal metabolites were endogenous plant growth regulators and this was confirmed by chemical characterization in the late 1950s. It is now understood that vascular plants, as well as some bacterial and fungi taxa, contain gibberellins. The routes, enzymes, genes, and mechanisms governing gibberellin production in plants and fungi have essentially been figured out. The finding that gibberellins cause the breakdown of the growth-inhibiting DELLA proteins supported the hypothesis that they work in plants by eliminating growth restriction. The discovery of the gibberellin receptor from rice in 2005 shed light on the process by which this is accomplished. The role of DELLA proteins as controllers of gene expression is a special emphasis of the current study on the activity of gibberellin. This overview tracks the development of gibberellin research, placing special stress on the early findings that made it possible for more recent developments[3]–[5].

Many plant parts only have a brief lifespan of a few weeks or months. The height of these organs' specific abscission zones is where they split from the plant. When a vascular casting technique was applied, the study of xylem vessels in abscission zones—a topic that has received little attention—revealed unique characteristics. All of the dicotyledon species that have been studied so far have heterogeneous metaxylem vessels that are adjacent to protoxylem and secondary xylem vessels with uniform patterns of lignified thickenings. When in the abscission zone, heterogenous metaxylem artery thickenings had spiral, reticulate, or scalariform elements and scarred elements on the proximal and distal edges. These boats' history and potential purpose are taken into consideration. According to data on the tomato blossom abscission zone (Lycopersicon esculentum Mill.), the procambium-cambium continuity contains localized variations in the pattern of cell differentiation and cell development that lead to the creation of heterogenous vessels.

The generation of methane from plant cells is estimated using a reasonably quick, quantifiable technique that is described. The process, which is a variation of Nelson's KMnO4 reduction method, basically entails a ferrous ammonium sulfate-KMnO4 titration procedure wherein ethylene is collected in an abundance of KMnO4 with the creation of ethylene glycol and manganese dioxide. These components are then removed from the KMnO4 absorption solution, and at the conclusion of the cycle, the leftover KMnO4 is titrated. Under uniform circumstances, the measurement result is transformed to equal milliliters of ethylene. 2. The ethylene value for apple apples as measured by the KMnO4 reduction technique is within the range previously reported for this type of tissue and was acquired by different researchers using other methods. Valencia oranges that were whole generated a lot less methane than fruit that had been sliced into pieces or injected with

Penicillium digitatum. Cotton and rose leaves both generated detectable levels of methane. It was discovered that young cotton leaves evolved more ethylene than adult cotton leaves of the same weight. 3. In vitro research using various common plant chemicals and a raw enzyme source derived from either apple juice or the green mold Penicillium digitatum showed that ethylene is indeed produced during breathing by the enzymatic breakdown of a variety of active substrates. It has been hypothesized and debated how it may have originated in living tissue.A crucial regulator of plant growth and defense that emerged during the shift of plants from an aquatic to a dry setting is jasmonate (JA) communication. Understanding the evolution of JA signaling is crucial for figuring out how plants grow, defend themselves, and produce specific molecules. It was possible to determine the ancestry of CORONITINE INSENSITIVE 1 (COI1), JASMONATE ZIM-DOMAIN (JAZ), NOVEL INTERACTOR OF JAZ, MYC2, TOPLESS, and MEDIATOR SUBUNIT 25 by tracing the genealogy of important protein domains that characterize JA signaling components. Despite having their orthologs in bryophytes, charophytes lack the genes encoding crucial JA signaling elements like COI1, JAZ, MYC2, and the JAZ-interacting bHLH factors. Charophyta and chlorophya phytoplankton were discovered to contain TIFY family genes. Through modifications to a number of essential amino acids, JAZs diverged from ZIM genes of the TIFY family. The middle Cambrian to early Ordovician eras, between 515 and 473 million years ago, are when JA communication first appeared, according to dating. Rapid biodiversification and catastrophic catastrophe disasters are hallmarks of this era. The development of JA signaling and plant defense may have been influenced by the greater hunting brought on by the diverse and shifting fauna.

A crucial part of how plants react to biotic and abiotic stress is played by salicylic acid (SA). Several essential proteins involved in SA production and controllers of SA signaling have undergone thorough characterization. The genesis, development, and early diversity of key components in plant SA signaling and biosynthesis, however, are still largely unclear. 10 key protein families involved in SA signaling and biosynthesis were found in this research across different green plant groups. We discovered that the essential SA signaling receptors, the nonexpresser of pathogenesis-related (NPR) proteins, formed distinct groups in the progenitor of seed plants and descended from terrestrial plants' most recent common ancestor (MRCA). TGACG motif-binding proteins (TGAs), important transcription factors for SA signaling, on the other hand, date back to the MRCA of streptophytes, supporting the idea that central SA signaling in plants has evolved gradually over time. SA is widely present in green plants, including chlorophytes and streptophyte phytoplankton, in contrast to the construction of the central SA signaling system in the progenitor of seed plants. However, the MRCA of terrestrial plants is where the entire isochorismate synthase (ICS)-based SA synthesis pathway was initially put together. We further revealed that the ancient abnormal inflorescence meristem 1 (AIM1)-based β-oxidation pathway is crucial for the biosynthesis of SA in chlorophyte algae, and this biosynthesis pathway may have facilitated the adaptation of early-diverging green algae to the high-light-intensity environment on land. Together, these results shed light on the early diversity and evolution of plant SA signaling and biosynthetic pathways and emphasize the critical function of SA in plant stress tolerance during plant terrestrialization.

Cytokinins (CKs) are a class of tiny signaling molecules generated from adenine that are essential for plant growth and a variety of embryonic processes. The biological roles of the standard CKs—isopentenyladenine (iP), trans and cis isomers of zeatin (tZ, cZ), and dihydrozeatin—have been thoroughly investigated, and their roles in numerous facets of plant metabolism are well established. The genes implicated in tRNA changes that result in the synthesis of tRNA-bound methylthiolated CKs are also well understood, particularly in bacterial and mammalian systems. The sources, futures, and potential roles of free methylthiolated CKs (2MeS-CKs) in living systems, however, are not well understood. The iP or Z-type CKs are changed by the addition of a thiol group (-SH) at position 2 of the adenine ring, which is then methylated, to produce 2MeS-CKs, which are free base or riboside derivatives. According to the available data, the tRNA breakdown route is the only source of these unique CK conjugates. The information on the likely processes involved in the production of free 2MeS-CKs in various domains of life is compiled in this study. Additionally, it illustrates CK characteristics of various species in which 2MeS-CKs have been found and proves a close relationship and delicate equilibrium between the generation of traditional CKs and 2MeS-CKs. Finally, it examines the findings that are currently known regarding the potential metabolic roles for 2MeS-CKs in various cellular systems [6]–[8].

CONCLUSION

The development regulators that control the biochemical and metabolic characteristics of the plant are called phytohormones. Different phytohormones perform various tasks in various plant settings. The combined impacts of the various phytohormones sustain the whole process from embryo growth to stalk and root development. Various transcription factors and signaling networks control the presence of various phytohormones at varying times and locations. At this chapter's end, we reviewed the short background, the normal frequency, and the various ways that phytohormones control plant development. A summary of phytohormones in nature can be gathered by investigating their various functions.

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CHAPTER 2

PHYTOHORMONES WHICH REGULATED PLANT GROWTH AND DEVELOPMENT

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ABSTRACT:

Whereas indole-3-acetic acid was the very first auxin to be discovered and is the main auxin in plants, auxin activity is also found in other chemicals found in plants. Auxins are chemicals formed from indoles that may regulate a cell's rate of division and extension as well as its identity or state of differentiation. Many growth and developmental processes during embryogenesis and post-embryonic maturation are regulated by auxin synthesis or reactivity. They include vascular maturation, leaf and blossom commencement, root growth, and the creation of lateral roots. Tropic growth responses are also included. Auxin can be produced from indole directly or from tryptophan via several unknown intermediates. Auxin pools that are necessary for typical development are produced by two distinct kinds of biosynthesis pathways. In this chapter, we discussed the natural occurrence of auxin, its biosynthesis, and its functional importance of it.

KEYWORDS:

Auxin Response, Acetic Acid, Auxin Biosynthesis, Growth Development, Root Hair.

INTRODUCTION

Higher plants have evolved successfully because of their capacity to create seeds, which serve as reproductive, dispersal, and survival units. To regulate these processes, synchronized cooperation between hormone signaling networks and environmental cues is necessary. The viable seed is made up of three genetically distinct compartments and is an entity that develops from the fertilized egg at the conclusion of the development program progression. That is mother seed-coat (2n) on the other, and filial endosperm (3n) and embryo (2n) on the one hand. The paternal and maternal gametes fuse to form the diploid embryo and the triploid endosperm, which is when the growth of the angiosperm seed begins. The endosperm begins to form in the majority of higher plants as a syncytium, in which nuclear divides do not result in cytokinesis. The endosperm becomes cellularized after a certain amount of caryokinesis. However, it is still unclear what controls the transition to cellularization, a crucial stage in seed growth. While it is typically kept in mature monocot seeds, the endosperm is typically consumed during seed development in dicots[1]–[3].

However, plants have a very high degree of endosperm growth conservation. When endosperm cellularization is compromised, the embryo is arrested, and the seed dies. It's interesting to note that for the endosperm to cellulate, auxin levels must be closely regulated. On the other hand, the growth of the three compartments that make up a seed depends heavily on strong interdependent control. It follows that it is not surprising that the genetic and hormonal levels of all molecular processes engaged in zygotic embryogenesis are closely synchronized. The classification of mutants has largely been used to analyze zygotic embryogenesis. The embryogenic phase concludes once the seed tissues have fully differentiated, and the maturation phase then starts. During this phase, storage substances (such as proteins and lipids) build up in the endosperm (monocots) or the cotyledons.

(eudicots). During maturation, programmed cell death takes place and desiccation tolerance develops; at the end, the primary seed enters a dormant state, stopping vivipary

The first hormone found in plants, auxin, has a significant impact on how plants grow and evolve. A number of transcription factors, including the auxin response factor, are one of the most significant of which is involved in the signal transduction pathway that auxin uses to operate. (ARF). Since the ARF was identified in Arabidopsis in 1997, it has been identified in a variety of plants, including vines (*Vitis vinifera*), tomato (*Solanum lycopersicum*), rice (*Oryza sativa*), maize (*Zea mays L.*), and Arabidopsis (*Arabidopsis thaliana*)[2]. Known in nature as indole-3-acetic acid (IAA), the plant hormone auxin is made in the apical meristem and is mainly derived from the well-known amino acid tryptophan (Figure.1). The manufactured auxins 2,4-dichlorophenoxyacetic acid (2,4-D) and naphthalene acetic acid are also present. (NAA).

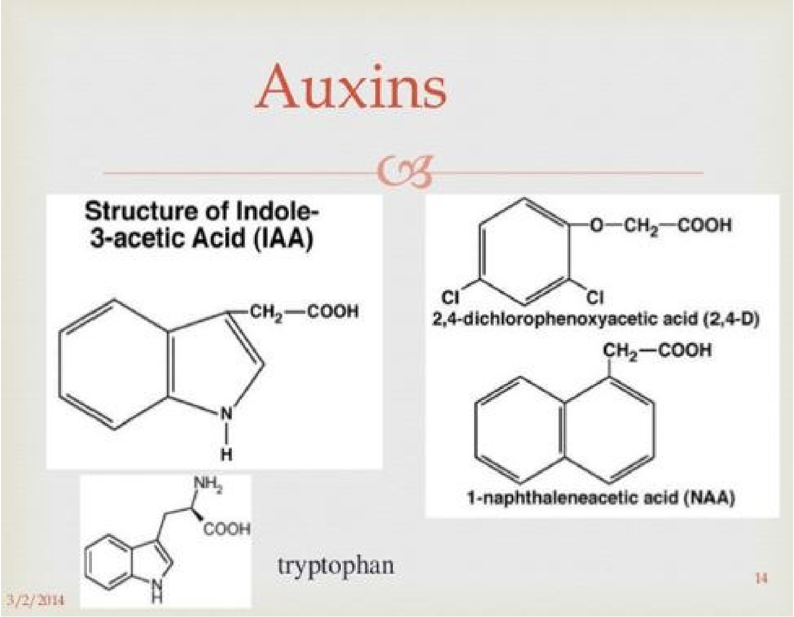

Figure 1: Auxins structure: Diagram showing the chemical structure of the auxin (Soil.evs).

The identification of IAA signaling pathways has advanced significantly, but little is still known about how environmental and developmental cues affect IAA biosynthesis. Auxin biosynthesis from scratch is crucial to many embryonic processes. Determining the molecular mechanisms of auxin biosynthesis may offer novel methods for answering complex questions about plant development, defining the functions of auxin in plant growth, comprehending auxin transport, and researching auxin's mechanisms of control over plant growth. In plants, auxin biosynthesis is a highly complex process. Numerous proposed mechanisms participate in the production of de novo auxin (Figure.2). IAA is a crucial component in the plant life cycle, so it makes sense that various plant species would share evolutionarily conserved core mechanisms for auxin biosynthesis.

However, different plant species may have distinct strategies and modifications to optimize their metabolic pathways. The tryptophan (Trp)-independent and Trp-dependent pathways have both been suggested as two main pathways for IAA biosynthesis in plants. Indole-3-glycerol phosphate or indole is the most probable precursor in Trp-independent IAA biosynthesis, but little is known about the biochemical pathway to IAA. (Figure.2). several routes have been proposed for the production of Trp-dependent IAA, including the indole-3-

acetamide (IAM), indole-3-pyruvic acid (IPA), tryptamine (TAM), and indole-3-acetaldoxime (IAOX) (Figure.2).

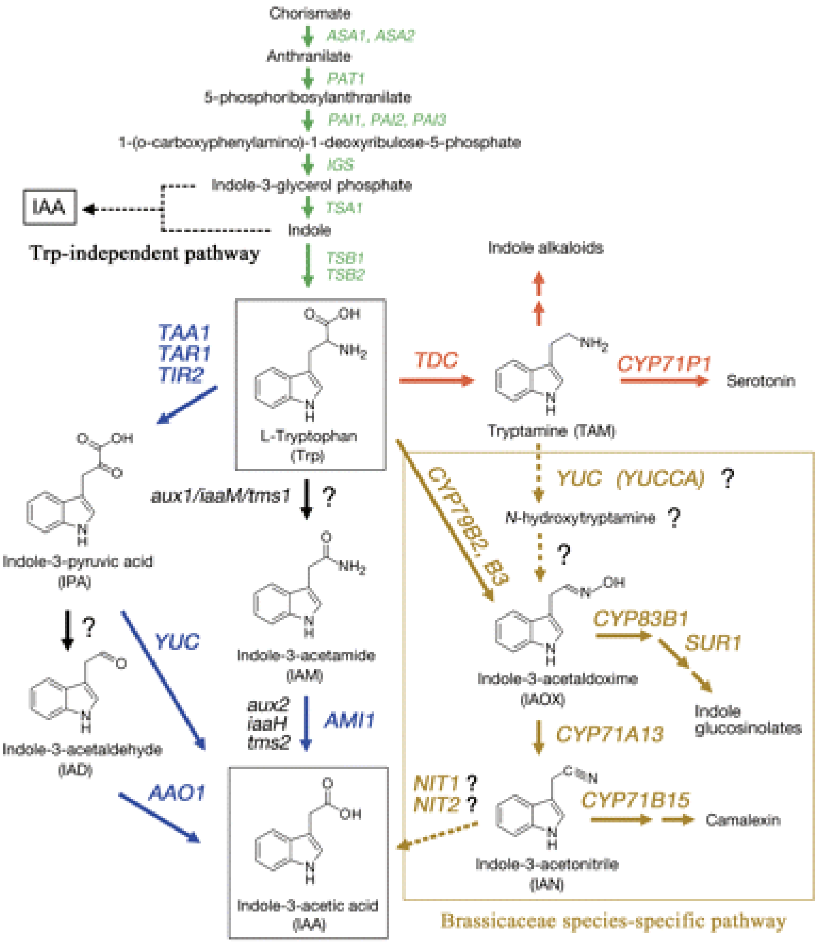

Figure 2: Biosynthesis pathway of IAA: Diagram showing the different biosynthesis pathways in the plants (academic.oup).

The roles of the genes that have been hypothesized to be involved in IAA biosynthesis in plants are listed. Although the plant hormone auxin IAA was the first to be discovered, little is known about the genetic underpinnings of the important enzymes involved in the IAA biosynthetic pathway(s), and it is not clear whether all pathways occur in all plant species[3]. Auxins play a crucial role in plant development because they are mainly responsible for cellular elongation, root formation, and apical dominance during vegetative growth. A downward concentration gradient of auxin, generated by the apical meristem during apical dominance, prevents axillary buds from activating via cytokinin initiation. Auxin, a hormone that promotes root growth, sinks into the roots as a result of this concentration gradient. (Figure.3). They are frequently utilized in the plant cultivation industry to induce root growth [3]. It's interesting to note that localized auxin concentrations can cause epinastic and hyponastic reactions in response to auxins. In order to improve photosynthetic function, plants like sunflowers often bend in the direction of direct sunlight, a process known as phototropism. The plant will slant in the direction of the concentrated auxin concentration during this process. It may also cause "leaf epinasty," in which leaves slant downhill due to disruptions in their growth, with adaxial surface cells expanding more than abaxial surface cells"[4].

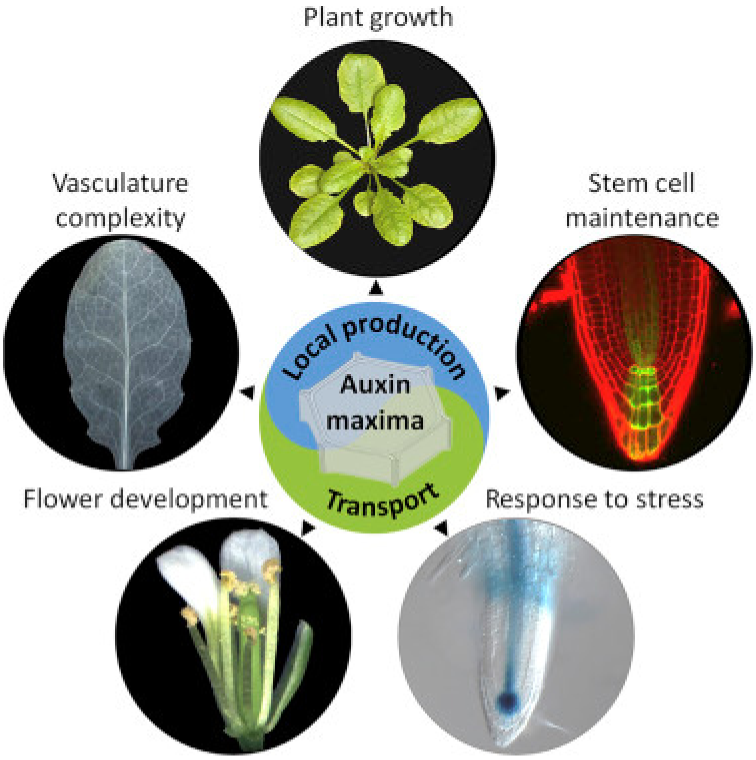

Figure 3: Function of Auxin: Diagram showing the different functions of the auxin plant (Science direct).

Auxin's primary roles, in brief, include cell elongation of branches and roots, IAA in the apical bud inhibits the development of lateral buds due to apical dominance. causes parthenocarpy, or the growth of fruit without fertilization, as in the case of tomatoes, and prevents premature leaf, flower, and fruit decline When used in grafting and stem cuttings, where it starts the growing process, encourages blooming, such as in pineapple Widespread use of 2,4-D as a pesticide kills unwanted weeds of dicot plants without harming monocot plants aids in xylem segmentation and cell division**.**

LITERATURE REVIEW

Undoubtedly, auxin is the most significant signaling molecule in plants, and in the past few decades, we have made amazing strides in knowing how it is produced, transported, and perceived. Recent studies on transcriptional responses to auxin have shed new light on the roles played by the domains of important transcription regulators in these reactions, notably implicating chromatin regulation in these reactions. Additionally, research is starting to pinpoint the precise transcription factors that auxin-responsive transcription factors directly target to modulate growth. The first understanding of how this single hormone can cause a variety of responses is developing along with mechanisms to tune the response to various auxin levels. The mechanism of auxin-directed transcriptional repression and the identification of new determinants of auxin response specificity are two important unresolved issues. The oldest land plants and other species can benefit from much of what has been discovered in model plants[4]–[6].

Recently, it has become clear how many hormone perceptions and signaling pathways are built, and it has also become clear that networks of interactions involving various hormones are what cause plant hormone reactions. Hormone responses are quantitative, just like growth, and they form the basis of a systems-based strategy for development and response. Although there have been many good reviews on auxin perception, polar transport, and signal transduction, auxin crosstalk has not received nearly enough attention despite being one of the best-characterized hormones in plant development. Therefore, this study provides a summary of recent advances in auxin-related hormone crosstalk. Although the mechanistic underpinnings of the points of crosstalk have been difficult to identify, the literature has long described the involvement of numerous hormones in specific processes. Crosstalk can be classified as either direct, indirect, or co-regulated. The metabolism of other hormones is one conclusion for auxin crosstalk, but microarray approaches are increasingly finding co-regulated genes and crosstalk nodes at shared signaling components. To fine-tune reactions and provide adaptive value to environmental circumstances, auxin crosstalk is frequently local and is spatially and temporally regulated.

Numerous plant growth and reproductive processes are regulated by the interaction between the phytohormones auxin and cytokinin. These hormones' biosynthesis, inactivation, transport, perception, and signaling processes have all been elucidated, showing a variety of regulatory mechanisms that can control the signal output from these pathways. These hormones interact with one another to support and sustain plant growth and development, according to recent studies. In this study, we concentrate on the interactions between auxin and cytokinin in a variety of developmental contexts, such as their control over apical meristems, root patterning, gynoecium and female gametophyte development, and organogenesis and phyllotaxy in the shoot

In the flowering plant's reproductive unit, the seed can grow into a new plant and guarantee the survival of the species in unfavorable environmental circumstances. It is divided into three parts: the seed covering, the endosperm, and the embryo. Coordination of the mechanisms that result in seed compartment differentiation, development, and maturation is necessary for proper seed development. The continuous transmission and reception of signals by the three compartments is the foundation for the coordination of these processes. Phytohormones are one of these signals; gradients of these hormones are produced in the various seed compartments, and their ratios make up the signals that encourage or inhibit specific seed growth processes. Auxin appears to play a key role among the hormones because it is the only one that can sustain high levels of an accumulation from fertilization to seed maturation. Pattern creation, cell division, and expansion are just a few of the processes of seed development that are impacted by the gradient of auxin produced by its PIN carriers. There are notable differences between Monocots and Eudicots species during seed maturation, despite the Spermatophytes' high degree of conservation in the regulatory processes that contribute to seed development. For instance, the endosperm in Monocots lasts until maturation and serves as a crucial compartment for the storage of nutrients, whereas in Eudicots it is reduced to a single cell layer as the developing embryo progressively replaces it. By taking into account the data present in two model plants, Zea mays L. for monocots and Arabidopsis thaliana for eudicots, this review gives an overview of the current knowledge on hormonal control of seed development. When contrasting the two species, we will focus on the influence that auxin has on the proper course of seed development

A crucial stage in the life cycle of higher plants is the generation of viable spores. Historically, the primary hormones that control seed development were thought to be gibberellin (GAs) and abscisic acid (ABA). Auxin, however, has only lately come into prominence as a crucial player that regulates a variety of cellular processes involved in seed development as well as the induction, regulation, and maintenance of primary dormancy in conjunction with ABA. (PD). The critical function of auxin as a signaling molecule that regulates seed life is examined and discussed in this overview. The growth of the endosperm and seed coat depends on the cellular machinery involved in auxin synthesis, transport, and compartmentalization within cells and tissues. As a result, auxin is a crucial substance involved in the development of the integuments, and the gene AGAMOUS-LIKE62 (AGL62), whose transcript is particularly expressed in the endosperm, controls how much auxin leaves the endosperm. Auxin involvement in PD is also supported by new biochemical and genetic data. The transcriptional regulator ABA INSENSITIVE3 (ABI3) is essential to this process because it reveals a cross-talk between auxin and ABA signaling. Future research projects that will help us understand how auxins affect seed growth and PD are also discussed[6]–[8].

The family of transcription factors known as auxin response factors (ARFs) is significant in the exertion of auxin in plants and is crucial in controlling the growth and development of plant reproductive and nutritional systems like roots, stems, leaves, flowers, fruits, and seeds. Foods from plants play a significant role in the nutritional composition of the human diet, and various plants have different primary edible parts. In this paper, we review recent research reports on ARFs and discuss their function in controlling the development of fruit, flower, and leaf tissue as well as other crucial life processes. We also discuss the difficulties and possibilities that ARFs will bring about in the future. The methods by which ARFs interact with other proteins or genes will need to be better understood. Additionally, it is important to keep in mind that more technical tools should be used to investigate ARFs, and the research should be focused on finding solutions to real-world issues. It is anticipated that gene editing and other techniques will be used in the future to enhance the nutrition and functionality of foods produced from plants

The development of the root hair is influenced by a variety of variables, including hormones, auxin-related environmental factors, and developmental cues that determine destiny. The soil environmental variables in particular are significant because they optimize absorption by controlling the growth of root hairs. Through the use of various hormones, these environmental variables have an impact on the development of root hair. Auxin seems to create the most intense networks with the pathways from environmental factors and hormones in root hair development, where these hormonal factors interact with one another to modulate root hair development. Additionally, the root hair-morphogenetic genes are genetically situated right upstream of the auxin action for root hair development genes. These findings imply that auxin functions as an organizing node for hormonal and environmental mechanisms that control root hair growth Transport, conjugation, deconjugation, conversion, and catabolism are all included in auxin biosynthesis. The ratio of auxin biosynthesis to auxin metabolism defines the actual level of the hormone in a particular cell, which has a significant impact on a variety of developmental processes, from seed germination to fruit ripening. Stable isotope labeling studies in combination with mass spectrometry have allowed for a thorough investigation of auxin biosynthesis and turnover as well as the discovery of numerous auxin conjugates. The conjugate moiety might indicate the metabolic fate, it seems. (e.g. storage and eventual hydrolysis to free hormone or catabolism). The gene families that translate for the recently discovered auxin-metabolizing enzymes differ in their auxin metabolite specificity. The patterns of these genes' expression will disclose a lot about the workings of auxin metabolism Plants use hormones to control their growth and development, but how does a plant make sure that the appropriate quantity of hormone is available at the appropriate time and location? We make an effort to compile data on the hormone auxin that is pertinent to this issue in this chapter. Indole-3-acetic acid (IAA), which has auxin activity, will receive the majority of our attention among the various compounds because it is the subject of the largest amount of research. IBA and 4-Cl-IAA are two additional naturally existing auxins that will be taken into consideration. You can read other evaluations to learn more about synthetic auxins and other substances that have auxin-like activity[9], [10].

CONCLUSION

In conclusion, auxins are natural chemicals that aid in efficient plant growth. Auxin encourages cell division, cell elongation, and shoot growth. It prevents roots from growing. Most of the time, roots and shoot tips are where auxin is created. It encourages the development of shoots. An increased auxin content causes stems to accelerate their development. The chart will demonstrate an upward association between the auxin concentrations and shoot length. It prevents the plant's roots from growing. Auxin content is inversely correlated with roots growth rate. The connection between auxin level and root length on a curve will be inversely related.Plant hormone collects mostly around the lowest portion of a root as it grows. Since auxin prevents development in lower parts, the top section grows primarily consequently. The resultant downward inclination of the root is referred to as positive gravitropism or developing following gravitation.

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CHAPTER 3

NATURAL OCCURRENCE AND FUNCTIONS OF THE ABSCISIC ACID PHYTOHORMONES

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ABSTRACT:

Plants are sessile creatures that cannot avoid unfavorable surroundings; as a result, they have evolved sophisticated reactions to the ever-changing habitat. Phytochemicals are necessary for the precise coordination of crop reactions to external signals, which include adjustments in metabolic, chlorophyll, gene function, ionic concentrations, etc. The primary phytohormone implicated in responses to abiotic stress is abscisic acid (ABA), while it is now obvious that its gene products are not isolated but rather linked to those of other chemicals in intricate systems. This chapter discussed the biosynthesis pathway and different functions of the abscisic acid required for the growth and development of plants. Furthermore, ABA is a chemical that is not only present in plants; it is also present in a wide variety of other creatures, including bacteria, microalgae, fungi, mammals, etc. Remarkably, various human cells can produce and release it. Those characteristics that make ABA a diverse variety of universal molecules will be learning further about abscisic acid.

KEYWORDS:

Abscisic Acid, Abscisic Biosynthesis, Abiotic Stress, Organism Plants, Plant Regulator.

INTRODUCTION

Nearly all of the organisms examined, including a variety of cyanobacteria, algae, bryophytes, fungi, and higher plants, had very low concentrations of ABA, the cormophytes' universal stress hormone (Figure. 1). Only a few studies have focused on the ABA biosynthesis that stress causes in cyanobacteria and phytoplankton. This excess ABA is discharged into the environment. External ABA application has been shown to have weak and conflicting impacts on the growth and metabolism of algae. The majority of investigations have used external ABA concentrations that are far above any physiological concentration range. Therefore, it is very challenging to discuss those facts satisfactorily. Even under moderate drought stress, endogenous ABA increases when organisms begin to colonize terrestrial habitats (such as aquatic liverworts and mosses).

Desiccation defense mechanisms are then stimulated, and the development of terrestrial organs is induced. The same can be seen in a variety of heterophyllous angiosperms, including aquatic ferns (Marsilea). Although they do not have a major regulatory role, the true stomata-bearing sporophytes of hornwort and mosses have particularly high ABA levels and their stomata react to ABA as do cormophytes. Large quantities of ABA are produced by fungi and released into the environment; these ABA levels do not appear to serve any purpose for the fungus. However, mycorrhizal associations, the rhizosphere of higher plants, and fungi's associations with cyanophytes and algae (lichens) may all be important sources of fungal ABA.

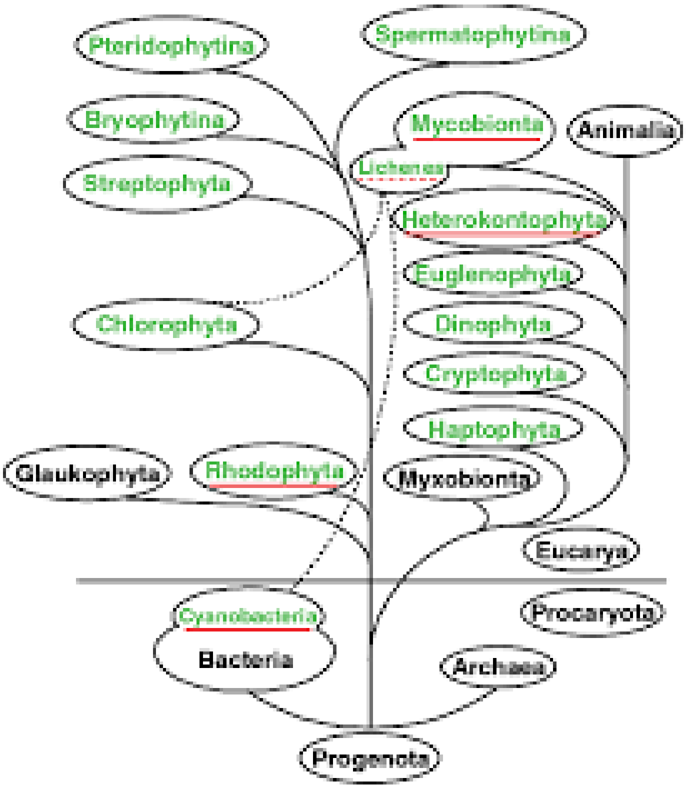


Figure 1: Abscisic acid Phylogenetic tree of the plants and fungi. Showing the different organisms for the biosynthesis of the abscisic acid (Semantic scholar).

ABA is a hormone produced by plants. ABA plays a role in a variety of developmental processes in plants, such as bud and seed dormancy, organ size regulation, and stomatal closing. The reaction of plants to environmental stresses, such as drought, soil salinity, cold tolerance, freezing tolerance, heat stress, and heavy metal ion tolerance, is particularly important. Abscisic acid (ABA) is an isoprenoid plant hormone, which is synthesized in the plastidal 2-C-methyl-D-erythritol-4-phosphate (MEP) pathway; unlike the structurally related sesquiterpenes (Figure. 2), which are formed from the mevalonic acid-derived precursor farnesyl diphosphate (FDP), the C15 backbone of ABA is formed after cleavage of C40 carotenoids in MEP. Zeaxanthin is the first committed ABA precursor; subsequent oxidation of xanthoxin to ABA occurs after a sequence of enzyme-catalyzed epoxidations and isomerizations via violaxanthin and final cleavage of the C40 carotenoid by a dioxygenation reaction. through abscisic acid[1], [2].

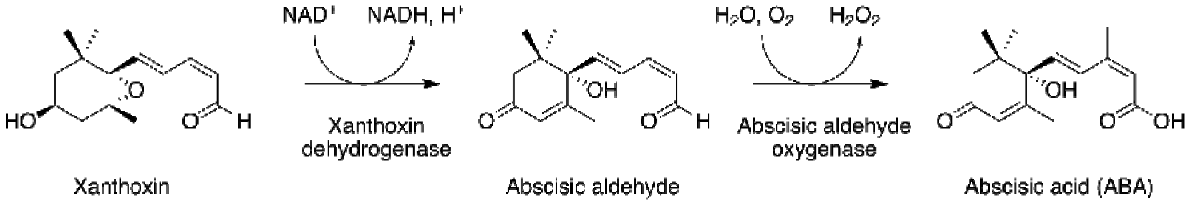


Figure 2: Biosynthesis of the Abscisic acid: Diagram showing the biosynthesis pathway of the Abscisic acid (Wikipedia).

Almost all plant tissues including roots, blossoms, leaves, and stems are synthesized to contain it.ABA-glucose-ester, an inactive form, is produced when glucose is attached to uridine diphosphate-glucosyltransferase in mesophyll (chlorenchyma) cells. in reaction to environmental stressors like heat stress, water stress, and salt stress, and released from the chlorenchyma. released when the vegetative tissues dry out and when roots come into contact with compacted dirt. green vegetables at the start of the winter season are synthesized. synthesized in developing seeds to create stasis.

Contrary to what was once believed, mobile within the leaf and capable of fast translocation from the leaves to the roots. The development of lateral roots is altered by accumulation in the roots, which enhances the stress reaction. Almost all cells that have chloroplasts or amyloplasts also produce ABA. The first specific inhibitor of ABA biosynthesis, Abamine has been devised, synthesized, developed, and trademarked. It allows for the control of endogenous ABA levels. Annual and biennial plants depend on seeds for life in addition to being significant reproductive and dispersal agents. These angiosperms pass away after blooming and seed development are finished. By preventing germination and encouraging the production of storage proteins, abscisic acid is crucial for seed maturation and imposes a period of dormancy in seeds.

It's crucial that the seeds don't sprout too soon in unusually mild weather just before winter or a dry season. The hormone gradually degrades throughout the winter, allowing the seed to emerge from dormancy and germinate in the spring when circumstances are favorable. Other environmental signals like exposure to a cold period, light, or water are frequently also required for germination to occur, as was covered in the Environmental Responses chapter. There is interesting evidence that ABA plays a part in maintaining seed dormancy in mangrove species with viviparous germination (Figure. 3), which means that seeds germinate while still attached to the parent plant. These mangroves have developed a technique for dispersing germinated seeds into the nearby ocean.

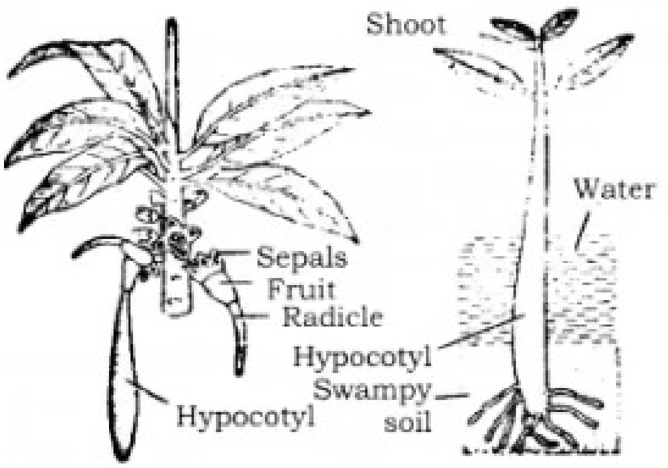
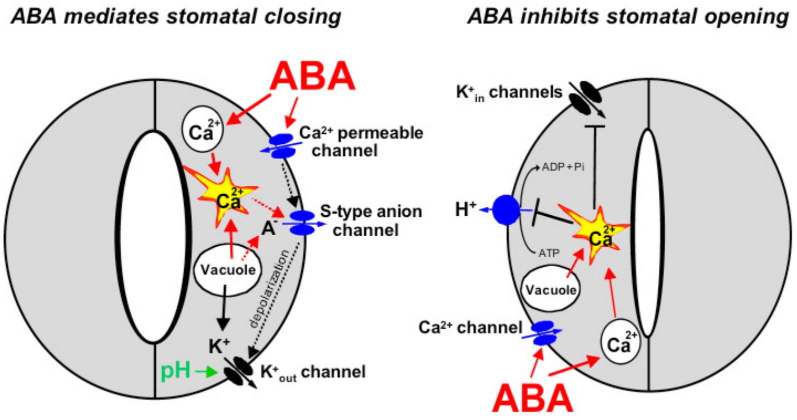


Figure 3: Viviparous germination: Diagram showing the Viviparous plant (Topper).

A further impact of ABA is to facilitate the transformation of the apical meristem into a dormant bud, which aids in the development of winter buds. In order to safeguard the meristem from mechanical harm and drying out over the winter, the newly emerging leaves that are growing above the meristem are transformed into stiff bud scales. The bud's abscisic acid also works to enforce dormancy so that the buds won't sprout early if a warm spell happens before winter is over. Bud dormancy won't be removed until after a protracted cold spell or the lengthening days of spring (photoperiodism). Additionally, abscisic acid controls the immediate drought reaction.


ABA mediates stomatal closing

ABA inhibits stomatal opening

Figure 4: Stomata opening and closing: Diagram showing the mechanism of the stomata opening and closing in presence of the ABA (university of californina).

Recall that two guard cells encircle each stoma, which are leaf pores. A large portion of the water a plant absorbs is released through its stomata as water vapor. A rise in ABA is triggered by low soil moisture, and this makes stomata close, decreasing water loss. Keep in mind that effective photosynthesis depends on the interchange of oxygen and carbon dioxide, which is prevented by stomatal closure. Blue light does not prevent the reaction to abscisic acid from occurring; rather, the signaling from drought via ABA overrides the signal from blue light to open stomata (Figure. 4).

LITERATURE REVIEW

Environmental conditions that are constantly changing put plants' lives in danger and severely hamper their growth, metabolism, and eventually their ability to produce. Despite being rooted, plants cannot escape stress but are well-equipped to endure and generate. Abscisic acid (ABA), an isoprenoid phytohormone, demonstrated its importance among the stress modulatory reactions by regulating growth, development, and stress responses as a signaling mediator. Under non-stressful circumstances, abscisic acid also regulates several metabolic, biochemical, and molecular processes in plants. It controls a variety of stress-related processes, including seed dormancy, stomatal closure, leaf abscission, senescence, fruit ripening, and legume-Rhizobium symbiosis. Under stressful circumstances, transcriptional and posttranscriptional levels of downstream reactions are controlled by ABA perception and signaling. The current overview addresses the homeostasis of ABA, its perception and signaling, as well as the physiological and molecular responses of ABA under stressful circumstances, such as those brought on by drought, heavy metals, salinity, and temperature changes. The recent molecular diagnostics reported through high throughput technologies reveal the role of ABA in the regulation of different physiological mechanisms through the integration of environmental cues via its positive and negative crosstalks with other phytohormones (like auxin, gibberellin, cytokinin, ethylene, salicylic acid, brassinosteroids, jasmonic acid, strigolactones, and melatonin) and potent chemical messengers like polyamines, sugars, NO and H2S mediated by several receptors, transporters, bZIP TFs, and regulatory proteins has also been focused in detail . As sessile organisms, plants cannot escape from adverse conditions and, therefore, they have developed complex responses to the changing environment. Phytohormones are necessary for the precise coordination of plant reactions to abiotic cues, which include adjustments in metabolism, photosynthesis, gene expression, ion levels, etc. The main phytohormone implicated in abiotic stress responses is abscisic acid (ABA), though it is now obvious that its signaling pathways are interconnected with those of other hormones in complex networks rather than acting in isolation. The molecular mechanisms by which ABA interacts with other phytohormones in response to various physiological processes are reviewed in this paper. Additionally, ABA is a molecule that is not only present in plants; it is also present in a wide variety of other species, including bacteria, algae, fungi, animals, etc. Interestingly, different human cells can produce and release it. This essay will also review the factors that endow the ABA with a variety of ubiquitous properties [3]–[5].

An essential phytohormone called ABA controls plant growth, development, dormant, and stress reactions. A wide variety of animals, including sponges (*Axinella polypoides*), hydroids (*Eudendrium racemosum*), human parasites (*Toxoplasma gondii*), and different mammalian tissues and cells, have recently been found to produce ABA. (leukocytes, pancreatic cells, and mesenchymal stem cells). ABA is a universal signaling molecule that stimulates diverse functions in animals through a signaling pathway that is remarkably similar to that used by plants; this pathway involves the sequential binding of ABA to a membrane receptor and the activation of ADP-ribose cyclase, which results in the overproduction of the intracellular cyclic ADP-ribose and an increase in intracellular Ca2+ concentrations. ABA stimulates the immune system in leukocytes, the release of insulin from pancreatic cells, the expansion of mesenchymal and colon stem cells, and the stress reaction (heat and light) in animal cells. Additionally, ABA causes cancer cells to differentiate and slows their development. When used as a growth regulator, ABA does not significantly harm animal cells, in contrast to some medications that have this impact. According to research, ABA is an endogenous immune regulator in animals and may one day be used to treat a number of human illnesses. The discoveries, signaling mechanisms, and applications of ABA in mammals are summarized in this paper

Abscisic acid and cytokinin, two phytohormones, were once believed to be present only in plants, but mounting evidence points to their presence in a variety of organisms. Few studies have looked at whether these "plant" hormones are present in fungi or whether their levels vary depending on the fungus's method of nutrition. This research looked at 20 fungi from temperate forests with various nutritional modes. (ectomycorrhizal, wood-rotting, saprotrophic). All of the fungi that were tested contained abscisic acid and cytokinin, proving that they are able to produce these two classes of phytohormones. Seven of the 27 cytokinins detected by HPLC-ESI MS/MS were found in all of the fungus samples. This implied that fungi share a uniform metabolic route for cytokinin that is unaffected by the type of nutrition they receive. The tRNA degradation pathway used by fungi to produce isopentenyl, cis-zeatin, and methylthiol CK is predicted to be the source of these compounds

Trifolium repense (white clover) and *Lotus japonicus*, which produce indeterminate and determinate nodules, respectively, were used to study the effects of the phytohormone abscisic acid (ABA) on plant growth and root nodule formation. Exogenous ABA had a minor impact on the quantity of nodules that *T. repense* plants produced after being inoculated with *Rhizobium leguminosarum*bv. trifolii strain 4S (wild type), but strain H1(pC4S8), which produces ineffective nodules, saw a dramatic decrease in nodule production 28 days after inoculation. (DAI). Exogenous ABA reduced the number of clusters produced by the wild-type strain at 14 and 21 DAI. ABA treatment also decreased the number of nodules in L. japonicus. Exogenous ABA thus prevents the development of root nodules following rhizobia inoculation. The step between root hair swelling and curling was blocked by ABA, as evidenced by the observation of root hair deformation. When the ABA concentration in plants was decreased by using abamine, a specific inhibitor of 9-cis-epoxycarotenoid dioxygenase, the number of nodules on lateral roots of abamine-treated L. japonicus increased dramatically, indicating that lower-than-normal concentrations of endogenous ABA enhance nodule formation. We postulate that the quantity of ABA regulates the development of root nodules

For plants to be productive and able to withstand stress, lateral roots (LRs) are essential. It is extremely difficult to comprehend how genes and hormones work together to control LR development in a constantly changing environment. Abscisic acid (ABA), which regulates LR development in a variety of plant species, is the main hormone that responds to stress. Exogenous ABA's impact on apple LR development hasn't been fully understood, though. To examine the regulation mechanism of ABA on LR development, "Qingzhen 1" was given exogenous 5 M ABA for 20 days. According to morphological observations, the 'Qingzhen 1' apple plants' root number, root length, plant height, and stem thickness were all lower than those of the control plants. This suggested that ABA inhibited both LR and shoot development. ABA treatment significantly reduced the concentrations of indole-3-acetic acid, zeatin riboside, and jasmonic acid while significantly increasing the endogenous ABA concentration. Furthermore, the expression levels of ABA-related genes (MdCYP707A2, MdABI1, MdAREB2, and MdABF3) were significantly upregulated, while the expression levels of auxin-related genes (MdYUCCA3, MdYUCCA8, MdPIN1, MdPIN2, MdPIN3, and MdARF19), root development-related genes (MdWOX5 and MdWOX11), and cell cycle-related genes (MdCYCD1;1 and MdCYCD3;1) were significantly downregulated at the early stage of ABA treatment, which act together on the inhibition of LR development. Together, the adjustments to hormone levels and gene expression prevented apple plants from developing LR in response to ABA

Strong plant immunity and virus tolerance is provided by a complex network of cellular receptors, RNA targeting pathways, and small-molecule signaling. Viruses must develop control mechanisms to balance host immune evasion and plant-damaging effects in order to maximize their fitness. Plant viruses belonging to the genus Potyvirus have large polyproteins led by the P1 protease encoded in their RNA genomes. The processing of polyproteins, the release of a downstream functional RNA-silencing suppressor, and viral replication are all regulated by a P1 autoinhibitory domain. Here, we demonstrate that P1Pro, a plum pox virus clone lacking the P1 autoinhibitory domain, causes extensive host transcriptome reprogramming and significant abscisic acid (ABA) accumulation. The connections between ABA and host pathways that regulate RNA stability, turnover, maturation, and translation were highlighted by a meta-analysis. Host RNA abundance and diversity changes brought on by P1Pro infection or ABA was comparable. Plant resistance to potyviral infection is promoted by ABA, according to genetic and hormone treatment assays. Finally, self-control of polyprotein processing kinetics was supported by quantitative mathematical modeling of viral replication in the presence of defense pathways as a viral mechanism that reduces the intensity of the host antiviral response. Overall, our results show that ABA plays a significant role in plant antiviral immunity, which is nevertheless circumvented by a self-replicating RNA virus[6]–[8].

Flooding significantly slows growth, which is a serious issue for soybean farming. A gel-free proteomic technique was used to examine the role of phytohormones in soybean under flooding stress. Abscisic acid (ABA) content in 2-day-old soybean roots did not decrease when they were flooded, but it did in untreated plants. In comparison to soybeans flooded without ABA, the survival ratio improved when ABA was added during the flooding treatment. The abundance of proteins involved in cell organization, vesicle transport, and glycolysis was lower in the roots of 2-day-old soybeans flooded with ABA than it was in the roots of soybeans flooded without ABA. To determine the transcriptional regulation, the nuclear proteins were also examined. The abundance of 34 nuclear proteins such as histone deacetylase and U2 small nuclear ribonucleoprotein increased by ABA supplementation under flooding; however, 35 nuclear proteins such as importin alpha, chromatin remodeling factor, zinc finger protein, transducin, and cell division 5 protein decreased. Cell division cycle 5 protein, C2H2 zinc finger protein SERRATE, CCCH type zinc finger family protein, and transducin had significantly lower levels of mRNA expression when exposed to ABA. These findings imply that ABA may play a role in improving soybean flooding tolerance via regulation of zinc finger proteins, cell division cycle 5 protein, and transducing as well as energy conservation via the glycolytic system[9], [10].

CONCLUSION

Abscisic acid (ABA) is a crucial hormone that plays a significant role in regulating adaptations to diverse abiotic stimuli and has notable effects on plant defense against microbial agents. Depending on when it acts, ABA has a variety of functions in plant defense versus bacteria and fungus, activating or suppressing reactions.Many variables can control abscisic acid flows inside the vascular tissue as they travel through the rhizome to the target tissues inside the stalk. The tissue of the root system, stalks, and leaflets have morphological, functional, and developmental factors.ABA is a phytohormone found in fruits and vegetables that can be obtained naturally through dietary intake. Its advantages for human health have previously been investigated. It has been shown that ABA is essential for memory, inflammation, glucose metabolism, and tumor growth. Studying the molecular mechanism of the ABA along with the other cross-talk hormones developed a new approach for the treatment of various diseases of humans.

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CHAPTER 4

BRASSINOSTEROIDS PHYTOHORMONES BIOSYNTHESIS AND THEIR ROLE IN PLANT DEVELOPMENT

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ABSTRACT:

Many biotic and abiotic stressors that affect plants can significantly reduce their ability to reproduce. In response to diverse environmental challenges, plants go through several cellular and physiological changes that are regulated by distinct plant hormones. Recently, interest in using phytohormones to reduce stress has increased. A class of polyhydroxylated steroidal phytohormones known as brassinosteroids (BRs) is necessary for the growth, development, and productivity of plants. During the whole plant life cycle, these hormones have a role in controlling the division, extension, and differentiation of various cell types. During the past few decades, BR studies have captured the attention of plant scientists because of their adaptable capacity to tolerate multiple ecological challenges. Several studies have demonstrated the beneficial effects of BRs on how plants react to diverse biological and environmental stressors. This chapter discusses the discovery, occurrence, and chemical structure of BRs in plants. We also have insight into the biosynthesis pathways and functional role in the plant,

KEYWORDS:

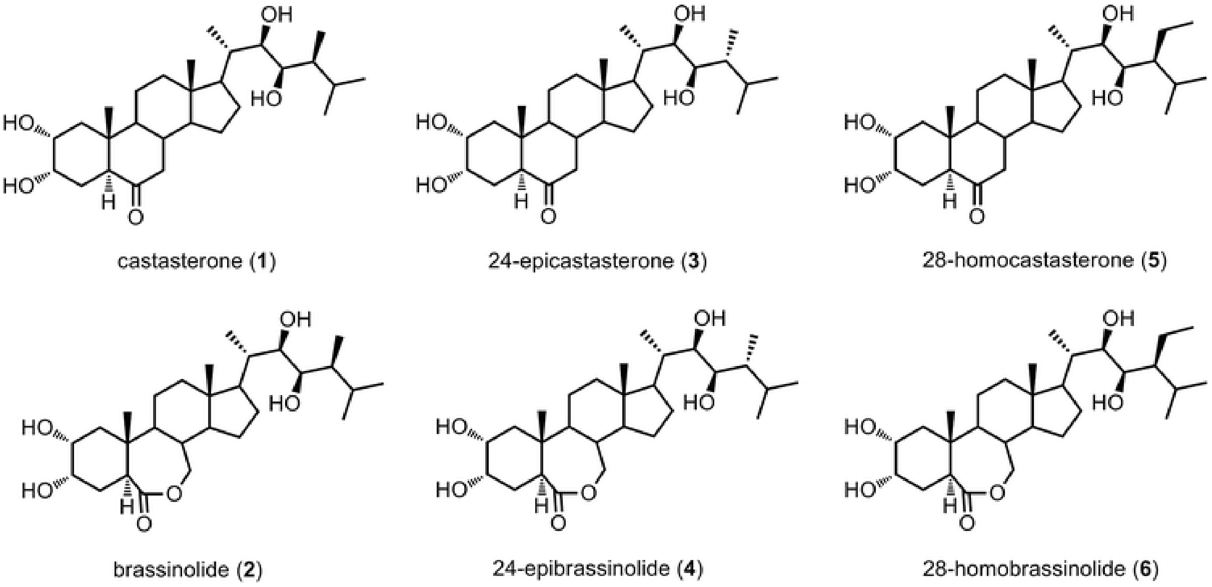
Cell Elongation, Cell Division, Growth Development, Plant Hormones, Plant Growth.

INTRODUCTION

The polyhydroxysteroid class known as brassinosteroids (BRs or, less frequently, BS) has been identified as the sixth class of plant hormones. Brassinosteroids may be useful as an anticancer drug for endocrine-responsive cancers to cause apoptosis and inhibit growth. When Mitchell et al. observed that treatment with organic extracts of rapeseed (Brassica napus) pollen promoted stem elongation and cell division, these brassinosteroids were first investigated in the 1970s. When pollen from Brassica napus was shown to stimulate stem elongation and cell divisions, and the biologically active molecule was extracted, brassinolide was the first isolated brassinosteroid. Only 10 milligrams of brassinosteroids were produced from 230 kg of Brassica napus pollen. Over 70 BR compounds have been extracted from plants since their discovery [1].

The sixth family of plant hormones is known as brassinosteroids (BRs). The molecular similarities between BRs and androgens, estrogens, corticoids, and ecdysteroids are striking. (Figure.1). Both lower and upper plants, particularly angiosperms, as well as all of the plant's organs, including roots, stems, leaves, flowers, anthers, pollen, seeds, and grain, have been found to contain them. BRs are crucial to the growth and evolution of plants. They induce a wide range of physiological and morphological reactions, in addition to a tolerance for biotic and abiotic stress.

BRs were first identified in Brassica napus pollen due to their capacity to stimulate development.BRs have been found to act as elongation and division triggers in plant cells. The term "brassins" was later given to BRs. The most active BR, brassinolide (BL), was discovered in 1979. The isolation of Brassinosteroid Insensitive 1 (BRI1), a receptor kinase that initiates an intracellular signaling cascade in reaction to extracellular BR perception, was the most important discovery. Since the discovery of BL, a sizable number of chemically distinct BRs, including green algae and land plants, have been found throughout the plant world, which suggests that BRs developed early during the evolution of plants. After finding BR-deficient mutants in A. thaliana, BRs were discovered as plant hormones.Castasterone (CS), Typhasterol (TY), Brassinolide (BL), 6-deoxocastasterone (6-deoxoCS), 28-norcastasterone (28-norCS), and Teasterone (TE) are the BRs that are most frequently found in a variety of plant types in a variety of environments (Figure.1).



castasterone (1) 24-epicastasterone (3) 28-homocastasterone (5)

brassinolide (2) 24-epibrassinolide (4) 28-homobrassinolide (6)

Figure 1: Naturally occurring Brassinosteroids: Diagramed showing the different naturally occurring Brassinosteroids (research gate).

There are presently three BR biosynthesis pathways that can produce BRs of the C27, C28, or C29 type (Figure. 2). While later stages distinguish the BR biosynthesis pathways, early steps of their synthesis are common to each type and can occur via the mevalonate (MVA) or non-MVA pathway. (cycloartenol- and cycloartanol-dependent). The C28-BR biosynthesis pathway has so far uncovered and described the majority of the reactions, enzymes, and genes (primarily in Arabidopsis thaliana, from which the majority of the genes in this pathway are derived).

Campesterol and 22-hydroxycampesterol biosynthesis are the two main steps in their production. In contrast to C29-BRs, whose biosynthesis begins with -sitosterol and results in 28-homoBL, C27-BRs' immediate substrate, cholesterol (CR), is ultimately converted to 28-norBL. Not all of these two routes' indirect compounds have, however, been found [2]. Brassinosteroid insensitive-1 (BRI1) and BAK1 form a co-receptor complex that recognizes brassinosteroids at the cellular level. (BRI1-associated receptor kinase 1). In the lack of BRs, BKI1 (BRI1 kinase inhibitor 1) inhibits the kinase BRI1. When BR binds to the co-receptor complex, BKI1 is released, starting a chain of phosphorylations that deactivates another kinase called BIN2 (brassinosteroid insensitive 2). The transcriptional regulators are inhibited by BIN2. On the other side, when BR inhibits BIN2, several developmental pathways are activated by transcriptional factors.

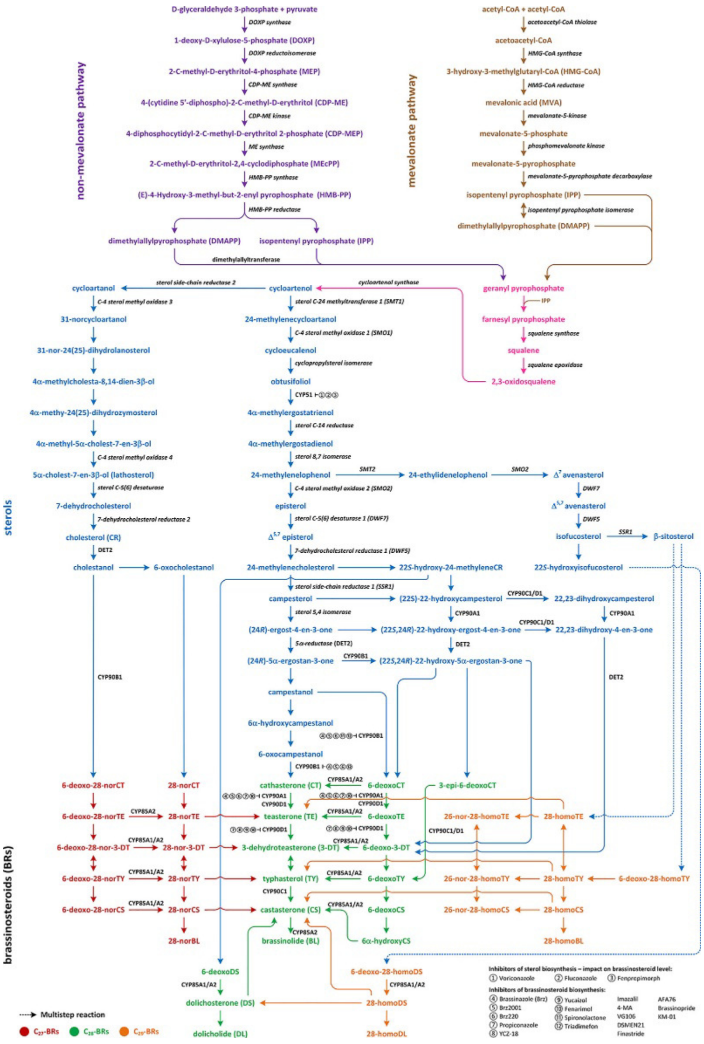


Figure 2: Biosynthesis pathway of brassinosteroid: Diagram showing the biosynthesis pathway of the brassinosteroid (Forinter).

The complex network of pathways that lead to BR biosynthesis is largely controlled by transcriptional modulation of BR biosynthetic genes. The biosynthetic route for BR has been elucidated by a number of genetic and biochemical investigations. It starts with campesterol, a precursor for the synthesis of brassinolide, the most active form of BR. (BL). Firstly campesterol is converted to campestenal which was initially believed to branch into two parallel pathways, namely the early and late C-6 oxidation pathways involving a chain of reductions, hydroxylations, epimerizations and oxidations which eventually converge at castesterone that leads to the formation of BL Mevalonic acid is a precursor in the triterpenoid pathway and is converted into 2,3-oxidosqualene through condensation. This compound then goes through additional modification to produce important plant sterols like sitosterol and campesterol.

Campesterol can be modified by two distinct enzymes, a C-22 hydroxylase dwarf4/CYP90B1 (DWF4), and a C-3 hydrogenase constitutive photomorphogenesis and dwarf/CYP90A1 (CPPH), depending on the presence of substrate and enzymes. (CPD). The pathway branches to a third early C-22 hydroxylation pathway because DWF4 can operate on a variety of biosynthetic intermediates, including campesterol and campestenol. CPD, a C-23 hydroxylase that metabolizes campesterol and other intermediates and has recently been found to engage in a C-3 oxidation as well, has been shown by LC-MS and various genetic studies to form several other branches. The intermediates produced by the aforementioned reactions undergo additional modification before merging with the late C-6 oxidation pathway, showing some degree of crosstalk between the parallel pathways and demonstrating the intricate networking of BR biosynthesis. De-etiolated-2 (DET2), a 5'-reductase, CPD, a C-3 oxidase, DWF4, a C-22 hydroxylase, rotundifolia3/CYP90C1 (ROT3), and CYP90D1, C-23 hydroxylases are just a few of the important genes recently characterized to improve the perspective of BR biosynthesis. Interesting enough, monocots like rice and maize lack the CYP85A2 enzyme necessary for the C-6 oxidation process, indicating that castesterone is the final product of BR synthesis in rice. In order to enhance the biological activity of BR in rice, it has recently been demonstrated that an alternative pathway for the biosynthesis of functionally less active C29-BRs exists in addition to castesterone.

By bio-degrading their C-26 demethylated C28-BR analogs to decrease BR activity in planta, C29-BRs even seem to play a part in regulating BR levels. BR are used nearby synthesizing cells as opposed to being transported over great distances like other hormones. However, they go through passive or active intracellular transport from their location of synthesis in the ER to the plasma membrane where its perception takes place. However, through their crosstalk with other hormones like auxins, BR are able to have a long-distance impact. It has been hypothesized that some carrier mechanism (BR conjugates produced by binding of BR to fatty acids or glucose) or through particular proteinaceous transporters mediates the short distance transport of BR. Potential possibilities for mediating BR transport include a number of proteins from the pathogenesis-related (PR) 10 family of proteins, protein families from the A or G classes of ABC transporters (ATP binding cassette), and a number of Sec-14 proteins. The spatial and temporal regulation of its homeostasis at the tissue or cellular level is highly important for normal growth and development in the absence of a mode for long distance transport of BR. It is possible to regulate BR biosynthesis in two different ways: first, by modifying the translation of the genes involved in BR biosynthesis at the level of endogenous BR, and second, by inactivating bioactive BR.

Feedback controls the majority of the BR-specific biosynthetic genes (DET2, DWF4, CPD, BR6ox1, and ROT3). Brassinosteroid insensitive 1 (bri1), a BR signaling mutant, exhibits significant accumulation of endogenous BR as their feedback regulation necessitates an intact BR perception and signaling system. Regulation at the level of transcription is mediated by two major BR signaling transcription factors brassinazole-resistant 1 (BZR1) and BRI1-EMS-suppressor1 (BZR2/BES1) as well as by several other novel transcription factors (CESTA, RAVL1, TCP1) that have been lately identified to regulate the expression of key BR biosynthetic genes such as CPD and DWF4 .Certain transcription factors that resemble the bHLH, such as CESTA and TCP, are implicated in the positive regulation of BR signaling. Another group of transcription factors in rice, known as ABA insensitive 3/vivaparous1 (ABI3/VP1) and related to ABI3/VP1 (RAV1), not only contribute to BR homeostasis by favorably regulating biosynthetic genes (D2, D11, and BRD1), but also support OsBRI1 expression.

The optimal amounts of bioactive BR in the cell are maintained by brassinosteroid catabolism/metabolism, which involves a variety of processes like acylation, sulphonation, glycosylation, etc. Brassinosteroid inactivator 1 (BIA1) and aberrant shoot 1 (abs-1) are two newly discovered genes from the family of BAHD acyltransferases that are involved in BR acylation to inactivate BR. Another BAHD acyltransferase, pizza (PIZ), collaborates with BIA1 in the duplicate process of BR inactivation. Similar to how bri1-5 enhanced 1 (BEN1) and Brassica napus sulfotransferase 3 (BNST3) inactivate active BR through multiple mechanisms involving reduction and sulfonation, they do so by having differential specificities to castesterone and BL. As part of the inactivation procedure, a group of glycotransferases enzymes, including UGT73C6 and its near homolog UGT73C5, catalyze the 23 O-glycosylation of CS and BL. The pool of dormant BR may temporarily be stored in these conjugations, which may also have other uses like transport, compartmentalization, irreversible inactivation, and security from cellular removal. Recent research has also demonstrated that environmental factors like salt and temperature duress can control BR biosynthesis.

Numerous plant mechanisms have been shown to involve brassinosteroids: Encourage cell extension and growth; use auxin to accomplish this. Its function in cell division and regenerating cell walls is unknown (Figure.3). Encouragement of vascular differentiation; research on BR signal transmission during vascular differentiation.is required for pollen elongation for pollen tubes to develop. The possibility that this action may be biologically important is supported by the acceleration of senescence in dying tissue cultured cells and the delayed senescence in BR mutants (Figure.3). can offer some protection to plants under drought and chilling duress. Brassinosteroids are present in comparatively high concentrations in the plant extract of *Lychnis viscaria*. The presence of *Lychnis viscaria* makes nearby vegetation more resistant to disease. The antigenotoxicity of 24-Epibrassinolide (EBL), a brassinosteroid isolated from Aegle marmelos Correa (Rutaceae), against maleic hydrazide (MH)-induced genotoxicity in the Allium cepa chromosomal aberration test was also examined. As a result of treatment with 24-epibrassinolide, it was demonstrated that the number of chromosomal aberrations caused by maleic hydrazide (0.01%) greatly decreased. According to some reports, BRs help plants fight off biotic and abiotic stress. Brassinosteroid treatment of cucumbers has been shown to speed up pesticide metabolism and removal, which may help to lower dietary intake of pesticide residue from non-organically produced vegetables.

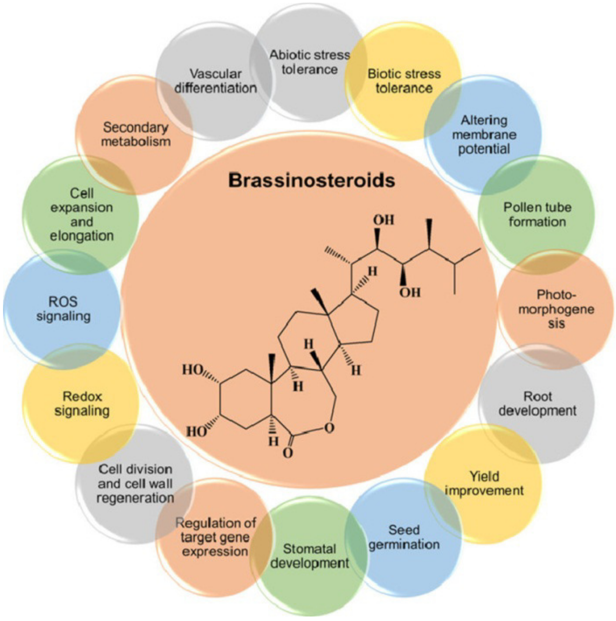


Figure 3: Functions of Brassinosteroids: Diagram showing the different functions of the Brassinosteroids (Research gate).

When used on rice seeds, BRs have reportedly had a range of effects. It has been demonstrated that seeds treated with BRs can lessen the growth-inhibiting effects of salinity stress. The treated seeds outperformed plants produced on both saline and non-saline medium when the fresh weight of the developed plants was analyzed, but when the dry weight was analyzed, BR-treated seeds only outperformed untreated plants that were grown on saline medium. Chlorophyll a and chlorophyll b concentrations dropped and pigmentation also decreased when tomatoes (Lycopersicon esculentum) were subjected to salt stress. When compared to untreated plants developed under the same circumstances on saline medium, rice seeds that had been BR treated significantly restored the pigment level.

A class of steroid hormones known as brassinosteroids (BRs) is crucial for the growth and development of plants. In addition to aiding in etiolation and reproduction, BR signaling encourages cell growth and mitosis. BR encourages the extension of the stigma as it is the phytohormone that was first discovered in the pollen granules of Brassica napus. Inflorescence stems architecture formation, floral transition, and other elements of plant reproductive processes depend on BR, according to recent studies [2].

LITERATURE REVIEW

A group of plant hormones with strong growth-promoting activity is known as brassinosteroids. Throughout the plant world, they can be found in trace amounts in young vegetative tissues, pollen, anthers, seeds, leaves, stems, and roots. About 60 phytosterols belong to the family of brassinosteroids. The paper provides a thorough overview of the previously identified brassinosteroids isolated from plants. Additionally, brassinosteroids' chemical properties are described. A group of plant hormones with strong growth-promoting activity is known as brassinosteroids. Throughout the plant world, they can be found in trace amounts in young vegetative tissues, pollen, anthers, seeds, leaves, stems, and roots. About 60 phytosterols belong to the family of brassinosteroids. The paper provides a thorough overview of the previously identified brassinosteroids isolated from plants. Additionally, brassinosteroids' molecular properties are presented [3].

From lower to higher plants, a broad variety of organisms contain brassinosteroids. They are steroidal plant hormones that may aid in promoting plant development and growth. It has long been understood that plants that are exposed to abiotic stresses will modify their brassinosteroid metabolism and that plants that interact with bacterial, fungal, and viral pathogens will also experience significant changes. This review explains how distinct mechanisms are activated by brassinosteroids to respond to various types of stresses [4]. The steroid hormones brassinosteroids play important roles in regulating cell division and elongation as well as other processes involved in plant development. In this overview, we talk about various approaches that have improved our comprehension of brassinosteroid function. Brassinosteroids-dependent regulatory modules controlling cell elongation were discovered through methods of monitoring whole-plant responses. The downstream elements of the brassinosteroid signaling cascade interact with other hormonal and environmental pathways directly in these regulatory modules. Brassinosteroid activity has been examined at the tissue and cellular levels of above- and below-ground tissues using alternative methods. Brassinosteroids' significance in cell cycle progression and the timing of cell differentiation has been established by these investigations. Additionally, they have shown that local hormone reduction defines organ borders. These investigations also revealed that brassinosteroid signaling from the epidermis can regulate organ growth. Thus, brassinosteroid-mediated growth regulation is highly dependent on intercellular communication. Deciphering the spatiotemporal spread of brassinosteroid activity and its influence on coherent growth and development is thus currently a challenge [5]. This summary generally includes works from 1999 to the beginning of 2003. Topics addressed include source-sink relationships and other endogenous interactions, as well as aspects of the biosynthesis and transport of brassinosteroids, their effects on cell division, expansion, and differentiation, and their impacts on whole plants.

We discuss some interactions with environmental signals as well as findings with potential uses in the future. Topics that warrant further investigation of the roles of BRs include phenotypic variability, reproductive physiology, senescence, branching, and apical dominance, whereas topics in which possible roles for BRs are relatively unexplored include lignification, phototropism, photoperiodism, and endogenous rhythms[6]. The plant world contains low concentrations of brassinosteroids (BRs), which promote growth, in pollen, seeds, and young vegetative tissues. Our understanding of steroids as signals regulating plant growth and development has significantly increased as a result of in-depth investigations into BR biosynthesis and metabolism as well as the recent discovery of BR-insensitive and BR-deficient mutants. This review looks at the microchemical and molecular genetic studies that have convincingly shown that BRs are crucial for a variety of developmental processes, such as cell growth, vascular differentiation, etiolation, and reproductive development. Also addressed are recent developments about the molecular mechanisms of BR-regulated gene expression and BR signal transduction [7].Plant steroid hormones known as brassinosteroids (BRs) are primarily recognized for their ability to stimulate organ development by combining the effects of cell division and growth. Additionally, BRs control a wide range of physiological and developmental reactions in plants, including tolerance to biotic and abiotic stresses, vascular differentiation, male fertility, flowering, senescence, and photomorphogenesis. The transfer of BR signals from the cell surface to the nucleus via sequential signaling modules has recently been characterized as a full-fledged core BR signaling pathway. Understanding exactly how this signaling pathway regulates the various BR-regulated actions is currently a significant challenge. The BRASSINAZOLE-RESISTANT1 (BRZ1) and BR-INSENSITIVE-EMS-SUPPRESSOR1 (BES1)/BZR2 transcription factors' recent discovery of direct targets leads to the conclusion that the BR signaling pathway regulates growth and primarily interacts with other signaling pathways at the transcriptional level [8]. Plant hormones in the family of brassinosteroids. From plants, more than 70 different compounds have been extracted. 42 brassinosteroid compounds and their conjugates are currently recognized. The various brassinosteroid metabolic pathways in plants are discussed in this overview. Dehydrogenation, demethylation, epimerization, esterification, glycosylation, hydroxylation, side-chain cleavage, and sulfonation are a few of the biochemical processes that brassinosteroid plants engage in. There are two types of structural alterations to the side chain and the steroidal skeleton that occur during the metabolism of brassinosteroids [1].

Brassinosteroids (BRs), which are steroid hormones, control how plants grow and evolve. The early and late C-6 oxidation pathways are connected at various stages and are also connected to the early C-22 oxidation pathway, according to a thorough analysis of the biosynthesis of brassinolide, a C28 BR. As a result, BR biosynthetic routes have extensive networking. The biosynthesis of C27 BRs was also demonstrated to occur similarly to that of C28 BRs. BR-deficient and BR-insensitive mutants have been used to learn more about the genes and enzymes involved in BR biosynthesis, as well as the control of those processes. Also addressed is the biosynthesis of sterols, which have recently been identified as plant growth regulators as well as BR precursors and membrane constituents. Also summarized [9] are a number of biochemical processes involving BRs, such as epimerization, oxidation, and conjugation.

In the recent years, there has been a lot of research done on the function of brassinosteroids (BRs) in plants. Mutant research has shown that BR synthesis, perception, and response are critical for typical plant growth and development. With the help of genetic and biochemical methods, several crucial components of the BR response have been identified. Molecular models that mimic animal signaling mechanisms like Wingless (Wnt), transforming growth factor (TGF), and receptor tyrosine kinase (RTK) signaling have also been suggested. Numerous studies have shown how BRs affect processes like cell elongation and seed development both on their own and in combination with other plant hormones. On the other hand, little is known about the relationship between BR sensing and particular physiological reactions like stress resistance. Regarding how these connections are made, there are still a lot of unanswered issues [10].

CONCLUSION

According to their many uses, Brassinosteroids have become strong phytohormones. Its numerous substrates and intricate regulatory systems are thought to be the cause of the broad spectrum of functions. Worldwide initiatives are underway in a significant and thorough manner to comprehend the intricate BR mechanism. Investigation on BR will take on new dimensions as a result of our comprehension of the structure of BR regulation and our analysis of its relationships among several phytohormones. It is anticipated that there will be a powerful addition to our understanding of the mode of BR activity shortly because of the accessibility of biological assets and the creation of ground-breaking new techniques. It might eventually lead to the dawning of a new phase in plant biology and stress biology.

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CHAPTER 5

AN OVERVIEW OF CYTOKININ PHYTOHORMONES BIOSYNTHESIS AND FUNCTION

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ABSTRACT:

The nature of cytokinin, as well as the biosynthesis pathway and its functions, are discussed in this chapter. Cytokinin has been discovered in the roots, stems, leaves, flowers, fruits, and seeds of entire plant species and is likely caught in all living organisms as well. The precise identification of that which systems or tissues are the sources of cytokinin production, however, has proven to be a challenging issue. Adventitious root development is followed by significant cytokinin production. The amount of cytokinin in the laminae increases noticeably as roots form on the petioles of removed bean leaves. Regarding the location of cytokinin production and the function of cytokinin in regulating the site of lateral root initiation, it is crucial to measure the amount of cytokinin along the main root using accurate techniques.Around the period of flower bud, phytohormone volume increases in the buds of rootless poplar shoots that have been removed. Several studies support the idea that the axis provides cotyledons with cytokinin.

KEYWORDS:

Auxins Cytokinin, Cytokinin Biosynthesis, Plant Hormones, Plant Growth, Soli Bacteria.

INTRODUCTION

The German physiologist J. Wiesner suggested in 1892 that the beginning of cell division is evoked by endogenous factors, specifically a correct balance among endogenous factors. This was the first time that specific substances were thought to be necessary for cell division to occur in plants. Later, in 1913, the Austrian plant physiologist G. Haberlandt observed that a substance that can cause cell division in the parenchymatic tissue of potato tubers diffuses from the phloem tissue . In 1941, Johannes Van Overbeek discovered that this factor was also present in the milky endosperm of juvenile coconuts and that it induced cell division and differentiation in developing Datura embryos.

In extending the work of Haberlandt, Jablonski, and Skoog (1954) discovered that the pith cells' ability to divide cells was caused by a material found in the vascular tissue. From autoclaved herring fish sperm DNA, Miller and his colleagues (1954) extracted and purified the cell division substance in crystallized form. Because of its capacity to encourage cell division, this active substance was given the moniker "Kinetin" and became known as the first cytokinin. Later research revealed kinetin to be 6-furfuryl-amino purine. Later, it was proposed to use the generic term kinin to refer to kinetin and other substances with comparable properties. Miller and D.S. Lethum (1963–1955) concurrently isolated and crystallized the first naturally occurring cytokinin from the milky endosperm of maize (Zea mays), which they named Zeatin. Cytokinins was the name Lethem ((1963) suggested for such substances [1].

A group of plant hormones known as cytokinins (CK) encourages cytokinesis, or cell division, in the roots and stems of plants. They influence apical dominance, axillary bud development, and leaf senescence in addition to being mainly involved in cell growth and differentiation. Adenine-type cytokinins, such as kinetin, zeatin, and 6-benzylaminopurine, and phenylurea-type cytokinins, such as diphenylurea and thidiazuron (TDZ), are the two different kinds of cytokinins.Roots are where the majority of adenine-type cytokinins are made. Cytokinins are produced by the cambium and other tissues that are constantly dividing. Plants haven't been discovered to contain any phenyl urea cytokinins. Cytokinins use the same transport mechanism as nucleosides and purines to engage in local and long-distance signaling. Normally, the xylem is where cytokinins are carried. Together with auxin, another plant development hormone, cytokinins have an effect. They complement one another and usually have opposing effects.

Although it does not trigger cytokinin reactions, adenine is the parent compound of naturally occurring cytokinins; the N6 position is denoted by an arrow. The most prevalent cytokinin in Arabidopsis is trans-zeatin, and its free base as well as its riboside and ribotide variants are displayed. An illustration of a naturally found aromatic cytokinin is benzyladenine, whereas kinetin is an artificial, aromatic cytokinin. Thidiazuron is a cytokinin of the diphenylurea family (Figure.1).

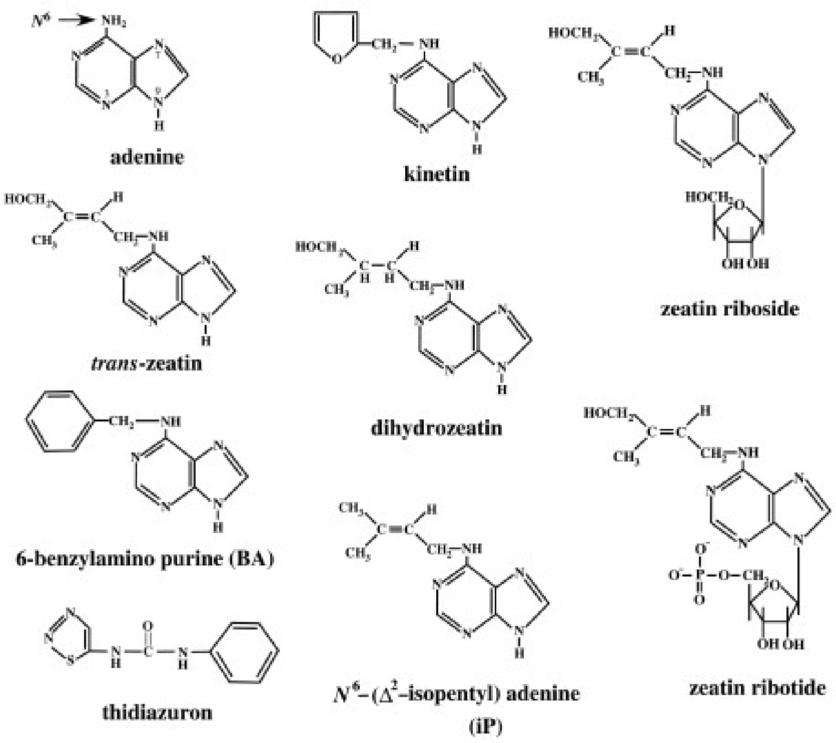

Figure 1: Structure of the cytokinin: Diagram showing the different structures of the cytokinin (ncbi).

The majority of species, including plants, have cZ as a modified base in their mature tRNAs. As a result, it was first proposed that the breakdown of tRNA might be a process for cytokinin biosynthesis because it was assumed that zeatin isomerase would convert the released cZ to active tZ. The cis and trans versions of zeatin do not appear to interconvert much, according to more recent findings. Furthermore, the quantity of cytokinins found in plants is probably not sufficiently explained by the slow turnover rate of tRNA. As a result, tRNA probably does not contribute to the biosynthesis of cytokinins, with the potential exception of cZ. First discovered in *Dictyostelium discoideum*, the enzyme turns AMP and dimethylallyl pyrophosphate (DMAPP) to the active cytokinin iPMP (N6-(2-isopentenyl)adenosine-5'-monophosphate). Later, it was discovered that the isopentenyltransferase (ipt) gene from Agrobacterium tumefaciens encoded an enzyme with a comparable function. IPT activity was found in crude extracts from a range of plant tissues, but the plant enzymes were not purified. IPT genes have also been found in several other bacteria. Nine ipt-homologues, known as AtIPT1 to 9, were found in the Arabidopsis genome sequence after in silico scans. According to phylogenetic analysis, the other seven AtIPTs created a distinct clade that was more closely related to the bacterial ipt gene than AtIT2 (At2g27760) and AtIPT9 (At5g20040), which produce putative tRNA-IPTs. This is supported by the finding that disruption of the other seven IPT genes led to decreased levels of tZ and its derivatives, whereas disruption of AtIPT2 and AtIPT9 led to a drop in the level of cZ but not tZ. The cytokinins iP (isopentenyladenine) and zeatin were secreted in response to the production of these seven genes (but not AtIPT2) in E. coli, demonstrating that they encode cytokinin biosynthetic enzymes. In contrast, CaMV 35S::AtIPT2 calli required exogenous cytokinin to regenerate shoots, whereas calli overexpressing AtIPT4 (At4g24650) under the guidance of the CaMV 35S promoter did not. Surprisingly, purified AtIPT4 used ATP and ADP as a substrate preference over AMP, in contrast to the bacterial ipt enzymes. Numerous AtIPT genes exhibit distinctive, tissue-specific patterns of expression that point to potential locations for cytokinin synthesis [2].

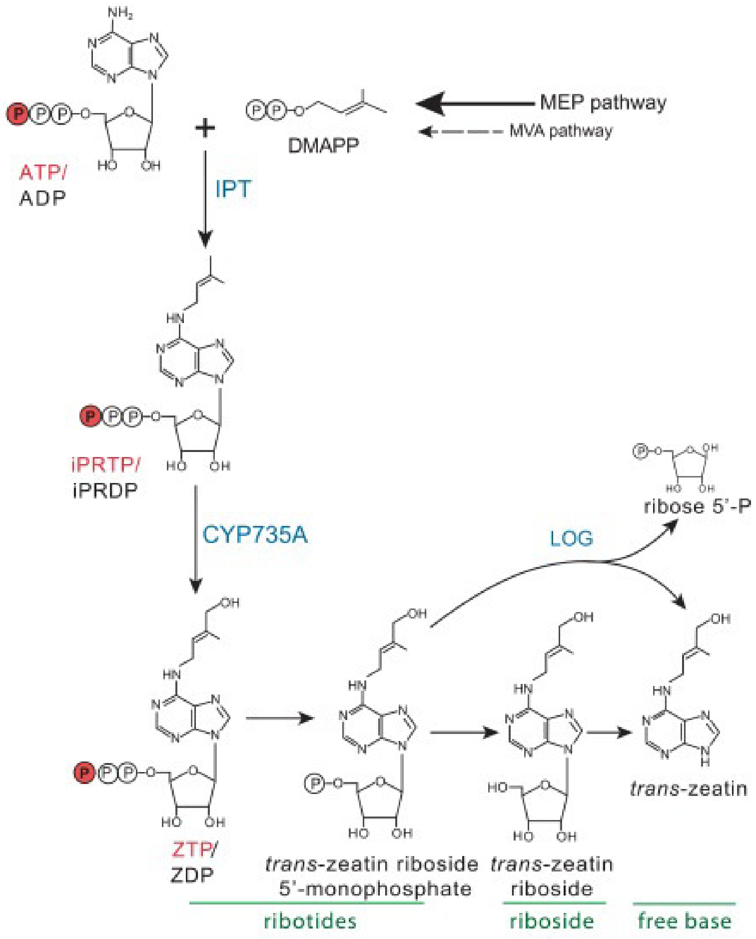

Figure 2: Biosynthesis pathway: Diagram showing the biosynthesis pathway of the cytokinin(ncbi).

The isoprenoid side chain on tZ could have come from either of two sources. IPT utilizes DMAPP, which comes from the plastid's methylerythritol phosphate (MEP) pathway, in one pathway. iP ribotide would result from this, and trans-zeatin would then be produced by hydroxylation of it (Figure 2). To create the DMAPP precursor, a second route makes use of the mevalonate (MVA) pathway, which lovastatin inhibits. According to a dual labeling research, the MEP pathway accounts for the majority of trans-zeatin synthesis in Arabidopsis. Isopentenyladenosine-5'-triphosphate (iPRTP) and isopentenyladenosine-5'-diphosphate (iPRDP) are the first products of the plant enzyme, and they can later be changed to tZ by hydroxylation of the isoprenoid side chain by a cytochrome P450 enzyme. (Figure 2).

A search using a (AtIPT4)/P450 co-expression system in Saccharomyces cerevisiae led to the discovery of the genes encoding these cytokinin trans-hydroxylase enzymes in Arabidopsis. Various candidate cytochrome P450s were expressed in this strain and two paralogous genes, CYP735A1 (At5g38450) and CYP735A2 (At1g67110) were found that encode proteins that catalyze the conversion of iP nucleotides, but not the nucleoside or free base forms, to produced tZ nucleotides. The two-step process of converting cytokinin ribotides to their active, free base versions was once believed to be how it happened. However, more recent research indicates that the LONELY GUY (LOG) family of enzymes is mainly responsible for the direct conversion of cytokinin ribotides into the free-base cytokinins. Genetic testing for errors in the upkeep of stalk meristems led to the discovery of these first in rice. There are seven genes in Arabidopsis that produce active LOG enzymes. With LOG7 (At5g06300) and LOG4 (At3g53450) playing the primary role in the shoot apical meristem (SAM) and LOG3 (At2g37210) and LOG4 in the root, respectively, disruption of multiple LOG genes results in severe retardation of shoot and root growth as well as defects in the maintenance of the apical meristems.

In Arabidopsis, the floral meristem and the L1 layer of the SAM are the only places where LOG4 mRNA is found. It has been proposed that LOG4 is essential for the synthesis of apically derived active cytokinins in the SAM proper[3].Cell division, as well as shoot and root development, are just a few of the processes that cytokinins play a role in. They are known to control apical dominance and the development of axillary buds. According to the "direct inhibition hypothesis," the ratio of cytokinin to auxin is what causes these effects. According to this hypothesis, auxin from apical buds moves down shoots to prevent the growth of axillary buds. This discourages lateral branching and encourages shoot development. Cytokinin travels from the roots to the shoots, ultimately indicating the development of lateral buds. This hypothesis is supported by easy experiments

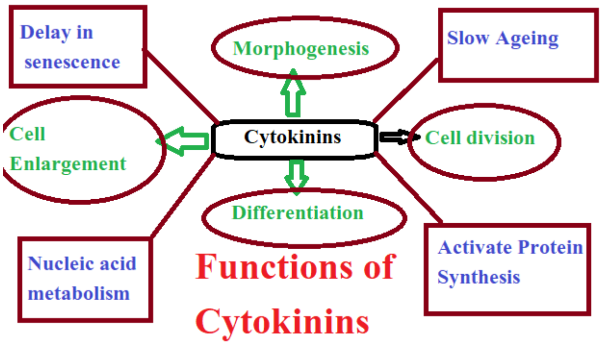

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Figure 3: Function of cytokinin: Diagram showing the different functions of cytokinin (Handwritten notes).

The axillary buds are unhindered, lateral development accelerates, and plants grow bushier when the apical bud is removed. Lateral supremacy is prevented by applying auxin to the cut stem once more. Furthermore, studies have shown that cytokinin does not affect tissue cells on its own. They enlarge but do not split when cultured with auxin but not cytokinin. The cells enlarge and specialize when cytokinin and auxin are combined (Figure. 3). The parenchyma cells make an undifferentiated callus when the levels of cytokinin and auxin are equal. A higher ratio of auxin induces the development of roots, whereas a higher ratio of cytokinin induces the growth of shoot buds. According to research, cytokinins slow down the aging process of plant organs by delaying the breakdown of proteins, triggering protein synthesis, and assembling nutrients from neighboring tissues. In a research that looked at how tobacco leaves age, it was discovered that transgenic leaves tended to stay mostly green while wild-type leaves yellowed.

It was proposed that cytokinin might have an impact on the enzymes that control the production and breakdown of proteins. Recently, it was discovered that cytokinins contribute to the disease of plants. For instance, cytokinins have been reported to cause *Pseudomonas syringae* tolerance in *Nicotiana tabacum* and *Arabidopsis thaliana*. Cytokinins appear to have possible uses in the biological control of plant diseases. The ability of *Pseudomonas fluorescens* G20-18 to produce cytokinins has been found as a critical factor in the effective management of *P. syringae* infection in *A. thaliana*. In spite of the fact that cytokinin action in vascular plants is thought to be pleiotropic, this family of plant hormones specifically induces the switch from apical growth to growth via a three-faced apical cell in moss protonema. This bud induction is a very specific cytokinin effect because it can be linked to the differentiation of a unique, particular cell.

LITERATURE REVIEW

In the hunt for substances that encouraged the division of plant cells in vitro, cytokinins were found. The N 6-substituted adenine derivatives that makeup naturally occurring cytokinins typically have an isoprenoid derivative side chain. These hormones have a significant impact on many physiological and developmental processes in plants, including seed germination, de-etiolation, chloroplast differentiation, apical dominance, interactions with pathogens, formation of flowers and fruits, and leaf senescence. Light and other phytohormones, for example, have an impact on these processes, and the physiological and developmental results show a highly integrated response to these various stimuli. The ratio rather than the absolute amount of these two hormones is crucial; for instance, the classic studies of Skoog and Miller (1957) demonstrated that undifferentiated callus cultures would develop into roots or shoots based on the relative amount of cytokinins and auxin in the medium.

A balanced ratio prevents differentiation of the cells, whereas high cytokinin to auxin ratios encourage shoot growth and low ratios encourage root development. The last ten years have seen significant advances in our understanding of the molecular mechanisms underpinning the action of other phytohormones thanks to genetic and molecular analysis of mutants. In such studies, cytokinin has lagged, but several intriguing new reports suggest that this is now changing. This review centers on the significant recent advancements in our comprehension of cytokinin signaling, perception, and metabolism. To comprehend the various cytokinin effects on plant physiology and its function as a developmental signal, all three parts must be analyzed [4].

Several phases of plant growth and development, including cell elongation, cell division, tissue differentiation, and apical supremacy, are regulated by the plant hormones auxins and cytokinins. A lot of research has been done on biosynthesis and fundamental mechanisms of action of auxins and cytokinins. Auxins and cytokinins can be made by microbes as well as plants. The role of phytohormone biosynthesis by microorganisms is not fully elucidated: in several cases of pathogenic fungi and bacteria these compounds are involved in pathogenesis on plants; auxin and cytokinin production may also be involved in root growth stimulation by beneficial bacteria and associative symbiosis. Pseudomonas, Agrobacterium, Rhizobium, Bradyrhizobium, and Azospirillum have well-studied genetic mechanisms for auxin biosynthesis and regulation, and a number of their physiological impacts have been linked to the production of bacterial phytohormones. Indole-3-acetic acid is produced by the indole-3-acetamide pathway, which is used by the pathogenic microbes Pseudomonas and Agrobacterium. They do, however, also have the chromosomally encoded indole-3-pyruvic acid system. Additionally, they possess genes that can hydrolyze conjugated types of auxins and cytokinins or conjugate free auxins. Near the auxin and cytokinin biosynthetic genes in Agrobacterium are a number of additional genes that control how sensitive the changed plant tissue is to auxins and cytokinins. Indole-3-pyruvic acid is used by the symbiotic bacteria Rhizobium and Bradyrhizobium to produce indole-3-acetic acid. Genetic determinants for the indole-3-acetamide pathway have also been found, but their function has not yet been proven. Both the indole-3-pyruvic acid and the indole-3-acetamide pathways are found in the plant growth-promoting bacteria Azospirillum, just like in Agrobacterium and Pseudomonas, though in Azospirillum the indole-3-pyruvic acid pathway is of primary importance. Additionally, biochemical proof of an indole-3-acetic acid route in Azospirillum that is tryptophan independent has been provided [5].

Plant growth regulators are phytohormones that are produced and exported by plant growth-promoting rhizobacteria (PGPRs). (PGRs). These PGRs might regulate plant formation and growth. PGRs are organic compounds that, at very low amounts, affect the physiological functions of plants. Among five classes of well-known PGRs, namely auxins, gibberellins, cytokinins, ethylene, and abscisic acid, the most common, best characterized, and physiologically active auxin in plants is indole-3-acetic acid (IAA) that stimulate both rapid (e.g. increases in cell elongation) and long-term (e.g. cell division and differentiation) responses in plants. Some bacteria also release substances that may help promote plant development indirectly, such as indole-3-butyric acid (IBA), tryptophan, and tryptophol, or indole-3-ethanol (TOL). On the other hand, cytokinins, which are typically found in trace quantities, promote cell division, resulting in the formation of root hairs and root development. About 90% of the microorganisms discovered in the rhizosphere are capable of releasing cytokinins when cultured in vitro, and microorganisms have been found to contain over 30 growth-promoting compounds of the cytokinin group.

Gibberellins (GAs), which are produced by soil microbes, number over 100 different types. The most well-known form of gibberellin is GA3 (gibberellic acid), and the plant hormone GA1 that is most active in promoting stem growth is GA1. Additionally, radioimmunoassay has found abscisic acid (ABA) in the supernatants of bacterial cultures thought to be the cause of stomatal closing. Its existence in the rhizosphere may be crucial for crop survival in soils that are water-stressed, as is the case in arid and semiarid climates. Strong plant growth regulator ethylene has an impact on a variety of facets of plant development, senescence, and growth. In addition to being known as a ripening hormone, ethylene encourages the development of exploratory root and root hair, speeds up germination, and removes seeds' dormancy. By reducing the levels of ethylene in plants and the rhizosphere of seeds, soil bacteria encourage plant development, particularly seed germination. The direct precursor of ethylene in plants, 1-aminocyclopropane-1-carboxylate (ACC), is hydrolyzed by the enzyme 1-aminocyclopropane-1-carboxylate deaminase. Ammonia and -ketobutyrate, the byproducts of this hydrolysis, can be utilized by the bacterium as sources of nitrogen and carbon for development. By acting as an ACC sink, soil bacteria reduce plant ethylene levels and help avoid some of the possibly harmful effects of high ethylene levels. The production of phosphatases, -glucanase, dehydrogenase, antibiotics, solubilization of mineral nutrients, stabilization of soil aggregates, enhancement of soil organic matter, and improvement of soil structure are all essential functions performed by soil bacteria along PGPRs. For sustainable crop yield, PGR-producing soil bacteria aid in reducing or supplementing the need for chemical fertilizers N and P [6].

The de novo organogenesis in vitro capabilities of the kohlrabi varieties Vienna Purple (VP) and Vienna White (VW) were examined. On Murashige and Skoog (MS) media supplemented with distinct cytokinins, including benzyladenine (BA), thidiazuron (TDZ), trans- or cis-zeatin, root, cotyledon, hypocotyl explants, and intact seedlings were all cultured. Intact seedlings and hypocotyl explants both caused shoot regeneration in response to all tested cytokinins, including cis-zeatin, with seedlings exhibiting the highest regeneration efficiency and shoot viability in both cultivars. On MS, the greatest frequency of shoot regeneration was attained with BA (50%), TDZ (47.5%), or transZ (37.5%) for VP and with BA (60%) or TDZ (50%) for VW. Measurements of the endogenous cytokinin and indole-3-acetic acid (IAA) contents in both hypocotyl explants and seedlings with regenerated shoots (HRSs and SRSs) suggested that the observed differences in organogenic response between these two types of explants were related to their cytokinin and IAA contents. While SRSs showed a higher IAA/bioactive cytokinins ratio, HRSs typically showed increased levels of total cytokinins. On a medium with BA (0.5 mg L1) added, shoots that had grown from seeds were successfully multiplied once more. On media supplemented with 2 or 4 mg L-1 indole-3-butyric acid (IBA), multiplicated shoots' ability to root was tested, with the greater IBA concentration resulting in more effective rooting. Rooted plantlets were successfully inserted into the ground, and flow cytometric analysis revealed no ploidy variations, demonstrating the speed and effectiveness of the outlined protocol for kohlrabi regeneration [7].

An essential horticultural technique called plant grafting is used to combine a scion and rootstock to create a new plant. One of the most popular methods employed by horticulturists to improve the quality and output of different products is this one. Grafting contributes to the enhancement of postharvest plant life as well as the health of the plants, their yield, and the purity of the plant products. The joining of vascular tissues is the primary procedure accountable for the successful production of grafted plants. Since this process affects graft success rates, it must be carefully examined. Plant hormones have recently attracted the attention of researchers because they are one of many factors that control the relationship between scion and stock. These phytohormones function as signaling molecules and can move throughout the graft junction. Auxins, cytokinins, and gibberellins are the primary plant hormones that play a significant role in the regulation of various important physiological processes taking place at the grafting site. In this review, we go over the molecular processes underlying graft development as well as the phytohormone-mediated control of graft union growth and development [8].Circadian systems sync up endogenous activities with outside cues. Hormone-clock feedbacks are a well-known integration mechanism in animals. Here, we used the promoter: luciferase system to examine the impacts of phytohormones on plant circadian rhythms. We report that numerous hormones regulate particular aspects of the plant circadian system in various ways. In particular, cytokinins slow down the circadian phase, auxins control the accuracy and amplitude of the clock, and brassinosteroids and abscisic acid alter the periodicity of the circadian rhythm. Since the rhythmic expression is predictably altered in a variety of hormone-related mutants, we were able to validate the pharmacology in hormone synthesis and perception mutants. We genetically analyzed one method for integrating hormone signals into the clock and demonstrated that the photoreceptor phytochrome B and the hormone-activated ARABIDOPSIS RESPONSE REGULATOR 4 are components in the input of the cytokinin signal to the circadian phase. Additionally, this signal's molecular-expression targets were discovered. We discovered that plants have many input/output feedbacks, suggesting that many hormones can work on the circadian system to adjust the clock to outside signals in order to keep the clock system functioning correctly

CONCLUSION

The large number of cytokinin substances that are present in abundance is controlled by a sophisticated system of biosynthetic and degradation processes. A wide variety of molecules and connected metabolic pathways establish the action mechanism of each cytokinin. Following ethylene, cytokinin where the second plant hormone for which receptors were found. The cytokinin receptors were discovered to be histidine kinase sensors, much like they were for ethylene. It is interesting to note that the animal kingdom lacks the two-component signaling method that cytokinin uses in the plant kingdom. Understanding the function of this essential plant growth factor will be made more difficult by the diversity of kinetin and their biochemical processes, which are connected to a relatively straightforward transduction cascade.

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CHAPTER 6

ETHYLENE PHYTOHORMONES BIOSYNTHESIS, THEIR ROLE IN PLANT GROWTH DEVELOPMENT, AND CELL SENESCENCE

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ABSTRACT:

During a plant's life cycle, its many organs, such as its roots, shoots, leaves, and flowers, grow and develop from its juvenile to its mature phases. The several sets of phytohormones control the plants' transitional condition. Ethylene is one of the hormones among those phytohormones that interacts with the other groups of phytohormones. These hormones' combined actions cause the plant to move between stages, mature and generate new organs. Each variation in ethylene concentration has an impact on how the other plant hormone pathways interact with it, which alters how plants develop. This chapter's emphasis is on the fundamental introduction of ethylene, its production process, and its role in plant growth and development. Additionally, areas, where there is little knowledge, have been emphasized for further study, enhancing prospective investigation of enhancing the same descriptive and analytical characteristics of plants as well as deepening our comprehension of the significance of ethylene all through development and senescence.

KEYWORDS:

Abscission Layer, Ethylene Biosynthesis, Ethylene Production, Growth Development, Hormone Synthesis.

INTRODUCTION

Ethylene has been used since the time of the ancient Egyptians, who would gash figs to hasten maturation (wounding stimulates ethylene production by plant tissues). The ancient Chinese would make offerings in enclosed areas to hasten the ripening of pears. Gas leaks from public lights were found to cause plant bending, stunted development, and aberrant stem thickening in 1864. In 1874, it was discovered that smoke helped pineapple farms grow. It was replaced with ethephon or naphthalene acetic acid, which stimulates the formation of ethylene when it was found that smoke contains ethylene. Since the late 19th century, ethylene has been recognized scientifically as having a function in plant physiology. Dimitry Neljubow, a Russian botanist, studied pea mobility in reaction to illumination gas in 1896. He found that ethylene, the active component of the light source, was what triggered pea behavior. He revealed his findings in 1901. Additionally demonstrating how the ethylene in lighting gas induced abscission in 1917 was Sarah Doubt. Farmers in Florida frequently lit kerosene lights to hasten the ripening of their harvests inside sheds because it was once thought that heat would hasten to ripen. The ethylene molecule emitted by kerosene lights, according to Frank E. Denny's discovery in 1924, is what causes the fruit to ripen.

In the same year, Denny released the individual experimental details and demonstrated through experimentation that using ethylene was preferable to using kerosene. Richard Gane, a British biologist, found in 1934 that the chemical component in ripe bananas could cause the ripening of green bananas as well as more rapid pea growth. He demonstrated that ethylene[2] could cause the same growth impact. When William Crocker, Alfred Hitchcock, and Percy Zimmerman reported that ethylene functions similarly to auxins in causing plant growth and the senescence of vegetative tissues in 1935, this strengthened their case. ethylene's status as a plant hormone is thus established.

The natural plant hormone ethylene is an unsaturated hydrocarbon vapor (alkene). It is the first gas known to function as a hormone and is the most basic alkene gas.It acts at trace levels throughout the life of the plant by stimulating or regulating the ripening of fruit, the opening of flowers, the abscission (or shedding) of leaves, and, in aquatic and semi-aquatic species, promoting the 'escape' from submergence by means of rapid elongation of stems or leaves.] In rice farming, this escape response is especially crucial. "Catalytic generators" produce ethylene gas from a liquid source of ethanol in commercial fruit-ripening rooms. Usually, gassing is done for 24 to 48 hours at a range of 500 to 2,000 ppm. When gassing, it is important to keep carbon dioxide levels under control because high-temperature maturation (20 °C; 68 °F) has been shown to result in CO2 levels of 10% in 24 hours.

Numerous labs have conducted several elegant studies that have clarified the ethylene biosynthetic pathway. Methionine, an amino acid, is converted in the first stage by AdoMet synthetase into S-adenosyl-methionine (AdoMet), which is then used to create ethylene (Figure.1). Many biosynthetic processes, including the synthesis of polyamines, use adoMet as a precursor. The first concerted and frequently rate-limiting step in the synthesis of ethylene is the conversion of AdoMet to 1-aminocyclopropane-1-carboxylic acid (ACC), which is catalyzed by the enzyme ACC synthase (ACS).

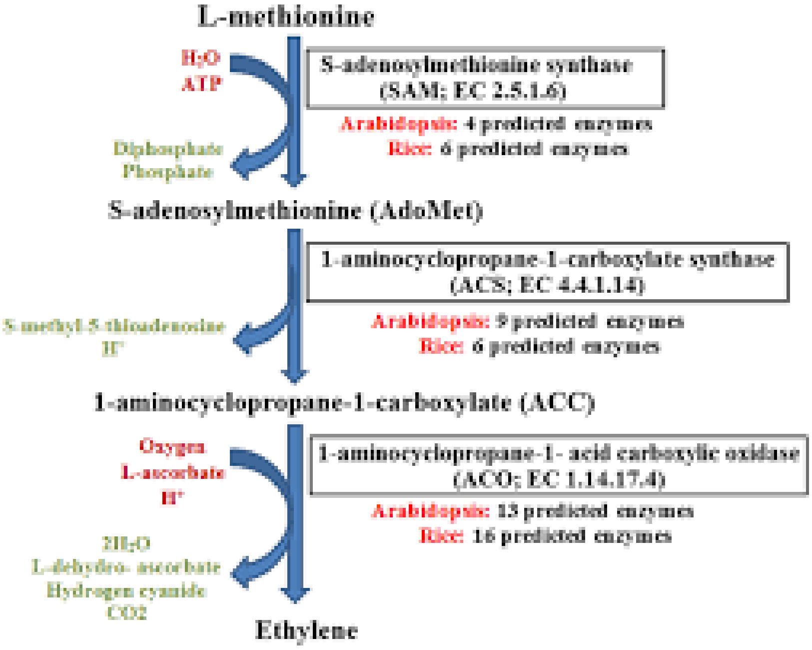

Figure 1: Ethylene biosynthesis: Diagram showing the biosynthesis pathway of ethylene (Journal of genetic engineering).

In the carefully scrutinized plant species, ACS is encoded by a multigene family, the members of which exhibit differential expression in reaction to various hormonal, environmental, and developmental cues. There are twelve ACS genes in Arabidopsis, designated ACS1 through ACS12. The ACS1 gene produces an inactive form of the ACS, and the ACS3 gene is probably a pseudogene. The Arabidopsis ACS gene family exhibits different transcriptional responses to multiple inducers, just like in other plant species. Although ethylene serves a variety of purposes, most of them are related to senescence, or aging. This encompasses flower wilting, fruit and leaf abscission, and fruit and leaf ripening. Additionally, ethylene helps some grains germinate as well as the sprouting of potatoes and bulbous plants. It causes the foliage to droop and the potato buds to emerge. Ethylene encourages the development of female flowers in monoecious plants, while gibberellic acid encourages the development of male blossoms. The triple reaction, which is mediated by ethylene, causes the shoots of buried seedlings to develop short and wide as well as bend horizontally[1]–[3].

The shoot can now plow through the debris thanks to this. In rice and other plants that are grown in water, ethylene induces stem elongation. It encourages ABA's (abscisic acid) disintegration, releasing ABA's grip on gibberellic acid. Many fruits, including apples, oranges, and avocados, emit ethylene as they get closer to maturity. Ethylene promotes the transformation of starch and acids into sugars during plant ripening. Unripe fruit, like avocados, can be stored in a sealed paper bag to hasten to ripen because the gas emitted when the first fruit ripens will hasten the maturation of the remaining fruit. Leaf, fruit, and floral petal abscission are caused by ethylene. Ethylene causes senescence and eventually programmed cell death at the location of the leaf's attachment to the stem when auxin levels drop. At the base of the petiole or fruit stalk, a special layer of cells called the abscission layer (abscission zone) develops (Figure 2).

The more distant separation layer and the more proximal protective layer are the two components of the abscission layer found in the petioles of some plants. Nutrients are taken up by the stem before abscission to prevent them from being wasted along with the leaf. At this point, the separation layer collapses, allowing the leaf to break free and descend to the ground safely without harming the rest of the plant. The seal is provided by the protective coating, which was strengthened with suberin. Autumn is a crucial time for temperate deciduous plants to absciss their leaves. This is a crucial reaction to the onset of winter because any branches that are still in the leaf would be in danger of breaking due to the snow load and the fact that the ground water is frozen and cannot sustain transpiration.

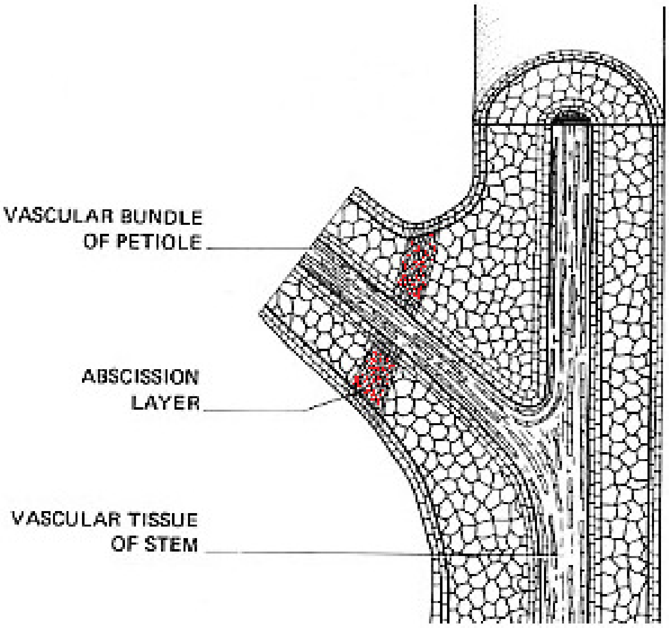

Figure 2: abscission layer: Diagram showing the formation of the abscission layer in the plant (Plant growth and movement).

However, plants will perish if the stomata stay closed for an excessive amount of time because closed stomata prevent gas exchange. As a result, if a drought lasts too long, the plant will start to sacrifice particular areas by letting specific leaves or stalks wither. Ethylene, which under certain circumstances can cause limited cell death, may control this process. Either ethylene prevents or encourages cell growth at the cellular level. It occasionally prevents cell growth. Occasionally, it promotes lateral cell growth. Transmembrane receptors in the endoplasmic reticulum (ER) of cells can sense the presence of ethylene. When ethylene binds to these receptors, a signaling chain is set off, which activates transcription factors and activates gene transcription.

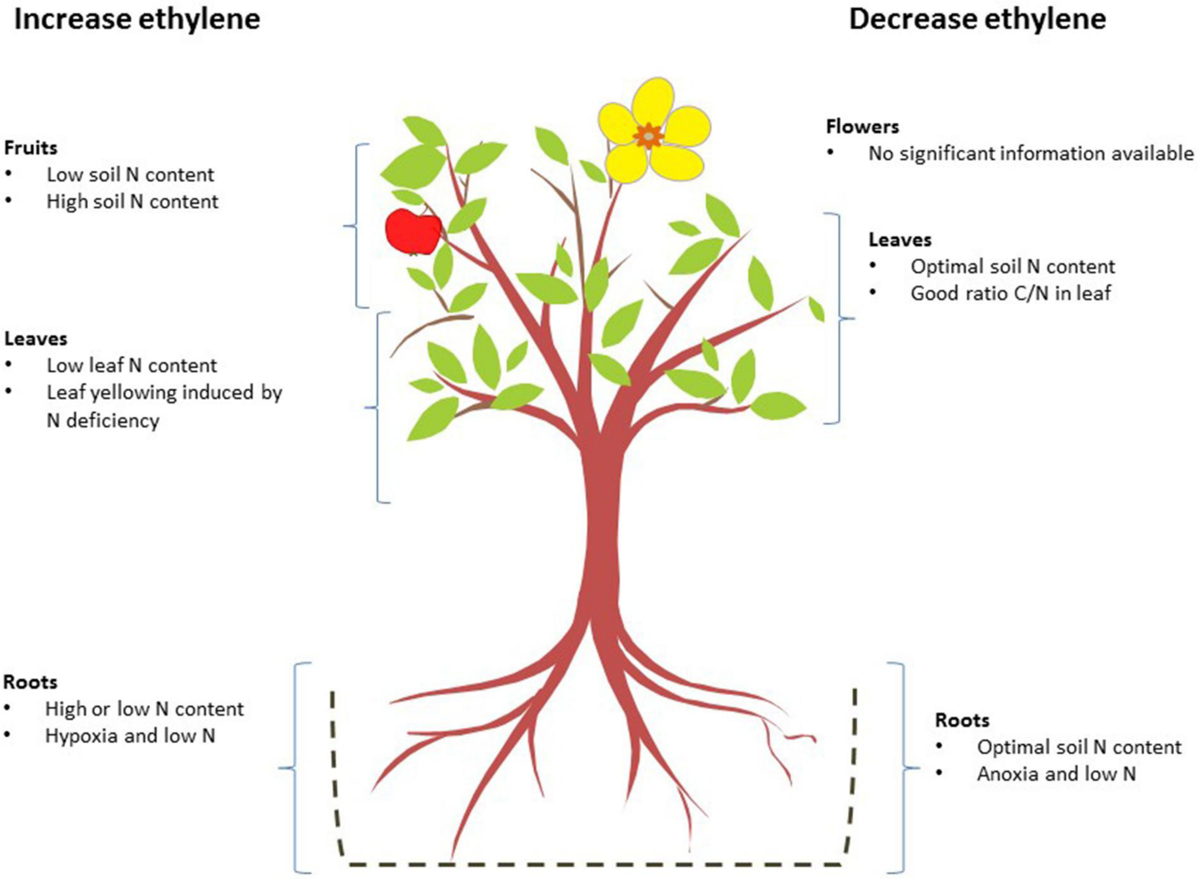

Figure 3: Function of ethylene: Diagram showing the different functions of ethylene in the plant(frontiers).

In agriculture, ethylene is extensively utilized. Equipment that produces ethylene can be purchased by commercial fruit growers to ensure that their harvest ripens swiftly and uniformly (Figure.3). Using fans and ventilation, horticulturists eliminate ethylene from conservatories to prevent ornamental plants from dropping their leaves. A family of five transmembrane protein dimers, including the ETR1 protein in Arabidopsis, detect ethylene. Numerous plants, including the model plant Arabidopsis thaliana, have had their ethylene receptor genes copied. Multiple genes in plant genomes contain ethylene receptors. Dominant missense mutations in any of the gene family, which includes five receptors in Arabidopsis and at least six in tomato, can confer insensitivity to ethylene. A plant that displays constitutive ethylene responses is the product of loss-of-function mutations in several members of the ethylene-receptor family [4]. Numerous other plant species have also had their ethylene receptor DNA sequences discovered. Cyanobacteria even have an ethylene-binding protein. This chapter has covered a summary of the plant hormone ethylene. Ethylene's function in food ripening and plant growth.

LITERATURE REVIEW

The first known gaseous biological signaling substance was ethylene, the simplest of the olefin gases. Plants produce it during specific developmental stages and in reaction to biotic and abiotic stresses. Many facets of plant growth, development, and responses to environmental cues are impacted by ethylene. Scientists began their investigation into the impacts of illuminating gas on plants in the 1800s, which eventually led to the discovery of ethylene as a plant hormone. This crucial area of study was established in 1901 when Dimitry Neljubow discovered that ethylene is the substance in lighting gas that has the greatest impact on plants. It is widely acknowledged that Richard Gane gave the definitive proof that plants biosynthesize ethylene in 1934. Early studies revealed that plants both biosynthesize and detect ethylene. Due to the lack of study on ethylene as a hormone from the 1930s to the 1960s and the difficulty in detecting ethylene, many scientists did not think that ethylene was actually a hormone produced by plants. However, the use of gas chromatography resulted in a rise in interest in ethylene studies in the late 1950s. The biochemical process for ethylene biosynthesis in plants was deciphered and membrane-bound ethylene-binding sites were identified and described between the 1960s and the early 1980s. The widespread application of molecular biological methods beginning in the 1980s and the use of the model plant system Arabidopsis thaliana are correlated with a second, more significant rise in the productivity of ethylene study. Many plant types are now using the knowledge learned from this model plant. In-depth models for the control of ethylene signal transmission and ethylene biosynthesis have surfaced in recent years. The most significant past findings regarding ethylene as a plant hormone are summarized in this paper.

More than 450 million years ago, a branch of freshwater charophyte green algae gave rise to land vegetation. Before the evolutionary shift to land, the extent of plant signaling systems is unclear. Despite holding a crucial phylogenetic place for illuminating the origins of such signaling systems, there is a dearth of sequence information for charophytes. Here, we perform de novo transcriptomics on five representative species of charophytes and identify potential homologs for the biosynthesis, transport, perception, and signaling of key plant hormones. We demonstrate that the filamentous charophyte Spirogyra pratensis has an ethylene hormone system that is similar to that of plants by focusing on the ethylene hormone found in plants. Spirogyra generates ethylene and responds to ethylene by elongating its cells. Indicative of unmistakably homologous ethylene-signaling pathways in Spirogyra and Arabidopsis, Spirogyra ethylene-signaling homologues partly rescue mutants of the angiosperm Arabidopsis thaliana and react post-translationally to ethylene when expressed in plant cells. These results suggest that this pathway was present in the shared aquatic ancestor before the land was colonized and that cell elongation may have been an ancestral ethylene response. This demonstrates the value of charophytes for tracing the evolutionary history of basic plant functions[4]–[6].

The plant hormone ethylene, which is frequently referred to as an "aging" hormone because it speeds up processes like ripening, senescence, and abscission, also controls many facets of growth and development throughout a plant's life cycle. There are numerous ways that the transcriptional output of the ethylene signaling pathway can be modified to fit the requirements of different developmental paths. Of special interest is the report by Lumba et al. in BMC Biology on how vegetative transitions are regulated through the effect of the transcription factor FUSCA3 on ethylene-controlled gene expression, providing an elegant example of how hormonal control can be integrated into a developmental pathway.

Since ethylene, a gaseous phytohormone, is involved in almost every stage of plant growth and development, it significantly affects crop output. This agronomic impact makes understanding ethylene signaling the Philosopher's Stone of the plant biotechnology world in applications including post-harvest transport of foodstuffs, consistency of foodstuff maturity pre-harvest, decorative flower freshness and longevity, and biomass production for biofuel applications. In reaction to environmental factors and events during the plant life cycle, plants biosynthesize ethylene, which sets off a signaling cascade that regulates over 1000 genes. A family of copper-dependent receptors, the bioinorganic chemistry of which has largely been ignored by the chemical world, are the essential elements in the perception of ethylene. The biological community has gained a great deal of information about the signal transduction pathways and mechanisms of ethylene signaling since the discovery of these receptors two decades ago. In this review, we emphasize these developments and significant chemical knowledge gaps that have yet to be explored but are essential for regulating and controlling ethylene signalling[6]–[8].

Ethylene, a volatile plant hormone, controls numerous plant developmental and stress reactions. Therefore, plants must have exact spatial and temporal control over the levels of ethylene production. There are two specific stages in the pathway for ethylene biosynthesis. S-adenosyl-L-methionine (SAM) undergoes a first process in which ACC-synthase changes it into 1-aminocyclopropane-1-carboxylic acid (ACC). (ACS). ACC-oxidase converts ACC into ethylene in a subsequent process. (ACO). Initially, the hypothesis that ACS is the pathway's rate-limiting enzyme led to a flurry of research into the mechanisms governing the stability and activity of the ACS protein. The quantity of evidence demonstrating that ACO is the rate-limiting step in the production of ethylene during specifically dedicated processes, however, has grown steadily over time. This suggests that there is strict control of the ACO protein family as well. With a focus on transcriptional, post-transcriptional, and post-translational control, we present a state-of-the-art overview of ACO evolution, functionality, and regulation in this study. In order to regulate the levels of ethylene production in plants, we also emphasize the significance of ACO being a key target for genetic engineering and precision breeding.

This review primarily concentrates on eudicot seeds and the interactions between auxin, cytokinins, gibberellins, ethylene, brassinosteroids, gibberellins, gibberellins, gibberellins, gibberellins, gibberellins, gibberellins, and gibberellins in regulating the interconnected molecular processes that control dormancy release and germination. Gene expression in seeds is controlled by signal transduction pathways, which are regulated by environmental and hormonal signals. The balance of forces between the embryo's development potential and the restraint imposed by the covering layers, such as the testa and endosperm, determines when species with coat dormancy release their dormancy from their seeds and when they germinate. Molecular methods using mutant and transgenic seeds of Arabidopsis thaliana and the Solanaceae model systems, tomato, and tobacco, which are altered in hormone biology, have greatly aided recent advancements in the field of seed biology. While ABA is a negative regulator of germination, it is a positive regulator of dormancy induction and most likely also preservation. GA breaks dormancy, encourages germination, and negates the impacts of ABA. In addition to promoting seed germination, ethylene, and BR counteract the impacts of ABA. In order to understand how hormones regulate seed dormancy release and germination, we offer an integrated view of molecular genetics, physiology, and biochemistry methods[9], [10].

CONCLUSION

The first hormone discovered in plants, ethylene is known to control several activities in plants' growth and responses to biotic and abiotic stressors. Because of its impact on fruit ripening and organ abscission, ethylene is well recognized for its commercial significance in agriculture. Unlike other plant hormones, ethylene is a gaseous hormone that may readily diffuse across membranes and is assumed to be generated at or near its site of action. During the past 20 years, considerable advancements have been achieved in the study of ethylene metabolism, perception, and function using the standard "triple response" phenotype. This chapter is mostly broken down into sections to provide an overview of the key elements of ethylene biology in plants. Ethylene biosynthesis and its control are covered in part one. And rest of the part discussed the various function of ethylene in the plants. Lastly, fascinating issues about the activity of ethylene are put up and will require additional investigation over the years.

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CHAPTER 7

AN OVERVIEW OF GIBBERELLIC ACID THEIR BIOSYNTHESIS AND THE FUNCTION

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ABSTRACT:

Gibberellins are a group of diterpenoid phytohormones that are produced by numerous microbes, fungi, and plants. The fungus *Fusarium fujikuroi* was the source of the first discovery of gibberellins. Gibberellins regulate a variety of cellular processes in plants, including the germination process, elongation growth, flower formation, and flowering period. Gibberellins come in a variety of types, including GA1, GA2, GA3, and others. GA3. The most extensively researched plant growth inhibitor is gibberellic acid. Gibberellins have pronounced impacts that encourage growth. They encourage fruit development, flowering, stem and root elongation, and the quickening of dwarf varieties' elongation to normal sizes. Such elongation mimics IAA-induced elongation in some ways, and gibberellin also promotes the formation of IAA. This volume covered an overview of the origin, synthesis, and functions of gibberellins in the plant system.

KEYWORDS:

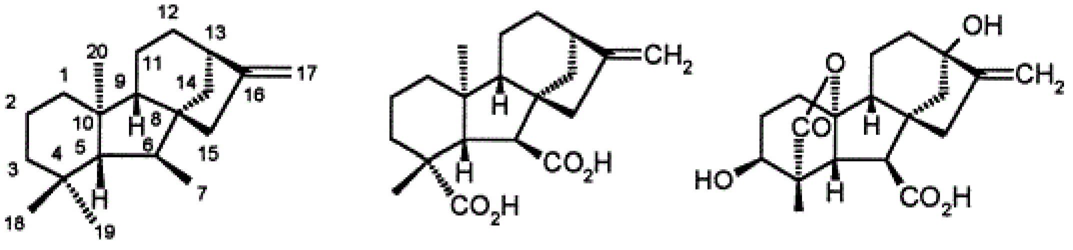
Abscisic Acid, Gibberellic Acid, Growth Regulators, Plant Hormones, Soil Bacteria.

INTRODUCTION

Since the beginning of 1800, when it was discovered that some rice plants had the illness bakane or bakanae (foolish seedling), gibberellins have been known to have an impact in Japan. Such rice plants were sterile, 50% longer than healthy plants, spindle-shaped, thin, and light green. Hori (1918) and Kurosawa (1926) discovered that the illness was brought on by the fungus Gibberella fujikori. The fungus is *Fusarium moniliforme* in its ideal state. Kurosawa discovered that the sterile fungus filtrate also caused disease signs to manifest in uninfected rice seedlings. Yabuta separated the active component and gave it the moniker gibberellin. (1935). Gibberellin was also made in crystalline form by Yabuta (1938); in reality, it was composed of six gibberellins. Only after World War II did Japanese art become known. In 1955, Brian et al. successfully isolated gibberellic acid, or GA3, in its purest state. Gibberellic acid (GA3)'s molecule was determined by Cross in 1961.

Plants and fungus produce gibberellic acid, also known as gibberellin A3, GA, and GA3Its molecular structure is C19H22O6. It is a whitish to pale-yellow solid after purification. Gibberellin, also known as GA, is a naturally occurring tetracyclic diterpenoid carboxylic acid, the majority of which have the carbon compounds ent-gibberellane (C20) or ent-20-norgibberellane (C19). Currently, 136 distinct GAs from higher plants, fungi, or bacteria has been discovered.Either 20 or 19 carbon atoms are present in them. The precursors of the C19 GAs are the C20 GAs, which have the complete complement of 20 carbons, such as GA12 (Figure. 1). The C20 GAs don't actually have any bioactivity. Despite the fact that there are many C19 GAs, many of them lack the molecular elements necessary for bioactivity, such as a 3-hydroxyl group and a 2-substituent[1]–[3].

The most active C19 GAs that meet these requirements are GA1 (Figure 1), GA3, GA4, and GA7. These GAs were among the very first to be isolated, which is unquestionably due to their elevated biological activity. GA1 is regarded as the hormone that is active in the majority of organisms. However, GA4 (13-deoxyGA1) appears to be more reactive than GA1 in Arabidopsis thaliana, and it is speculated that this makes it the active hormone. There is an indication that additional GAs may be involved in flowering control. The main GA in G. fujikuroi, also known as gibberellic acid, is manufactured economically from microbial fermentations. GA3 has numerous industrial applications in brewing, gardening, and agronomy [2].



ent-gibberellane GA_{12} GA_1

Figure 1: Gibberellin structure: Diagramed showing the structure of the different types of gibberellin (Science direct).

In their regular condition, plants produce a lot of GA3. Microorganisms can be used to make the hormone industrially. Gibberellic acid slows down plant decomposition and promotes plant growth when used sparingly, but ultimately plants build up a tolerance to it. GA induces the production of mRNA molecules that code for hydrolytic enzymes in the cells of germination-initiating seeds. Gibberellic acid is a highly powerful hormone that naturally occurs in plants and regulates growth. Applications of very low concentrations can have a profound impact because GA regulates growth, whereas too much will have the reverse effect. Typically, amounts of 0.01 to 10 mg/L are used.

In higher plants, the methylerythritol phosphate (MEP) route is typically used to create GAs. This process turns trans-geranylgeranyl diphosphate into functional GA. (GGDP). Three types of enzymes terpene syntheses (TPSs), cytochrome P450 monooxygenases (P450s), and 2-oxoglutarate-dependent dioxygenases are used in the MEP pathway to produce GA from GGDP. (2ODDs). The MEP route consists of eight steps [4]. Ent-copalyl diphosphate synthase converts GGDP to ent-copalyl diphosphate (ent-CDP). Ent-kaurene synthase transforms ent-CDP into ent-kaurene. Ent-kaurene oxidase transforms ent-kaurene into ent-kaurenol. (KO). KO transforms ent-kaurenol into ent-kaurenal. KO transforms ent-kaurenal into ent-kaurenoic acid. Ent-kaurenoic acid oxidase transforms ent-kaurenoic acid into ent-7a-hydroxykaurenoic acid. (KAO)KAO converts ent-7a-hydroxykaurenoic acid to GA12-aldehyde. KAO changes GA12-aldehyde into GA12. By oxidizing C-20 and C-3, GA12 is converted into the beneficial GA4 by two soluble ODDs called GA 20-oxidase and GA 3-oxidase (Figure. 2).In Arabidopsis and rice, one or two genes are responsible for encoding the enzymes that carry out the initial stages of GA biosynthesis. GA-deficient Arabidopsis dwarves are produced when the null alleles of the genes producing CPS, KS, and KO are present. The 2ODDs that facilitate the conversion of GA12 to bioactive GA4 are encoded by multiple gene families. Vegetative growth is impacted by AtGA3ox1 and AtGA3ox2, two of the four GA3ox-encoding genes in Arabidopsis [5]. AtGA3ox1 and AtGA3ox2 activity during seed germination is controlled by environmental cues. Overexpression of GA20ox in Arabidopsis raises the GA content.

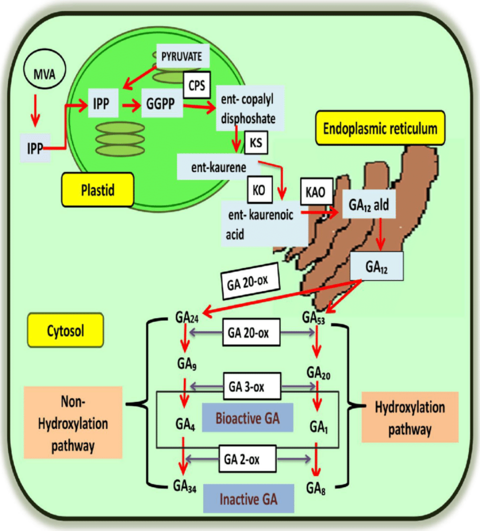


Figure 2: Biosynthesis pathway: Diagramed showing the biosynthesis pathway of the Gibberellins (Research gate).

Gibberellins serve several purposes. Below are a few of them: After GA3 is applied externally to dwarf plants, gibberellin promotes stem growth. These plants mimic the species' tallest varieties. Along with it, the stem's thickness and the quantity of leaves both decrease. Leaves also take a light green color. Gibberellins induce the internodes of genetically dwarf plants to elongate. Peas and maize seedlings are two examples. Gibberellin deficiency is the primary cause of dwarfism in these plants. Gibberellins encourage the lengthening of stems in rosette plants. A rosette is a grouping of foliage that is circular. Typically, rosette plants produce their leaves profusely and with slowed internodal growth. Immediately before blooming or the reproductive stage, gibberellins encourage bolting. An internode extension is bolting. You can find it in beet, broccoli, etc. The embryo ingests water and expands as the seed germination process takes place. Alpha-amylase, proteases, lipases, and other hydrolytic enzymes are produced by the embryo in response to gibberellins, which also cause their production. These enzymes break down the proteins, lipids, and carbohydrates found in the endosperm. As a result, nutrients needed for the creation of new cells will be released. The development of buds is reactivated by gibberellins (Figure. 3). Autumn-formed buds are inactive until the following spring. Gibberellin treatments can therefore be used to break the stasis of the buds. Plants age through a process called senescence. It happens as a result of protein, fat, chlorophyll, and RNA loss. As a result, the leaves acquire a reddish-yellow color.

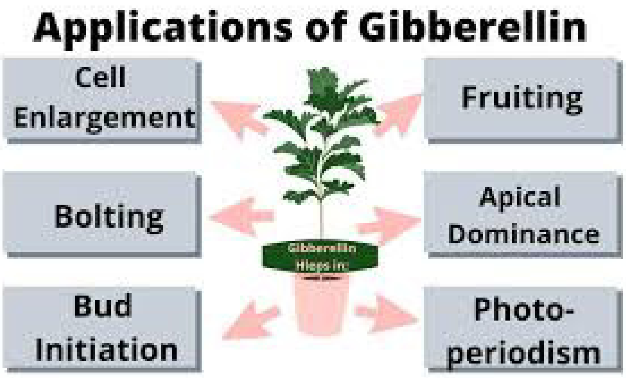


Figure 3. Functions of Gibberellin: Diagramed showing the different functions of the Gibberellin in the plants (EDUInput).

These leaves will ultimately disappear. Gibberellin is one of the proteins that plants use to slow down the aging process and is regarded as such. Gibberellins are typically used with auxins to regulate fruit growth and maturation. It has the power to cause parthenocarpy as well. Gibberellin also affects the maturation of the fruit. Apples and citrus fruits can have their ripening postponed with the aid of gibberellins. The market period can be extended by leaving the fruits on the plant for a longer time in this manner. The vegetables can also be stored in this way for a long time and safely. Apples that have received gibberellin treatment grow longer and have better form. It lengthens the sugarcane stem (*Saccharum officianarum),* increasing the output. In the stalk of sugarcane, carbohydrates are kept as sugar. In the brewing business, gibberellin speeds up the malting procedure. The procedure of steeping, germination, and drying grain to produce malt is referred to as malting. The malt is then employed in the production of beer or whiskey. GA treatment speeds up conifer development in young trees. As a result, seeds are produced earlier. When a seedling is exposed to water, gibberellins are either made in the germination process or released from storage as an inactive conjugate (Figure.4). Numerous hydrolytic enzymes are produced from scratch when active gibberellin appears in the seed's aleurone cells[4].

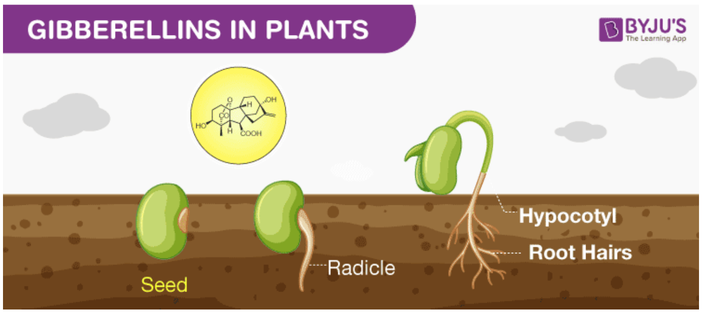


Figure 4: Gibberellin site: Diagramed showing the gibberellin precipitation site during the plant development (BYJU'S).

This foliage will eventually fall off. Gibberellin is considered one of the proteins used by plants to slow down the aging process. Gibberellins and auxins are frequently combined to control the development and maturation of the fruit. Additionally, it has the capacity to induce parthenocarpy. Gibberellin has an impact on produce ripening as well. Gibberellins can be used to delay the ripening of apples and citrus products. By keeping the products on the plant for longer, the market period can be prolonged. The vegetables can be safely and for a long period stored in this manner as well. Gibberellin treatment causes apples to grow longer and develop a superior shape. It increases production by lengthening the sugarcane stem (*Saccharum officianarum*). The sugar-containing carbohydrates are preserved in the sugarcane stem. Gibberellin expedites the malting process in the brewery industry. Malting is the process of steeping, germination, and drying barley to create malt. After that, the malt is used to make lager or whiskey. GA treatment hastens the growth of conifers in young trees. Seed production starts sooner as a result. Gibberellins are either produced during the germination process or released from storage as an inactive conjugate when a seedling is subjected to water. (Figure.4). Once active gibberellin is detected in the aleurone cells of the seed, a large number of hydrolytic enzymes are generated from start.

LITERATURE REVIEW

One of the most important plant development regulators is gibberellin. Due to their present and prospective uses in crop production as well as their role in the responses to environmental stresses, gibberellins, which were discovered over a century ago, are generating more interest in scientific research. The state of our understanding regarding the homeostasis and mechanisms of action of gibberellins is discussed in this overview. Additionally, the intricate network of interactions that eventually leads to precise gene expression is provided by the complex relationships between gibberellins and other plant growth regulators. The highlighted genes and proteins are those that are associated with gibberellin reactions in model and non-model species. The molecular processes governing the relationship between gibberellins and stress responses are also shown. To identify the precise mechanisms at play, this review seeks to present a thorough picture of the state-of-the-art of current perceptions of the interactions of gibberellins with other phytohormones and their responses to plant stresses. This information will help us better understand the biology of gibberellins and could expand the biotechnological toolkit required to enhance plant resilience, especially in the event of climate change

Numerous studies have been done on the impacts of plant hormones and how they affect plants' productivity, growth, and defense. However, little is known about their function in both people and animals. Recent research suggests that plant hormones function in mammalian systems as well and may be used to treat human diseases like cancer and diabetes as well as to promote healthy cell development. Plant hormones like indole-3-acetic acid (IAA) and gibberellins aid in apoptosis, ABA and cytokinin regulate glucose balance, act as antidepressants, and act as antitumor and anti-cancer agents, respectively. The primary objective of this review is to investigate and compare the relationships between plant hormones and their significant functions in animals, microbes, and plants, as well as their interactions, with a focus primarily on human health. This review will examine the impacts of the most significant and well-recognized plant hormones, such as IAA, gibberellins, ABA, cytokinin, and ethylene, on both people and animals

Salinity has a significant negative effect on plants due to its widespread distribution and high magnitude. The most significant endogenous compounds considered to be involved in the mechanisms of plant tolerance or susceptibility to salinity stress are believed to be phytohormones. Under salinity stress, phytohormones play a crucial role in controlling physiological reactions that ultimately result in adaptation to an unfavorable environment. By triggering a series of defense responses or boosting plant growth, ethylene and gibberellins (GAs) help to reduce the negative impacts of salinity stress. However, the actions of these two phytohormones interact with one another. The fact that GA is known to boost ethylene synthesis and that ethylene itself has an impact on its signaling creates a cross-talk between the two processes. In order to determine whether they have independent actions or whether their actions are contingent upon one another the current research focuses on both the individual and interactive effects of the two in salinity tolerance.

A wide variety of phylogenetically diverse organisms synthesize the potent and complicated diterpenoids known as gibberellins (GA), which are phytohormones. It has since been recognized that plants, fungus, and bacteria all have analogous metabolisms, which were first identified in the phytopathogen Fusarium fujikuroi. Interesting biosynthetic pathways that produce these sophisticated natural products appear to have separately evolved in each of these large groups of organisms. Here, we present our current knowledge of the diverse GA metabolism in each group with a focus on the traits, especially pertinent enzymatic type, that distinguish their GA biosynthetic pathways from one another. An overview of the required metabolic integration as well as the various catabolic processes involved in breaking down bioactive GAs in plants is given, as are the steps that are shared by the biosynthesis of GA and other isoprenoid and related diterpenoid natural products in plants.

Microorganisms like bacteria, fungi, actinomycetes, protozoa, and algae are abundant in soil. The rhizosphere of the earth is typically home to microscopic life that interacts with plants.

The capacity of microbes to produce the "classical five" phytohormones auxin, gibberellin, cytokinins, ethylene, and abscisic acid is what leads to microbial-plant interactions. Jasmonate and salicylic acid are also known to function as bacterial hormones that support a sustainable agro system, in addition to these modulators. Azospirillum species are known to generate auxins, gibberellins, and cytokinins. The production of auxin by fungi like Pistolithus tinctorius promotes plant development, and various bacterial species have an impact on root length by increasing surface area and inducing the growth of tumors and galls. Gibberellins are tetracyclic diterpenoid acids that play a variety of developmental, reproductive, and floral roles in plants, whereas cytokinins promote plant growth and induce tumor and gall formation. It has been demonstrated that ethylene is produced in culture by Pseudomonas solanacearum, Mycobacterium hiemalis, and primarily spore-forming bacteria. A stress-related signaling molecule called abscisic acid (ABA) has been found in all kingdoms of life, including bacteria that are linked with plants, fungi that are harmful to them, some cyanobacteria, algae, lichens, protozoa, and sponges. The fungus P. patulum produces salicylic acid, which works well as a medicine for plants. SA affects how plants react to biotic and abiotic stress. Throughout the lifetime of the plant, it also controls biochemical and physiological processes. A signaling molecule known as jasmonic acid is thought to be produced by the fungus Lasiodiplodia theobromae and is engaged in plant defense. Nevertheless, there are few reports outlining strategies that concentrate on the production, extraction, and detection of microbial phytohormones, despite the extensive research that has been done in this field. The methods used to isolate and purify these phytohormones are the main emphasis of this review.

Abiotic stresses that adversely affect plant development include salinity, drought, extreme temperatures, etc. Global crop losses are primarily due to such harsh environmental circumstances. Herein lays the significance of in-depth analyses of how the plant interactome functions under stress. The creation of a tolerant phenotype can benefit from an ideal definition of the molecular elements in the interactive stress pathway. The main control mechanisms of stress reactions are phytohormones. Gibberellins or gibberellic acids (GAs), a class of hormones that promotes germination, play a key part in these processes. Under conditions of stress like salinity and cold, optimum plant development is restricted by reduced GA accumulation. On the other hand, increased GA synthesis encourages stress-escaping reactions and stimulates plant development under shade and submersion. By controlling the expression of GA biosynthetic genes or GA-catabolic genes like GA2ox and DELLAs, plants can sustain such cellular homeostasis. In reaction to abiotic stress, GA-mediated signaling interacts with other phytohormones such as auxin, ABA, and others to integrate multiple hormone signaling cascades. The development of plants under abiotic stresses has served as the backdrop for our discussion of the GA metabolism, emerging GA-regulatory signaling pathways, and their possible interactions with other phytohormones

The fundamental classes of phytohormones, their localization, and their role in controlling sporophyte and gametophyte growth and development in pteridophytes are highlighted in the review. It has been explored how gibberellins and gibberellin-like compounds (antheridiogen and antheridiogen-B) affect the determination of sexual polymorphism. A biologically active meristem produces antheridiogen, which contains a gibberellin skeleton in its structure. The male gametophyte forms at high antheridiogen amounts, while the female gametophyte develops in its absence. Publications dealing with studies on the content and possible involvement in the regulation of physiological processes of abscisic acid (ABA) (in regulation of spore dormancy breaking), auxins and cytokinins (in frond formation), ethylene and jasmonic acid (in resistance formation) in pteridophytes have been analyzed. The summarizes the present state of research on the fundamental phytohormone complex components in the Polypodiophyta division[5]–[7].

Plant growth regulators are phytohormones that are produced and exported by plant growth-promoting rhizobacteria (PGPRs). (PGRs). These PGRs might regulate plant formation and growth. PGRs are organic compounds that, at very low amounts, affect the physiological functions of plants. Among five classes of well-known PGRs, namely auxins, gibberellins, cytokinins, ethylene, and abscisic acid, the most common, best characterized, and physiologically active auxin in plants is indole-3-acetic acid (IAA) that stimulate both rapid (e.g. increases in cell elongation) and long-term (e.g. cell division and differentiation) responses in plants. Some bacteria also release substances that may help promote plant development indirectly, such as indole-3-butyric acid (IBA), tryptophan, and tryptophol, or indole-3-ethanol (TOL). On the other hand, cytokinins, which are typically found in trace quantities, promote cell division, resulting in the formation of root hairs and root development. About 90% of the microorganisms discovered in the rhizosphere are capable of releasing cytokinins when cultured in vitro, and microorganisms have been found to contain over 30 growth-promoting compounds of the cytokinin group. Gibberellins (GAs), which are produced by soil microbes, number over 100 different types. The most well-known form of gibberellin is GA3 (gibberellic acid), and the plant hormone GA1 that is most active in promoting stem growth is GA1. Additionally, radioimmunoassay has found abscisic acid (ABA) in the supernatants of bacterial cultures thought to be the cause of stomatal closing. Its existence in the rhizosphere may be crucial for crop survival in soils that are water-stressed, as is the case in arid and semiarid climates. Strong plant growth regulator ethylene has an impact on a variety of facets of plant development, senescence, and growth. In addition to being known as a ripening hormone, ethylene encourages the development of exploratory root and root hair, speeds up germination, and removes seeds' dormancy. By reducing the levels of ethylene in plants and the rhizosphere of seeds, soil bacteria encourage plant development, particularly seed germination. The direct precursor of ethylene in plants, 1-aminocyclopropane-1-carboxylate (ACC), is hydrolyzed by the enzyme 1-aminocyclopropane-1-carboxylate deaminase. Ammonia and -ketobutyrate, the byproducts of this hydrolysis, can be utilized by the bacterium as sources of nitrogen and carbon for development. By acting as an ACC sink, soil bacteria reduce plant ethylene levels and help avoid some of the possibly harmful effects of high ethylene levels. The production of phosphatases, -glucanase, dehydrogenase, antibiotics, solubilization of mineral nutrients, stabilization of soil aggregates, enhancement of soil organic matter, and improvement of soil structure are all essential functions performed by soil bacteria along PGPRs. For sustained crop yield, soil bacteria that produce PGRs reduce or replace the need for chemical fertilizers N and P[8]–[10]

CONCLUSION

Any member of the family of plant hormones known as gibberellin is found in seeds, juvenile leaves, and roots. The name comes from the hormone-producing fungus Gibberella fujikuroi, a member of the phylum Ascomycota, which produces excessive growth and low yield in rice plants. Gibberellins have pronounced impacts that encourage growth. They encourage fruit development, flowering, stem and root elongation, and the quickening of dwarf varieties' elongation to normal sizes. Such elongation mimics IAA-induced elongation in some ways, and gibberellin also promotes the formation of IAA. When a plant is exposed to cold temperatures, a larger quantity of gibberellins is produced. They promote fruit without seeds, breakage and budding, cell elongation, and seed germination. By releasing the seed from its dormancy and serving as a chemical messenger, gibberellins trigger seed germination. Only a small number of the up to 136 distinct gibberellin molecules that have been identified so far, including GA1, GA3, GA4, and GA7, are bioactive. Along with the development of molecular genetics and functional genomics, recent studies on GA biosynthesis, metabolism, transport, and signaling have made significant progress. These studies have also examined the interactions between GA and other plant hormones and environmental signals. Studying the gibberellin biosynthesis route and signaling cascade offers fresh insight into how to crop quality, stability, and life span are developed.

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CHAPTER 8

AN OVERVIEW OF JASMONATES PHYTOHORMONES BIOSYNTHESIS PATHWAY AND FUNCTION

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ABSTRACT:

In the plant system environmental stress is regulated by the phytohormones known as jasmonates. Jasmonates originated from the phospholipids that acclimatizedthe stress response by slowing the normal growth of the plant and collaborating with the other hormones to develop multiple responses under stress conditions. Apart from the plant stress response, they are also involved in the development of the flower and fruit. Due to the phospholipids' nature of jasmonates, they can transport a signal to their proximate plant against biological and environmental stress. The processes of jasmonate signaling pathways, the processes of cross-talk with some other hormonal, and the identification of the underlying pathways of plant self-defense are the main areas of emphasis of contemporary jasmonate study. In the chapter we mainly discussed the jasmonate's biosynthesis pathway, and its function in the plant system.

KEYWORDS:

Biosynthesis Pathway, Cell Death, Delayed Dehiscence 1, Jasmonic Acid, Plant Development.

INTRODUCTION

While jasmonic acid itself was extracted from *Lasiodiplodia theobromae* by Alderidge et al. in 1971 the molecular structure of jasmonates and their name were first discovered in 1962 through the isolation of methyl jasmonate (MeJa) from jasmine oil derived from *Jasminum grandiflorum.* JA and its derivatives are lipid-based plant hormones that control a variety of processes in plants, from growth and photosynthesis to the formation of reproductive organs. JAs are particularly important for plant defense against herbivory, plant responses to unfavorable environmental circumstances, and plant responses to other types of abiotic and biotic challenges [1]. Some JAs have the ability to be released as volatile organic compounds (VOCs), allowing plants to communicate in advance of potential threats [2].

Following the original discovery of MeJA as a flowering plant odor and of JA in the fungus *Lasiodiplodia theobromae's* culture medium, several JA compounds were found to be present in all land plants. Fruits contained significant amounts. The presence was found in all organs harboring plastids, according to later screening. It was discovered that such a basal level rose quickly in response to injury or other environmental signals. Marchantia polymorpha, the most primitive lineage of extant terrestrial plants, has recently been found to contain 12-oxo-phytodienoic acid (OPDA), but not JA. Physcomitrella patens also exhibited OPDA but not JA. OPDA has been found in large amounts in the spikemoss *Selaginella martensii*, one of the earliest vascular plants. Numerous lipoxygenase (LOX) pathway intermediates, including JAs, are present in both green and brown phytoplankton. In the 1980s, the biosynthesis route for JA from -LeA esterified in chloroplast membranes was discovered. A suggested sequence initially included a LOX, a hydroperoxide cyclase, a reductase, and ß-oxidation of the carboxylic acid side chain. The two-step reaction of membrane-associated allene oxide synthase (AOS), whose extremely unstable product is cyclized by an allene oxide cyclase (AOC) to OPDA, was later demonstrated to be the single-step of hydroperoxide cyclase. In addition to the enzymatic processes, the unstable epoxide spontaneously hydrolyzes to form - and -ketols and undergoes non-enzymatic cyclization to form racemic OPDA. This needs to be considered in both JA and OPDA quantification as well as enzyme tests. Chloroplasts contain all of the OPDA production enzymes. (Figure.1). Peroxisomes are where the second part of JA biosynthesis takes place. Here, acyl-CoA-oxidase (ACX), multifunctional proteins (MFPs), and the L-3-ketoacyl-CoA-thiolase (KAT) decrease OPDA before activating it to form co-esters through fatty acid CoA-synthetases and 4-coumaroyl: CoA-ligases (Figure.1) [3].

The stereochemistry of intermediates and products plays a significant role in JA biosynthesis. The naturally existing cis-(+)-7-iso-JA's enantiomeric form (7R, 7S) is established in the AOC-catalyzed step. Epimerization to the more dependable (-)-JA was initially thought to occur. But it is now evident that (+)-7-iso-JA-Ile, an isoleucine conjugate of JA with the (7R,7S) configuration, is necessary for JA sensing and communication since the discovery of the most bioactive JA compound.

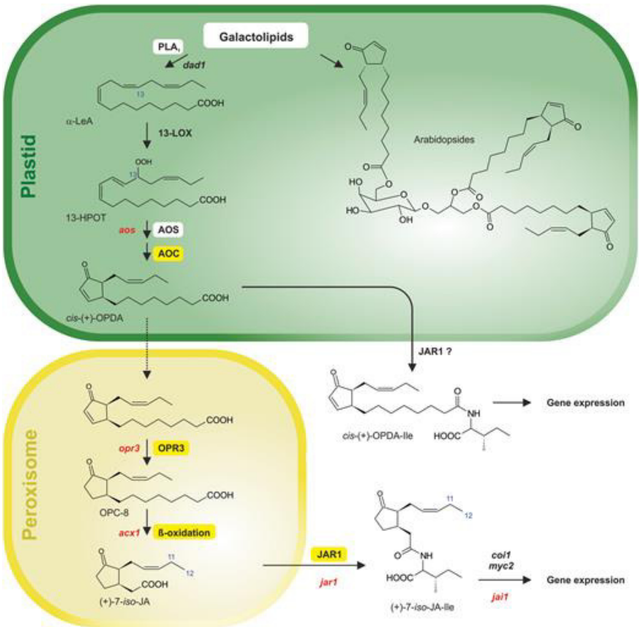

Figure 1: Biosynthesis pathway: Diagram showing the biosynthesis pathway of the jasmonate acid phytohormones (Academic.oup).

The three main principles that govern the regulation of JA biosynthesis are: (i) the necessity for the release of -LeA as the substrate upon external stimuli; (ii) the positive feedback loop in JA's expression of the JA biosynthesis genes; and (iii) tissue specificity. Additional regulatory factors may occur by concurrent activity between the AOS and HPL, and other branches of the LOX pathway, by the negative regulators JAZs, post-translational control (e.g. OPR3), heteromerization (e.g. AOCs of Arabidopsis), Ca2+ signaling, and the mitogen-activated protein kinase cascade. Even though more recent data contest the existence of a positive feedback loop in JA formation, they still demonstrate this control of JA biosynthesis gene expression, which suggests that post-translational modifications may be involved [3]. Even though jasmonate (JA) controls a wide range of physiological functions in plants, its impact on wound healing is best known. After herbivory or mechanical injury, JA biosynthesis is quickly triggered, which causes the expression of the necessary response genes. For instance, when a tomato is wounded, defense molecules are produced that prevent the insect's stomach from breaking down the leaf. The volatile emission of substances generated from JA is another indirect effect of JA signaling. MeJA on leaves has the ability to disperse through the air to adjacent plants and increase transcript levels associated with wound response. Generally speaking, this emission can intensify the signaling and synthesis of JA and encourage adjacent plants to prepare their defenses for herbivory.

In addition to their function in defense, JAs are also thought to contribute to cell demise and leaf senescence. Numerous kinases and transcriptional regulators linked to aging can interact with JA. Additionally, JA can cause mitochondrial mortality by causing the buildup of reactive oxygen species. (ROSs). These substances cause apoptosis, or planned cell death, which compromises the cell by damaging mitochondrial membranes. The functions of JAs in these processes imply mechanisms by which the plant protects itself against biotic threats and restricts the spread of infections. (Figure.2). Along with the mechanisms listed below, JA and its derivatives have also been linked to symbiosis and the growth of plants. One of the earliest discoveries was that JA inhibits root growth, which was discovered through research on mutants overexpressing JA.

Figure 2: Function of the jasmonate: Diagram showing the different functions of the jasmonate in the plant (MDPI).

It is still unclear what causes this phenomenon, but mutants in the COI1-dependent signaling pathway frequently exhibit less inhibition, indicating that the COI1 pathway is somehow required for preventing root development. JA has numerous functions in the growth of flowers. Male sterility manifests in Arabidopsis JA signaling or synthesis mutations, usually as a result of delayed development. In Arabidopsis, the same alleles that increase male fertility also increase female fertility in tomatoes. Also, 12-OH-JA overexpression can prevent flowers from blooming. The sprouting of dormant seeds is stimulated by JA and MeJA while the germination of non-dormant seeds is inhibited (Figure.2). Genes encoding vegetative storage proteins are JA responsive, and high amounts of JA promote the accumulation of storage proteins. Particularly, the production of tubers is induced by tuberonic acid, a JA metabolite. Although the exact function of JAs in the symbiosis between plants and microbes is still unknown. JA presently seems to control nodulation regulation and signal exchange between legumes and Rhizobium. On the other hand, increased JA levels in mycorrhizal plants seem to control how carbohydrates are partitioned and how well they can withstand stress[4]. The emergence of predatory plants like the Venus flytrap has been linked to JAs. According to research, the evolution of plant carnivory may have been aided by the repurposing of the jasmonate signaling pathway, which regulates defense against herbivores in noncarnivorous plants. The release of enzymes and nutrient transporters, which are essential for plant digestion, can be regulated by jasmonates, which can also be used to indicate the closing of traps. The jasmonate route is not utilized by all carnivorous plants in the same manner, though. Butterworts have evolved potentially JA-independent mechanisms for controlling stomach enzymes, setting them apart from Venus flytraps and sundews.

LITERATURE REVIEW

Jasmonates are crucial signaling molecules that include the plant hormones jasmonic acid, and methyl jasmonate, and the intermediates they generate in the octadecanoid pathway. These occur frequently in the plant world and are important in processes involving plant growth and development as well as responses to biotic and abiotic stress. Jasmonates have recently been demonstrated to play a role in biological processes. We discuss the most current research on the biosynthesis, control, and signaling of jasmonates. We also discuss the discovery of [(+)-7-iso-JA-L-Ile] as the biologically active hormonal form of jasmonate, which closes the biggest information gap about the signaling pathway that activates downstream genes in the jasmonate-signaling cascade. The discovery of numerous Arabidopsis thaliana mutants was essential for unraveling the signaling pathways underlying jasmonate-mediated reactions. Finally, since some of the key enzymes in the jasmonic acid biosynthesis pathway were discovered in a stigma/style expressed sequence tag database (TOBEST) of this Solanaceae species, the role of jasmonates in Nicotiana tabacum L.'s reproductive system is briefly discussed [5].

Short chain cyclic fatty acids were produced when six plant species processed the 18O-labeled 12-oxo-cis,cis-10,15-phytodienoic acid (12-oxo-PDA). Zea mays *L., Solanum melongena* L., *Linum usitatissimum L., Avena sativa L., Helianthus annuus L.,* and wheat were the plant types that were examined. (Triticum aestivum L.). Jasmonic acid, a naturally occurring plant component with the ability to control development, was one of the items. The route is the same as the one we recently reported for the pericarp of Vicia faba L. to produce jasmonic acid. The 12-oxo-PDA ring double bond must first be filled before six carbons from the carboxyl side chain can be removed by -oxidation enzymes. Studies on the substrate specificity of 12-oxo-PDA showed that neither the stereochemistry of the side chain at carbon 13 nor the existence of the double bond at carbon 15 was essential for either enzyme step. Numerous plant species possess enzymes that convert 12-oxo-PDA to jasmonic acid, suggesting that this metabolic route may be common to all plants[6, p. 1].

Jasmonic acid (JA) and the related compounds known as jasmonates (JAs), which are both precursors and derivatives of JA, are crucial molecules in the control of numerous physiological processes involved in plant growth and development, particularly the mediating of plant reactions to biotic and abiotic stresses. Numerous studies have been conducted on JAs biosynthesis, perception, transport, signal transduction, and activity. In this review, we will discuss the initiation of JA signaling with a focus on environmental signal perception and transduction, JA biosynthesis and metabolism, transport of signaling molecules (local transmission, vascular bundle transmission, and airborne transportation), and biological function (JA signal receptors, regulated transcription factors, and biological processes involved) [7].

The functions of jasmonic acid (JA) and related compounds in controlling plant growth are discussed in this chapter. The expression of many genes, including the genes for proteinase inhibitors in tomato plants and the genes for vegetative storage proteins in soybean plants, is strongly induced by JA-related compounds, which are broadly distributed in higher plants. A number of enzymes convert linolenic acid into JA. Lipoxygenase, a common enzyme in plant tissues, catalyzes the early reaction in the synthesis of JA. Methanol, ethanol, or acetone can be used to quickly extract molecules connected to JA from plant-based materials. After collection, the substance needs to be homogenized as soon as possible with enough solvent to stop the compounds' enzymatic changes. Due to the existence of two chiral carbons at the C-1 and C-2 positions of a cyclopentane ring, JA has four stereoisomers. Maslenkova et al. investigated how JA affected chloroplasts isolated from barley plants' capacity to evolve oxygen. According to the oxygen evolution's dynamics, JA reduced the value of the overall number of oxygen-evolving centers. In the barley chloroplasts, JA has an impact on the degree of granular region structuring or the structural stability of the electron transport chain [8].

Higher plants contain jasmonic acid (JA), a naturally produced growth regulator. This substance, or a related substance called methyl jasmonate, has been implicated in several physiological functions during plant development and in reaction to biotic and abiotic stress. We created JA with 13C as an internal standard with isotopic composition of [225]:[224] 0.98:0.02 as opposed to [225]:[224] 0.15:0.85 for natural material in order to precisely measure JA amounts in plant tissue. Fire ionization detection and mass spectrometry results from GC analysis show that the internal standard contains 92% 2-(+/-)-[13C]JA and 8% 2-(+/-)-7-iso-[13C]JA. The JA concentrations in young leaves, flowers, and fruit of soybean plants were the greatest. (highest in the pericarp). The hypocotyl hook, plumule, and 12-h axis in soybean seeds and seedlings were the youngest organs with the greatest concentrations of JA. JA levels rose roughly 5-fold within 2 hours in soybean leaves that had undergone dehydration which resulted in a 15% reduction in fresh weight before falling to about control levels after 4 hours. On the other hand, there was a delay of 1-2 hours before abscisic acid buildup peaked. These findings will be reviewed in relation to various JA biosynthesis pathways, the function of JA in plant development, and how plants respond to environmental cues [9].

Anthers in an Arabidopsis T-DNA mutant known as delayed dehiscence1 discharge pollen grains after pollination has already begun. A delay in the stomium degeneration pathway is the root cause of the delayed dehiscence1 defect. An enzyme in the biosynthesis route for jasmonic acid, 12-oxophytodienoate reductase, is encoded by the gene disrupted in delayed dehiscence1. With the help of exogenous jasmonic acid, we were able to restore the mutant phenotype and produce sperm from previously male-sterile plants. According to in situ hybridization research, all floral organs accumulated DELAYED DEHISCENCE1 mRNA in the early phases of floral development. Later, filaments in the pistil, petals, and stamens in particular aggregated with DELAYED DEHISCENCE1 mRNA. The stomium and septum cells of the anther, which are involved in pollen discharge, did not contain DELAYED DEHISCENCE1 mRNA. Both the accumulation of DELAYED DEHISCENCE1 mRNA and 12-oxophytodienoate reductase activity was abolished by the T-DNA insertion in delayed dehiscence1. According to these studies, the timing of anther dehiscence inside the blossom may be influenced by jasmonic acid signalling [10].

Here, in-depth analyses of the two oxo-phytodienoate reductase genes, OPR7 and OPR8, in JA-deficient mutants of maize (Zea mays), show the diverse roles of jasmonic acid (JA) in the plant. Most tissues with single mutants generate wild-type levels of JA, but all organs with the double mutant opr7 opr8 have significantly lower levels of JA than single mutants do. Strong developmental flaws in opr7 opr8 included the development of a feminized tassel, the beginning of female reproductive buds at each node, and extremely long ear shanks.

Exogenous JA was able to correct these defects. These findings demonstrate that JA is necessary for the determination of male sex and the inhibition of female reproductive organ development. Additionally, opr7 opr8 showed delayed leaf senescence, along with decreased ethylene and abscisic acid levels, and brace roots that were not anthocyanin-pigmented. The extreme susceptibility to a root-rotting oomycete (Pythium spp.) renders opr7 opr8 nonviable in nonsterile soil and under field circumstances, proving that these genes are essential for maize survival in nature. The fact that opr7 opr8 is vulnerable to beet armyworms supports the significance of JA in insect defense. The global roles of JA in maize development and immunity to pathogens and insects are supported by robust genetic data overall, according to this study [11].

Plants are crucially protected by glutathione from oxidative stress, climatic stress, xenobiotics, and some heavy metals. The transcription of the genes for glutathione synthesis, -glutamylcysteine synthetase, glutathione synthase, and glutathione reductase increased in Arabidopsis plants exposed to cadmium or copper. Other toxic and nontoxic metals did not affect mRNA levels, but only those metals whose toxicity is believed to be reduced by phytochelatins elicited a reaction. According to feeding studies, the production of these genes was not activated by oxidative stress, which is brought on by exposure to H2O2, oxidized glutathione, or low glutathione levels. The fact that jasmonic acid triggered the same group of genes also raises the possibility that it plays a role in the copper and cadmium signal transduction pathways. The notion that the glutathione concentration is regulated at various levels is supported by the fact that jasmonic acid treatment increased mRNA levels and the ability to synthesize glutathione but had no effect on the glutathione content in unstressed plants [12].The essential signaling molecules jasmonic acid (JA) and its derivatives, collectively known as jasmonates (JAs), coordinate the plant's reaction to biotic and abiotic stresses as well as a number of developmental processes. It has long been understood that the COI1 F-box and additional SCF modulators play a significant part in the JA-signaling pathway. A series of transcription factors, including MYC2, control downstream JA-dependent transcriptional re-programming. The "missing link" in JA signaling has recently been defined by the discovery of JAZ family members as COI1 targets and repressors of MYC2. It has been suggested that the hormone's active version is JA-Ile, and COI1 is a crucial part of the receptor complex. The module COI1/JAZs/MYC2 has been identified as the central JA-signaling pathway by these new discoveries [13].

According to recent research, cross-talk among signaling pathways reliant on ethylene, jasmonic acid, and salicylic acid (SA) controls how plants react to biotic and abiotic stressors. Previous research has shown that the Arabidopsis ecotype Cvi-0 activates a cell death pathway resembling the hypersensitive response (HR) in reaction to ozone (O3) exposure. The influence of SA and JA signaling on O3-induced cell demise has now been established. Salicylate hydroxylase (NahG) expression in Cvi-0 decreased O3-induced cell mortality. Pretreating Cvi-0 with methyl jasmonate (Me-JA) decreased O3-induced H2O2 content and SA concentrations while entirely eliminating O3-induced cell death. When exposed to O3, Cvi-0 produced just as much JA as Col-0 did, but it was much less sensitive to external Me-JA. The responses to O3 of the JA-signaling mutants jar1 and fad3/7/8 were examined, and this research also revealed an antagonistic connection between JA- and SA-signaling pathways in regulating the severity of O3-induced HR-like cell death [14].

CONCLUSION

Jasmonic acid (JA), its amino conjugated (JA-Ile, for example), and its derivatives have recently come to light in plants as essential signaling molecules involved in stress protection and growth. The study on JA has generated a lot of attention and is becoming more prevalent quickly, demonstrating the significance of these plant hormones for plants and animals. In contrast to salicylic acid, which is linked to plants' responses to necrotrophic infections, JA was first identified as a stress hormone involved in biotic stress (diseases and herbivores) that prevents damage to offers a great and symbiont pathogen. JA is also connected to how plants react to abiotic stress.Additionally, current findings have shown that JA regulates a variety of physical mechanisms, including the expansion of reproductive organs, root growth, and plant oxidative stress. JA also contributes to the biosynthesis of several chemical compounds (e.g., phytoalexins and terpenoids). Few plants, primarily *Arabidopsis thaliana*, and *Oryza sativa* L. have JA signaling pathways that have been extensively studied, demonstrating the hormone's critical function in plants.

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CHAPTER 9

AN OVERVIEW OF THE SALICYLIC ACID PHYTOHORMONES

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ABSTRACT:

Salicylic acid is a plant hormone which mostly synthesized in the biotic and abiotic stress of plants. Salicylic acids performed a systemic acquired response against the infection from the pathogen. Its complicated SA communication pathway may be broken down and its crucial involvement in both healthy and diseased plants is confirmed by the identification of its targets and the comprehension of its molecular mechanisms of action in biological processes. From the studies and countless others, we summarized that plants possess a well-developed system of chemical messengers that induce (inhibit or promote) growth and developmental responses. These chemical messengers are termed "hormones". In this chapter, we discussed the origin of salicylic acid in the plant. Furthermore, we looked at the biosynthesis pathways and biological functions of the salicylic acids in the plant.

KEYWORDS:

Acquired Resistance, Disease Resistance, Plant Acid, Systemic Acquired, Salicylic Acids.

INTRODUCTION

Willow has a lengthy history of use in medicine. Dioscorides, whose writings were highly influential for more than 1,500 years, used 'Itea' (which was possibly a species of willow) as a treatment for 'painful intestinal obstructions,' birth control, for 'those who spit blood,' to remove calluses and corns and, externally, as a 'warm pack for gout.' Willow bark, when burned to ashes and steeped in vinegar, removes corns and other similar risings in the feet and toenails, according to William Turner in 1597. Some of these treatments may explain how salicylic acid, which can be made from the salicin found in willow, works. However, the idea that Hippocrates used willow as a painkiller is modern fiction. Decoctions containing salicylate were known to lower fevers and ease pain by Hippocrates, Galen, Pliny the Elder, and others. It was applied to cure these ailments in China and Europe. Ancient Egyptian, Sumerian, and Assyrian writings all make reference to this treatment.

The bark is infused by the Cherokee and other Native Americans for treating fever and other ailments. 2014 saw the discovery of salicylic acid residues on pieces of seventh-century pottery in east-central Colorado. The willow bark was found to be successful in lowering fevers, according to a 1763 report by the Reverend Edward Stone, a vicar from Chipping Norton in Oxfordshire, England. German chemist Johann Andreas Buchner discovered and gave the term salicin to a willow bark extract in 1828. Salicin is named after the Latin name for the white willow (Salix alba). A greater quantity of the substance was discovered in 1829 by French pharmacist Henri Leroux. Italian scientist Raffaele Piria succeeded in converting the substance into a sugar and a second component, which when exposed to oxygen becomes salicylic acid. German scientists also discovered salicylic acid in the plant meadowsweet (*Filipendula ulmaria*, formerly known as *Spiraea ulmaria*) in 1839.

When taken in large amounts, their extract results in digestive issues like gastric irritation, bleeding, diarrhea, and even death. The Scottish doctor Thomas MacLagan tested salicin as a treatment for acute rheumatism in 1874, and he published his results in The Lancet in 1876. German researchers attempted sodium salicylate at the same time, but with fewer results and more negative side effects. Salicylic acid (SA), is a hormone with a phenol-like molecule, (Figure.1). Since it is the forerunner of the painkiller aspirin, it was initially isolated from a white willow bark extract (Salix alba) and is of considerable interest to human medicine. SA is essential for plants' protection against biotrophic pathogens. SA has a comparable ability to methylate as JA does. Methyl salicylate, like MeJA, is flammable and can serve as a long-distance signal to nearby plants to alert them to pathogen assault. SA plays a defense function as well as a role in how plants react to abiotic stress, specifically drought, extreme heat, heavy metals, and osmotic stress.

Figure. 1: Structure of salicylic acid: Diagram showing the molecular structure of the salicylic acid (Shutterstock).

A crucial hormone in plant natural defense, salicylic acid (SA) promotes cell demise, acute reactions, and resilience in both local and general tissue to biotic assaults. Seed germination, cell development, metabolism, stomatal closing, senescence-associated gene expression, reactions to biotic and abiotic stressors, baseline thermotolerance, and crop production are some of the effects of SA on plants. (Figure. 2). A potential function of salicylic acid in communicating disease resistance was first revealed by infusing leaves of robust tobacco with SA. This led to increased resilience to infection by tobacco mosaic virus (TMV) and stimulation of pathogenesis-related (PR) protein buildup after SA injection. Plant cells undergo a series of events as a result of disease exposure[1]–[3].

Salicylic acid plays an important role in the growth and development of the plant for important physiological roles such as increasing the plant’s response to stress conditions (biotic and abiotic) by increasing the resistance of the plant to System Acquired Resistance (SAR) by stimulating or changing the internal paper dissection endogenous signaling to withstand a large number of stresses (Figure.2). Salicylic acid acts as a stimulant or transmitter of the cell to withstand environmental stress conditions such as dryness, coldness, temperatures strain of heavy components, and circumstances of ammonia tension and also increases the plant’s ability to withstand salt tension salt, particularly harmful sodium chloride compound NaCl .Additionally, it has the capacity to form conjugates with some amino acids, including proline and arginine, which improves the plant's capacity to withstand external stressors while also maintaining systemic acquired resilience.

Salicylic acid's ability to promote the creation of antioxidants is one of its most significant impacts. when subjected to thermal duress and other stresses, an antioxidant can prevent the damaging effects of free radicals from the group Reactive Oxygen Species (ROS). A hereditary component of drought stress is that it inhibits the oxidation of cytokinein, oxytin, and algebraic compounds. Antioxidant enzymes like manganese superoxide dismutase have their genes stimulated by it. It has been discovered that raising salicylic acid content internally triggers the defensive function of harmful bacteria, increasing the plant's reaction to tolerance and resilience to different illnesses impacting plants.

The SA plays numerous other crucial physiological functions, including promoting protein synthesis, ion uptake, nutrition transfer, increased CO2 representation, stomata movement regulation, and stimulation of blooming and other physiological processes. It also contributes to increasing the percentage of nucleic acids and amino acids and the accumulation of dry matter and speeds up the formation of various plant dyes and increasing their levels such as chlorophyll and carotene and prevents the representation of ethylene gas, and it is contrary to the work of ABA responsible for the fall of leaves. Additionally, it is crucial for boosting metabolic rates, which aid in the plant's ability to conserve energy through the use of alternate routes and a shift in the concentration of DNA and amino acids.

The phenylalanine ammonia-lyase (PAL) and isochorismate synthase (ICS) pathways in plastids enhance SA biosynthesis[3]. It has been found that SA is originally collected at the local infected tissue during plant-microbe interactions as a part of the defense mechanisms, and then it is disseminated throughout the plant to cause systemic acquired resistance at non-infected distant sections of the plant. In order to develop defenses against viruses and other harmful external factors, plants were able to raise their internal content of SA.

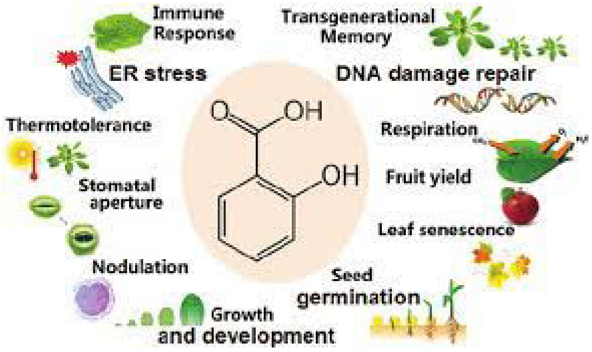

Figure 2: Functions of the salicylic acids: Diagram showing the functions of the salicylic acids in the plant (Research gate).

It is well known that plants have two pathways for producing SA, beginning from chorismate: isochorismate synthase (ICS) and phenylalanine ammonia-lyase (PAL) (Figure.3). Not all of the enzymes that catalyze these processes have been found in plants, though. In various plant taxa, the significance of these routes for the production of SA differs. The ICS pathway is crucial in Arabidopsis, whereas rice's PAL pathway appears to be more crucial for SA buildup. As is the case in legumes, it is also possible for both routes to contribute evenly. Additionally, the control of SA production within the plant may vary. For instance, the baseline SA levels in rice seedlings are significantly greater than those in roots.

In a plant, salicylic acid can go through a number of changes. The majority of them make SA dormant. SA glucoside (SAG) can be created when SA is glucosylated. The vacuole has a big capacity for storing this substance. Another SA sugar compound that can develop in plants is Salicyloyl Glucose Ester (SGE) as a consequence of glucosylation. Methylation renders SA more soluble and enhances its membrane permeability. This product, which the plant can emit, acts as a signal for relationships between plants and insects. Amino acid (AA) linkage, which may be implicated in SA degradation, is another significant change. SA is hydroxylated to produce 2,3- and 2,5-dihydroxybenzoic acid. (2,3-DHBA and 2,5 DHBA). A glycosyltransferase that can change MeSA into MeSA glucoside (MeSAG) has recently been discovered.

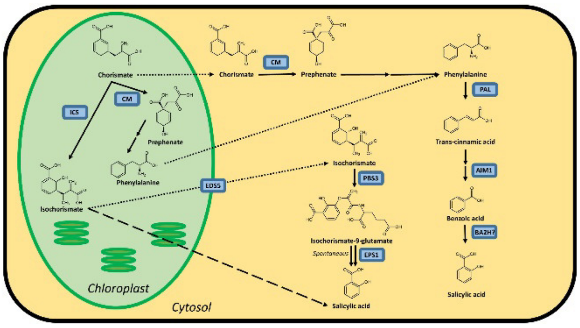

Figure 3: Biosynthesis pathway: Diagram showing the biosynthesis pathway for the synthesis of the salicylic acids in the plant(Frontiers).

The result of sprouting at this early embryonic period is determined by a complicated interplay between SA and both ABA and GAs. GAs play a part in SA production and the SA pathway in Arabidopsis. In comparison to seeds ingested in water and wild-type plants, the ingestion of 50 M GA3 by seeds for 24 hours and the amplification of a GA-stimulated gene from beechnut (FcGASA4) in Arabidopsis plants cause a 2-fold rise in SA levels. Additionally, FcGASA4-overexpressing lines and Col-0 embryos cultivated in the presence of GA3 show higher expression of the ICS1 (isochorismate synthase) and NPR1 (nonexpressor of PR-1) genes, implicated in SA biosynthesis and sensing, respectively. It's interesting to note that under 150 mM NaCl stress, exogenous GA3 (50 mM) barely enhances the germination of the SA-deficient sid2 mutants, whereas exogenous SA (50 mM) partly restores seed germination in the GA-deficient mutant ga1-3.

Despite the fact that these findings point to a beneficial interaction between SA and GA, it was found that SA and GA had a hostile relationship when it came to barley germination, which could be explained by using a greater dosage of SA. By inducing a WRKY regulator, SA inhibits the germination and post-germination development of barley seeds while also suppressing the production of the GA-induced enzyme -amylase (Amy32b). (HvWRKY38). Since SA and ABA upregulate HvWRKY38 expression in aleurone cells while GAs repress it, this transcription factor may function as a convergent node of the SA and ABA signal pathways that inhibit GA-induced seed germination. The enhanced production of ABA-regulated proteins, such as late embryogenesis abundant (LEA) proteins, dehydrins, and heat shock proteins, in Arabidopsis seedlings sprouted in the presence of 0.5 mM SA is additional evidence confirming the interaction between ABA and SA signaling.

LITERATURE REVIEW

A crucial communication component in plants is salicylic acid (SA). There are two suggested routes for SA production in plants. According to biochemical experiments involving isotope feeding, plants generate SA from cinnamate, which is made by the action of phenylalanine ammonia lyase. (PAL). Pathogen-induced SA buildup is decreased by PAL gene silencing in tobacco or pharmacological suppression of PAL action in Arabidopsis, cucumber, and potato. On the other hand, genetic research suggests that isochorismate is the primary source of the majority of SA. Isochorismate Synthase (ICS) and Isochorismate Pyruvate Lyase initiate two processes in microbes that produce SA from chorismate. (IPL). Despite having two ICS genes, Arabidopsis does not have any genes that produce IPL-like proteins. Therefore, it is unclear exactly how SA is produced in plants. PBS3 and EPS1, two newly discovered Arabidopsis genes, are crucial for SA buildup brought on by pathogens.

EPS1 encodes a member of the BAHD acyltransferase subfamily, while PBS3 encodes a member of the acyl-adenylate/thioester-forming enzyme family. An essential precursor or regulating protein for SA biosynthesis may be created directly by PBS3 and EPS1. There may be more complexities than originally realized in the mechanisms and control of SA biosynthesis in plants[4]–[6].

After a disease exposure, plants generate salicylic acid (SA) as an immunological cue to promote systemic acquired resistance. It's the only significant plant hormone whose target hasn't been established. In Arabidopsis, the breakdown of the transcription component nonexpresser of PR genes 1 (NPR1), which serves as a molecular switch, is necessary for systemic acquired resistance. Here, we demonstrate that the SA receptors NPR3 and NPR4, paralogues of NPR1, bind SA with various sensitivities. NPR3 and NPR4 help the Cullin 3 ubiquitin E3 ligase facilitate NPR1 breakdown in a way that is SA-regulated. As a result, the double mutant of NPR3 and NPR4 in Arabidopsis acquires more NPR1 and is resistant to the development of systemic acquired resistance. This mutation also has problems with defense and pathogen-effector-triggered programmed cell death. In reaction to a virus assault, our research demonstrates the process of SA sensing in deciding cell demise and survival.

Salicylic acid cannot be accumulated by transgenic tobacco or Arabidopsis thaliana that expresses the bacterium enzyme salicylate hydroxylase. (SA). Due to this flaw, plants are not only unable to produce systemic acquired resistance, but are also more vulnerable to bacterial, viral, and fungus invaders. Even host-pathogen combos that ordinarily lead to genetic resilience are now more susceptible. As a result, SA buildup is necessary for the manifestation of various plant disease defense mechanisms.

An essential communication component in plant protection is salicylic acid. The process of salicylic acid production and communication in plants has been greatly improved over the last two years. Salicylic acid is produced from chorismate via isochorismate in a route resembling that of some microorganisms. At least two pathways, one of which needs the NON-EXPRESSOR OF PR1 (NPR1) transcript and the other of which is autonomous of NPR1, facilitate salicylic-acid communication. Upstream impulses are modified by salicylic acid-based feedback circuits. These feedback loops might serve as a hub for the fusion of embryonic, ambient, and other defense-related signals, allowing plants to fine-tune their defensive reactions.

Salicylic acid (SA), which caused heat production at values as low as 13 ng g f. wt. 1 in the thermogenic inflorescences of Sauromatum guttatum Schott (voodoo lily), has recently been discovered as the natural catalyst for heat production. Other thermogenic and non-thermogenic plant types have since had their SA levels measured. SA levels during heat generation surpassed 1 g g f wt in male cones of at least four thermogenic cycads and five thermogenic inflorescences of aroid species. SA was not found in the thermal blooms of Bactris major Jacq or the water lily Victoria regia Lindl (Nymphaeaceae). (Palmae). Levels of salicylic acid varied substantially in the floral parts of seven non-thermogenic species and in the leaves of 27 non-thermogenic species .Salicylic acid (SA) is synthesized by plants in response to a challenge by a diverse range of phytopathogens and is essential to the establishment of both local and systemic-acquired resistance (SAR). Pathogenesis-related (PR) protein buildup is brought on by SA administration. Pathogen vulnerability to both avirulent and lethal pathogens is increased by mutations that either result in decreased SA synthesis or diminished detection of SA. However, we only have a basic understanding of the main signaling elements that activate SA biosynthesis and connect to the buildup of PR proteins. We discuss the advances made in identifying the NPR1 and MPK4 as well as the methylation, amino acid conjugation, and S-nitrosylation pathways that contribute to SA-signaling and sensing. We also look at newly available information on pathogens' tactics for suppressing SA-mediated plant defense, including ABA regulation and coronatine production[7]–[9].

Following a pathogen assault, it has been demonstrated that SA plays a significant communication function in activating a number of plant defense reactions. These reactions include enhancing host cell demise, promoting local and general disease resilience, and controlling the dissemination of pathogens. The various methods by which SA exerts these effects include changes in the activity or creation of specific enzymes, greater translation of defense genes, potentiation of a number of different defense reactions, and/or the production of free radicals. Numerous genes encoding proteins implicated in the SA-mediated defense pathway(s) have been identified through the examination of mutated plants displaying abnormal reactions to pathogen invasion. An SA-independent route may also be used to trigger some defense reactions, according to growing data. (s). A short discussion of the SA-independent pathway (s) and its capacity to interact with the SA pathway is also included in this overview, which mainly centers on new findings regarding the SA signaling pathway(s) that contribute to disease resistance.

Plants that have been sensitized to pathogen invasion display increased salicylic acid (SA) buildup, enhanced activation of plant defense genes, and systemic acquired resistance (SAR) to subsequent infection by a variety of pathogens. There is strong proof that SA is essential in starting SAR. Two bacterium genes that produce enzymes that turn chorismate into SA in two steps have been inserted into tobacco. The mutant (CSA, constitutive SA biosynthesis) plants displayed a 500–1,000-fold greater buildup of SA and SA glucoside compared to normal plants when the two enzymes were targeted to the chloroplasts. In CSA plants, defense genes, especially those that code for acidic pathogenesis-related (PR) proteins are produced constantly. The plant shape was unaffected by this expression, but the CSA plants displayed resilience to virus and fungus attacks that were comparable to SAR in non-transgenic plants.

The creation and pharmacological assessment of salicylic acid-containing double glycolate oxidase/lactate dehydrogenase inhibitors are reported. In a simple, two-step synthesis process, the desired molecules are produced. These substances demonstrated low micromolar IC50 values for the two important glyoxylate-metabolizing enzymes. Docking experiments confirm that they work against both enzymes as noncompetitive inhibitors from a mechanistic perspective. Hyperxaluric mouse in vitro and in vivo tests are also a part of the biochemical assessment. The three main hyperoxaluria categories are responsive to the chemicals. Additionally, potential sources of negative effects, such as kidney poisoning or cyclooxygenase suppression, have been researched and ruled out. This makes the drug-like chemotype a strong option for the therapy of primary hyperoxalurias[10].

CONCLUSION

Salicylic acid (SA), which functions as a natural signal regulating both regional and systemic plant resistance against pathogens, has been the subject of much investigation in recent years. Moreover, it has been shown that SA contributes to how plants react to abiotic challenges such as osmotic stress, heat, toxicity from heavy metals, and drought. In this regard, SA looks to be an "effective therapeutic drug" for plants, just as it is for humans. In addition to its role in regulating physiological and biochemical processes under biotic and abiotic stress, SA is essential for the regulation of these processes throughout the plant's entire lifespan. Understanding the molecular mechanism of the synthesis and the mode of action in the different physiological conditions opens a gateway to studying the complete signaling pathway.It will be straightforward to examine the many plant defense mechanisms against pathogens and illness by examining the signaling route. The number of salicylic acid derivatives is growing every day, and they can help treat a variety of human diseases.

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CHAPTER 10

CAROTENOID-DERIVED PHYTOHORMONES KNOWN AS STRIGOLACTONES PLAY IMPORTANT ROLE IN PLANT AND FUNGI SYMBIOSIS

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ABSTRACT:

Carotenoid-derived signaling molecules and plant hormones are known as Strigolactones (SLs). The main function of the Strigolactones (SLs) is to that accessible by the fungi and root-parasitic plants to identify their plants. Apart from that they are also involved in many plant developments like root shoot development. Strigolactones are synthesized by the conical and non-conical pathways in plants. The carotene progenitor proceeds through conversion, cleaving, or further alteration to create caprolactone, which goes through additional oxidizing and alteration to create a variety of strigolactone molecules. A unique method for the sensing of SLs includes an enzymatic sensor of the serine hydrolase type attacking the SLs and becoming covalent changed. As a result, target proteins like transcription factors are ubiquitinated and destroyed by the binding of the ligand with other molecules, such as an F-box protein. In this chapter, we discuss the discovery of Strigolactones, their biosynthesis pathway, and their function. We also cover their site of the perception in the plant and their role in parasitism and plant fungi symbiosis.

KEYWORDS:

Mycorrhizal Fungi, Plant Growth, Plant Hormones, Shoot Branching, Strigolactones Sis.

INTRODUCTION

The first strigolactones were discovered in cotton plants' stems in 1966. However, it took some time to figure out how it affected the development of other species. It was evident from earlier research with Striga lutea that a substance generated in the roots was promoting this process because root preparations from the host plants were required for the infected seed to begin growing. A succession of experiments following the separation of strigolactones demonstrated that this substance was required to trigger the sprouting of Striga species. Later, it was discovered that two related substances, sorgolactone, and alectrol, had the same impact. Because they both had the distinctive lactone group, they were categorized as strigolactones. Only minimal quantities of strigolactones, on the order of 5 parts per million, were required to trigger the sprouting of infected plants

A class of organic substances called strigolactones is created by a plant's roots .These compounds have been categorized as phytohormones or plant hormones based on how they work. So far, three distinct metabolic mechanisms linked to strigolactones have been discovered: First, they encourage the growth of parasitic organisms that reside in the stems of the target plant, including Striga lutea and other members of the Striga family. Second, strigolactones are essential for parasitic fungi, particularly arbuscular mycorrhizal fungi, to recognize the plant because they form a mutualistic relationship with these plants and supply them with phosphorus and other soil minerals. Third, it has been discovered that strigolactones are hormones that suppress branching in plants. When present, these substances halt excessive bud growth in stem ends, which stops the branching process in plants. Although stigolactones are a varied collection, they all share a fundamental molecular structure, as demonstrated in the (Figure.1). The tricyclic lactone, which is shown in the image as the A, B, and C parts, and the hydroxymethyl butenolide, which is shown as the D portion of the molecule, are what make up the structure. It's essential to note that while the ABC portion of most strigolactones varies across species, the D ring remains largely consistent, raising the possibility that the biochemical activity of the molecule depends on this component. Numerous studies have shown that when the C-D portion of the molecules is altered, the function of the molecules is gone[1]–[3].

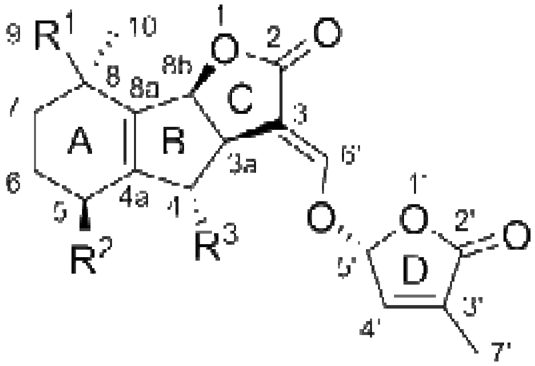

Figure 1: Structure of the Strigolactones: Diagram showing the general structure of the Strigolactones (Wikipedia).

Experiments with carotenoid-deficient mutants and carotenoid biosynthesis inhibitors have indicated that SLs are biosynthesized through the carotenoid pathway before they were discovered as a new family of plant hormones controlling shoot bending. We were then significantly assisted in our understanding of SL biosynthesis by a set of heterozygous mutants with enhanced stalk growth. These mutants include Arabidopsis more axillary growth (max), pea (Pisum sativum) ramosus (rms), petunia decreased apical dominance (dad) and rice dwarf/high-tillering dwarf (d/htd), which have been obtained in genetic studies that aimed to reveal a novel shoot branching regulator other than classical hormones such as auxin and cytokinin (CK). First, it was discovered that the CAROTENOID CLEAVAGE DIOXYGENASE 7 (CCD7) and CCD8 mutants of the plants Arabidopsis max3 and max4, pea rms5 and rms1, and rice d17 and d10 were SL-deficient mutants.

Then, it was revealed that two new iron-binding proteins, rice D27, and Arabidopsis AtD27, were involved in the production of SL. Recombinant D27, CCD7, and CCD8 proteins from Arabidopsis, peas, and rice were used in 2012 by Alder et al. to carry out an outstanding in vitro biochemistry study. They demonstrated that successive processes involving these three enzymes result in the production of carlactone (CL), a non-canonical SL-like molecule, from all-trans-carotene via 9-cis-carotene and 9-cis-apo-10'-carotenal (Figure 2). Recently, a thorough study of the D27, CCD7, and CCD8 enzymes' enzymatic properties was conducted. Later, LC-MS/MS study using liquid chromatography-tandem mass spectrometry (LC-MS/MS) demonstrated that CL is the native substance in Arabidopsis and rice. Furthermore, CL is transformed into 4-deoxyorobanchol (4DO) and ORO, both of which are natural conventional SLs in rice, in feeding studies using stable isotope-labeled CL. This suggests that CL is an intermediate of SL biosynthesis in vivo. Importantly, the exact shape of endogenous CL was found to be (11R) at the D-ring's C-11 location, which correlates to C-2' in native SLs. (Figure 2). Therefore, it is believed that the stereospecificity of the CCD8-catalyzed process to produce (11R)-CL is essential for the stereochemistry of SLs

In vascular plants, the CYP711A subgroup of cytochrome P450 oxygenases performs the conversion of CL into both canonical and non-canonical SLs. In Arabidopsis, CYP711A was first connected to the production of SL. It was demonstrated that the CYP711A1-defective Arabidopsis max1 mutant showed the same hyper-branching trait as max3 and max4. Grafting studies have indicated that MAX1 works after MAX3 and MAX4. Additionally, the native CL level was dramatically elevated in the max1 mutation, indicating that CL is a substrate for MAX1.

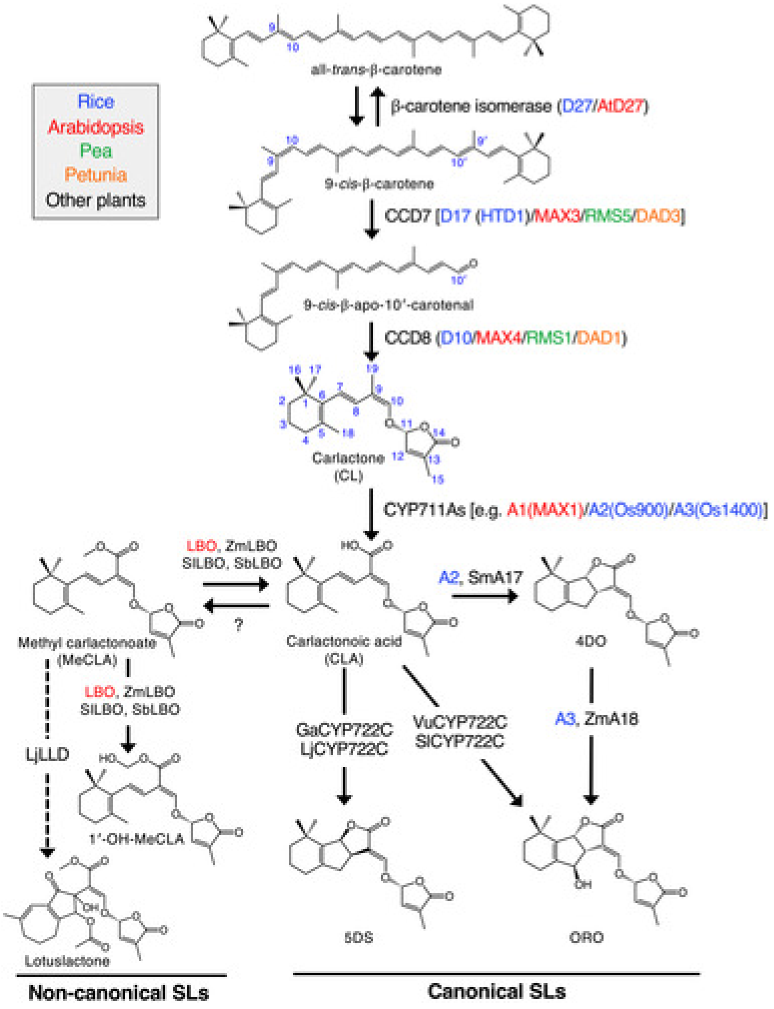

Figure 2: Biosynthesis pathway: Diagram showing the biosynthesis pathway of the Strigolactones (Online library).

Recombinant MAX1 protein was found to be responsible for the conversion of CL into carlactonoic acid (CLA) in Arabidopsis via 19-hydroxy-CL. This finding raises the possibility that MAX1 catalyzes three-step oxidations of the methyl group at the C-19 location to a carboxylic acid (Figure 2). The substrate specialization of MAX1 may also be required for the effective creation of the (2'R)-configured SLs because it favored (11R)-CL to (11S)-CL as a substrate. Additionally, they demonstrated that although CYP711A17v1/v3 of Selaginella moellendorffii and CYP711A18 of maize (Zea mays) could both initiate the A2- and A3-type reactions, respectively, converting CL to 4DO via CLA (CYP711A2-type) and converting 4DO to ORO (CYP711A3-type) were not universal reactions. According to these findings, CYP711As are crucial for the production of both canonical and non-canonical SLs.

Endogenous strigolactones have been assigned three functions: (1) promoting the sprouting of parasitic plants, (2) regulating arbuscular mycorrhizal fungi (AMF) to increase the plant's effective soil interaction, and (3) controlling the stem canopy. Tricyclic lactones are released by plants, and in modest quantities, they appear to promote the growth of parasitic vegetation. Strigolactones have also been discovered in the root secretions of plant species that these obligatory pathogens have not taken over. Regulating AMF growth is the second function of strigolactones that has been proposed. AMF are believed to have developed 400 million years ago and may have helped plants colonize the land, but we are just now starting to understand how important they are for regulating nitrogen absorption. The mutualistic relationship that these obligatory biotrophic creatures establish with more than 80% of land plants makes them both environmentally and commercially important. AMF hyphal growth is increased by strigolactones, which are released by plant roots and may also increase the likelihood that hyphae will associate with the plant roots. The regulation of plant stem growth appears to be a third crucial function of strigolactones. Strigolactones or chemically similar substances serve as signaling hormones that regulate the morphology of the plant canopy, according to recent scientific developments involving grafting studies

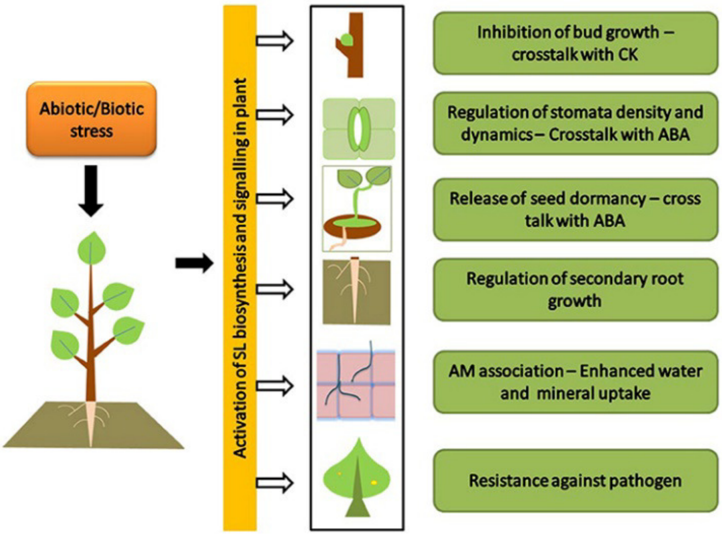

Figure 3: Function of Strigolactones: Diagram showing the different functions of the Strigolactones in the plants (Frontiers).

The dual receptor/hydrolase protein DWARF14 (D14), a member of the / hydrolase superfamily, detects strigolactones in plants. The biochemical activity of the protein depends on a complete catalytic trio despite the fact that these hydrolases are thought to have low substrate turnover .According to research on molecular dynamics, the ligand binding region is adaptable and the catalytic trio is crucial for ligand binding and placement. The D-ring is chemically bonded to the serine in the active site as a consequence of strigolactone hydrolysis. A loose D-ring produced by the hydrolysis of strigolactone acts as a molecular adhesive at the receptor's entryway and mediates contact with another protein. binding of an undamaged, non-hydrolyzed strigolactone result in a changed DWARF14 protein surface that facilitates protein contact. The D-ring is chemically bonded to the histidine in the active site as a consequence of strigolactone hydrolysis. When strigolactone is hydrolyzed, the D-ring is simultaneously chemically linked to the serine and histidine in the active site, changing the shape of DWARF14 and opening the door for protein contact. According to kinetic data, the undamaged strigolactone initiates a signaling chain before being hydrolyzed as the last stage to render the strigolactone molecule inactive.

In almost every conceivable farming setting, the joint functions of strigolactones in the control of plant root-fungal interactions as well as in the formation of stem and foliage cover are crucial factors to take into account. The three hypothesized functions of strigolactones in controlling root and plant growth can work in concert. Think about how phosphorus supply affects AMF and plants, for instance (Figure.3). Strigolactone concentrations are influenced by soil minerals, particularly phosphorus, and as a result, strigolactones may control AMF association, parasitic plant growth, and stem budding. Throughout the plant's life cycle, shoot growth regulates the extent of the foliage cover and main respiration. The study of strigolactones, as well as the movement of these substances within a plant, is still in its early stages. Because strigolactones are carried acropetally and prevent axillary budding, they may control crop canopy development in response to nutritional status when phosphate supply is constrained. Clearly, a deeper comprehension of the genetic and biochemical regulation of this significant family of terpenoids is required for future concerns in agricultural development regulation.

LITERATURE REVIEW

Strigolactones are a group of carotenoid-derived plant hormones that affect numerous metabolic processes in plants as a result of external duress. Additionally, they serve as external cues recognized by both infected plants and mycorrhizal fungi. Possible biological uses were stimulated by these compounds' unique molecular structure and method of action in plants. An summary of the most current uses of strigolactones and their related compounds as antitumor, anti-inflammatory, and antiviral medications is provided in this minireview.

SLs exert their control over physiological and developmental processes by directly or indirectly affecting the actions of other hormones and/or components of other growth regulators' signaling pathways. These, among many others, include modulation of hormone content, transport, and distribution within plant tissues, interference with or complete dependence on downstream signal components of other phytohormones, as well as acting synergistically or antagonistically with other hormones to elicit plant responses. The impacts of SL relationships with other hormones on cells and entire plants have been extensively studied, but more work needs to be done to clarify the exact biochemical processes that underpin these processes. More so in the cases of salicylic acid, abscisic acid, cytokinins, gibberellin, and jasmonates, for which very little information has been published about their endocrine interactions with SLs.

Plant hormones are key regulators of how plants grow and evolve. Hormones control the rate of plant development, while metabolism gives the energy necessary for plant life. Strigolactones (SLs) are a novel class of phytohormones that control the metabolism of plants, which in turn controls their growth and development. This group of phytohormones is derived from carotenoids and has been implicated in a wide range of physiological functions including regulation of plant architecture (inhibition of bud outgrowth and shoot branching), photomorphogenesis, seed germination, nodulation, and physiological reactions to abiotic factors. Arbuscular mycorrhizal fungus (AMF) spores are also induced by SLs to undergo hyphal branching, which is crucial for establishing the link between recipient plant roots and AMF. The biochemical functions of SLs are described in this overview, along with the importance of relationships between SLs and other phytohormones to plant metabolic responses.

Strigolactones (SLs), which are primarily biosynthesized in roots, control a variety of facets of plant growth and development. In this paper, we discuss current studies on the function of SLs and how auxin, cytokinin, and ethylene interact to modulate root growth and development. In eudicot plants, SLs control main root growth and prevent adventitious root development when nutrients are abundant. In the near term, SLs suppress lateral root growth in both grass and eudicot plants while promoting the lengthening of generative roots and increasing the quantity of adventitious roots in grass plants. SLs can have a variety of impacts on the lengthening of root filaments, depending on the type of plant, the growing environment, and the SL content. Lack of nitrogen or phosphate inhibits the growth and development of roots by causing the buildup of endogenous SLs. Genetic studies show that SLs and auxin, cytokinin, and ethylene are cross-regulated in the control of root growth and development. We address the ramifications of these studies and take into account their potential for utilizing SL signaling components in the design of agricultural plants that more effectively utilize soil resources.

Numerous naturally occurring phytohormones have demonstrated tremendous promise in the avoidance and therapy of numerous cancer types. Strigolactones (SLs), a unique family of plant hormones made in the roots, control the budding of new above-ground shoots by preventing undifferentiated meristem cells from self-renewing. Here, we investigate the development and longevity of six breast cancer cell lines treated with synthesized SL analogs. We demonstrate that "non-cancer" lines are only slightly affected by SL analogs' ability to suppress growth and cause death in breast cancer cells. We also evaluated the capacity of SL analogs to suppress the development of mammosphere cultures that are usually loaded with cancer stem-like cells in light of the treatment issue of cancer return, which is believed to be caused by drug-resistant cancer stem cells. We demonstrate that SLs are powerful antagonists of breast cancer cell lines produced as mammospheres' ability to self-renew and to survive and that even brief exposure to SLs causes permanent effects on mammosphere separation and cell mortality. According to an immunoblot study, SLs analogs suppress PI3K/AKT activation while inducing the stress response, which is mediated by the P38 and JNK1/2 MAPK modules. All things considered, this research suggests that SLs may be effective antitumor drugs whose actions may be regulated by stress and survival signaling pathways[4]–[6].

In this study, we made molecular counterparts of natural strigolactones with a butenolide D-ring substituted by a -lactam and assessed their biochemical activity. An RCM on appropriately modified amides was essential for producing the,-unsaturated lactam. Plant hormones known as strigolactones (SLs) have a variety of physiological roles. They are necessary for creating an advantageous mycorrhizal plant/fungus relationship because they act as soil communication molecules. In addition to these auxinic functions, SLs have lately been effectively researched as antitumoral drugs. The hormone receptor's enzyme action is peculiar to the SL sensing system. The butenolide D-ring is essential for maintaining cellular activity, according to SARs data. A lactam could be used to replace the butenolide, which could provide insight into how vision works. The binding mechanisms of the synthetic substances to the plant receptor for SLs were then proposed by a focused in silico study.

Strigolactones are phytohormones with various signaling functions that share a structure with two lactones joined by an enol-ether linkage. Strigolactones are produced by a process that includes the iron-binding protein D27, the carotenoid cleavage dioxygenases 7 and 8 (CCD7 and CCD8), and carotenoids. We demonstrate that D27 is an enzyme that changes all-trans-carotene into 9-cis-carotene, which is then broken down by CCD7 into a 9-cis-configured aldehyde. When CCD8 links carotenoids with strigolactones and conducts chemical rearrangement on 9-cis-apo-10′-carotenal, it creates carlactone, a substance with strigolactone-like pharmacological properties. Understanding the structure of carlactone will be essential for comprehending strigolactone biology and could be useful in the fight against parasitic weeds. Strigolactones (SLs), a newly identified family of phytohormones, play a significant role in controlling plant development and growth. Although the biosynthesis process for these compounds is well known, little was previously understood about the molecular processes underpinning SL sensing and signal transmission in plants. Other phytohormones share some of their sensing and signaling properties, such as the hormone-mediated contact between the receptor and the F-box protein, the destruction of suppressor proteins, and the stimulation of transcription factors. Some SL signaling characteristics, however, appear to be unique to the SL signaling system. These include the SL receptor's enzyme function and the instability brought on by SLs. The information on the SL signaling system in plants is summarized in this review.

The new plant growth factors karrikines and strigolactones share many chemical characteristics, but little is known about how they affect plant behavior. A Michael-type addition for both molecules has previously been suggested as a possible chemical process. We now suggest a different mechanism for karrikin and strigolactone mode of action that includes degradation of the butenolide ring based on structure-activity experiments with karrikins[7].

CONCLUSION

The unique class of plant hormones known as strigolactones has gained recognition over the past ten years.

These participate in the regulation of important parts of growing-up activities such as horizontal branch extension and the formation of leaves and roots, among many others. Moreover, strigolactones control how plants react to abiotic challenges including dehydration and phosphorus deficiency. Several activities for strigolactones within the regulation of plant growth and physiological stress, in addition to some of their known species-specific effects, are summarised below according to present understanding. We will also go through its biosynthesis pathway and its function in symbiosis.

The potential to use strigolactones and their potential symbiosis mechanism as tools to optimize species of critical agronomic value has been raised by the recently identified actions of such chemicals as phytohormones.

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CHAPTER 11

OTHER PHYTOHORMONES; PLANT PEPTIDES, NITRIC ACID, POLYAMINES, KARRIKINS, AND THE TRIACONTANOL

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ABSTRACT:

Plant growth and development are regulated by a different set of hormones known as phytohormones. Apart from the phytohormones plant also synthesized some growth regulator molecules which are categorized as the other phytohormones. These types of phytohormones include nitric acid, plant peptide hormones, polyamines, Karrikins, and Triacontanol. In this chapter, we discussed the importance of these hormones in brief.

KEYWORDS:

Growth Developments, Growth Regulators, Nitric Oxide, Receptor Like, Seed Germination**.**

INTRODUCTION

For growth and development, plants need sun, water, air, minerals, and other elements. In addition to these exterior needs, plants also rely on specific chemical molecules to communicate, govern, and modulate their development. Plant growth regulators or plant growth hormones are the group names for these. In the same way that plants need air, water, sunshine, and food to grow and develop, they also need certain organic compounds to control that growth and development. Plants naturally generate what is referred to as "Plant Growth Regulators," which are chemicals. These are straightforward organic compounds with various molecular make-ups. Phytohormones, plant growth agents, or plant growth hormones are other names for them.

They have the ability to both speed up and slow down plant development. The following traits are displayed by plant growth factors or hormones: Cellular differentiation and extension, growth of foliage, blooms, and stalks, leaf wilting, fruit ripening, seed stasis, etc. Plant hormones can be broadly divided into five categories: auxin, gibberellins (GAs), cytokinins, abscisic acid (ABA), and ethylene. There are additional constituent substances, both natural and manufactured, that have similar effects on plant development. There are some additional growth regulators besides the primary ones like auxin, Gibberellin, ABA, and jasmonate, etc. among the additional recognized plant development factors are:

All tiny released peptides that are engaged in cell-to-cell communication are referred to as plant peptide hormones. These tiny peptide hormones are essential for the growth and development of plants, as they regulate defense mechanisms, cell proliferation and expansion, and pollen self-incompatibility. Water stress detected in the roots is known to be transmitted to the stomata in the leaves by the tiny peptide CLE25, acting as a long-distance communication. The biggest family of receptor-like molecules in plants, membrane-localized receptor kinases, have been discovered as the particular receptors for different peptides that play a major role in various facets of plant growth and development. The following protein groups have constituents that are signaling peptides. Activating molecular protections against predators requires a long-distance communication, which systemin serves as. The peptide nature of this plant hormone was first established. The CLV3/ESR-related ('CLE') peptide family is encoded by the CLV3 gene, which produces a tiny released peptide that acts as a short-range ligand for the membrane-bound CLV1 receptor-like kinase, which, along with the receptor-like protein CLV2, serves to sustain stem cell equilibrium in Arabidopsis shoot apical meristems. An early nodulin gene called ENOD40, or simply ENOD, is thought to putatively produce two short peptides, one with 12 amino acids and the other with 18. There is debate over whether peptides themselves or mRNA are in charge of bioactivity. The "conditioning factor" phytosulfokine (PSK) was first discovered in cell preparations of asparagus and carrot.POLARIS (PLS) — The PLS peptide, which is expected to be 36 amino acids long but lacks a release signal, likely performs its role in the cytoplasm.

Although the PLS peptide itself has not yet been biochemically separated, loss-of-function mutants have increased cytokinin sensitivity and decreased auxin reactivity. While extracting systemin from tobacco leaves, the 49 amino acid peptide known as fast Alkalinization Factor (RALF) was discovered. It induces fast medium alkanalization but does not trigger immune reactions like systemin. ROT4/DVL1 (ROTUNDIFOLIA4/DEVIL1) — The proteins ROT4 and DVL1 have a significant degree of genetic similarity and are 53 and 51 amino acids, respectively. They are two of the 23 peptide family members. On the lengthwise plane of organs, ROT4 and DVL1 are engaged in controlling the growth of polar cells.

Polyamines are weakly base, low-molecular-weight compounds that have been discovered in all of the species so far. They have an impact on the mitotic and meiosis processes and are crucial for the growth and development of plants. Polyamines have been connected to the regulation of aging and planned cell demise in plants. The biochemical role of polyamines is only partially understood, despite the fact that it is well known that the production of polyamines is tightly controlled. They attach to DNA in their cationic ammonium form, and in contrast to Mg2+, they reflect molecules with cations that are found at regular intervals in their structure. which are penalties (points). Additionally, it has been discovered that they support translational frameshifting that has been encoded into the ribosomes.

Cell development is slowed or stopped when the production of polyamines is inhibited. Exogenous polyamines are given to reestablish the development of these cells. The majority of mammalian cells have an ATPase that transports polyamines on their cell membrane, making it easier for foreign polyamines to be absorbed. Some chemotherapeutics presently in research have this system as their target because it is extremely active in cells that proliferate quickly.

Additionally, polyamines influence a number of ion channels, such as NMDA and AMPA receptors. They inhibit inward-rectifier potassium channels, causing the currents to be internally rectified and preserving the cellular energy represented by the K+ ion gradient across the cell membrane. Additionally, polyamine helps to start the translation of the Colicin E7 operon's SOS response and down-regulates proteins necessary for colicin E7 absorption, giving colicin-producing E. coli a survival edge under stressful circumstances.The blood-brain barrier's porosity can be improved by polyamines. They are regarded as plant hormones because they play a role in controlling the aging of plant tissues. They also play a fundamental role in the control of planned cell demise.

An important indication in endocrine and defensive reactions is nitric oxide (NO). (e.g. stomatal closure, root development, germination, nitrogen fixation, cell death, stress response). NO regulates the activities of plant cell organelles and can be generated by an as-yet-unidentified NO synthase, a particular form of nitrite reductase, nitrate reductase, mitochondrial cytochrome c oxidase, or non-enzymatic mechanisms. (e.g. ATP synthesis in chloroplasts and mitochondria). In plants, nitric oxide can be produced by any of four routes:

(i) L-arginine-dependent nitric oxide synthase, (although the existence of animal NOS homologs in plants is debated), (ii) plasma membrane-bound nitrate reductase, (iii) mitochondrial electron transport chain, or (iv) non-enzymatic reactions. It is a communication protein that primarily combats oxidative stress but also participates in relationships with plant pathogens. Nitric oxide treatments have been shown to extend the time before withering in plants and cut flowers. Additionally, NO controls the growth of peripheral and adventitious roots, root filaments, association (such as with organisms in nitrogen-fixing root clusters), regulation of stomatal opening, and some plant-pathogen interactions. Cellular structures such as mitochondria, peroxisomes, and chloroplasts are known to generate nitric oxide.

It contributes to the reactions to reactive oxygen species and antioxidants. The N-end regulation of proteolysis mediates nitric oxide detection in plants, which regulates abiotic stress reactions like hypoxia brought on by inundation, salinity stress, and dry stress. Auxin, ethylene, abscisic acid, and cytokinin are examples of plant chemicals with communication networks that interact with nitric oxide. Most vascular species have stomates that can be penetrated by atmospheric nitric oxide, which can have impacts varying from death to foliage blemishing. Karrikins are not plant hormones because they are not made by plants but rather by burning plant matter, where they are discovered in the dust. In many species, karrikins can aid in seed development. Some have proposed the presence of an as-yet-unidentified karrikin-like natural hormone in plants based on the observation that plants lacking the karrikin receptor exhibit a number of developmental traits (increased biomass buildup and increased susceptibility to dehydration, for example).

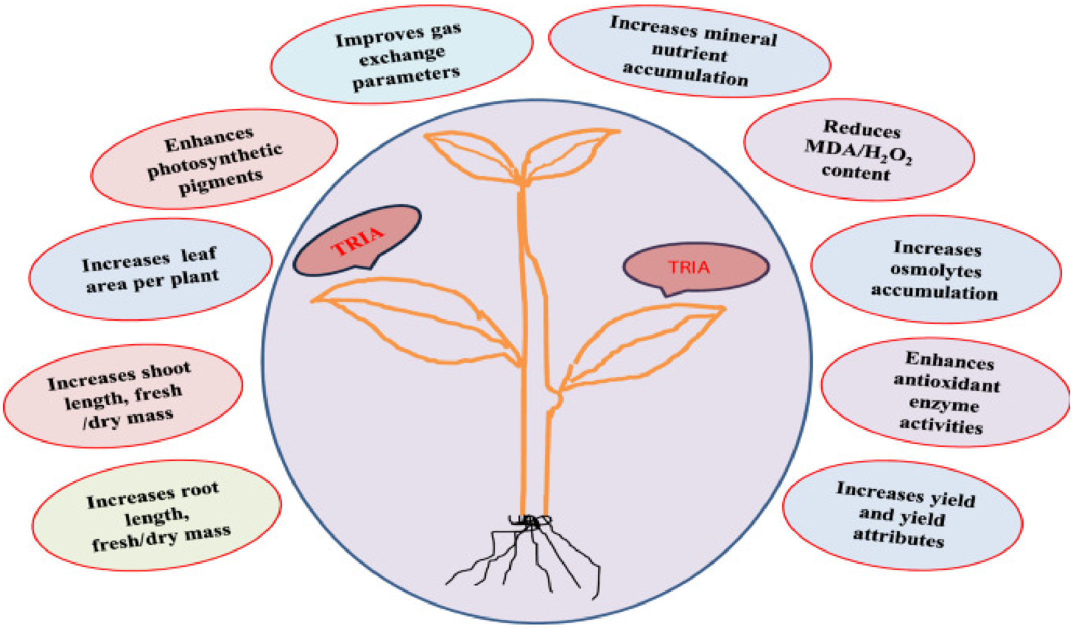

Figure 1:Triacontanol function: Diagram showing the different functions mediated by the Triacontanol (Springer link).

Numerous elements of the strigolactone signaling pathway and the cellular karrikin signaling pathway are shared. Karrikins from bushfires are primarily found in the debris at the fire's location. After-fire rains drive the karrikins into the earth, where latent seeds are found. Such seeds may receive a "wake-up call" from the karrikins and water, resulting in the sprouting of the earth's seed bank. "Fire-followers" are plants that rely on karrikins to develop; they appear, expand rapidly, bloom, and generate new seeds that fall to the ground. Until the next fire creates new karrikins, these spores can survive on the earth for decades. The term "fire ephemerals" refers to plants that live in this way. They flourish as a result of the fire's removal of rival flora and provision of sunshine and nutrition to newly sprouting plants. Smoke and karrikins cause responses in plants across many families, which suggests that these responses have separately developed in various groups.

Other plants than just fire-followers react to karrikins. Trees, vegetables, cabbage, and other seeds from numerous blooming groups react to karrikin communication. Interestingly, other research has discovered that seeds from species that are supposedly fire-adapted do not exhibit karrikin sensitivity. The reliance on karrikins distinguishes plants that react to karrikins from plants that follow fire. Because karrikins imitate the strigolactone hormones that plants initially needed for development, their impact on how plants react to them is critical. On the other hand, fire-followers have tailored their reactions in accordance with the accessibility of karrikins. Triacontanol is a fatty alcohol that stimulates development, particularly starting new basal breaks in members of the rose family.

Alfalfa (lucerne), beeswax, and some viscous leaf surfaces all contain it. Triacontanol accelerates cell reproduction in plants, resulting in bigger roots and branches. Triacontanol has been demonstrated to improve hormone efficacy and root enzyme activity when administered to plants during their peak development phase. This increases the plant's total performance. Triacontanol essentially works by improving a plant's fundamental processes, such as speeding up photosynthesis and creating more sugar or glucose. A plant produces more carbohydrates and absorbs more sunshine when photosynthesis is functioning properly in that plant (Figure.1). The plant then uses its root system to transfer more carbohydrates to the rhizosphere, which is where food exchange, metabolism, and development occur close to the earth. More carbohydrates being available causes more metabolism and nutritional interaction between the soil's microbes and plants.

The microbial activity in the root zone rises when the bacteria obtain more carbohydrates from the plant, and they work more effectively to mine the nutrients, as in the case of nitrogen fixation. These microbes in particular track the soil's vital minerals. The plants continue to use these nutrients to create more complicated nutrients and chemicals necessary for their quick development and defense against specific other microorganisms. The crop's production is maximized by these intricate chemicals. Overall, even though sufficient amounts of triacontanol have other advantages, simply increasing photosynthesis makes plants more effective in a variety of ways.

LITERATURE REVIEW

Karrikins are a family of chemically characterized plant growth factors that were found in the fumes produced when burning plant matter. Karrikins are effective at waking up seeds of numerous species that have evolved to habitats with frequent fire and smoke. Karrikins have recently been found to regulate seed germination and plant development in species that would only occasionally experience fire, indicating that their importance may go far beyond fire ecology. Recent research that demonstrates how carefully and precisely Arabidopsis thaliana seedlings react to karrikins in smoke serves as an example of this. If karrikins are created in the environment by processes other than fire, such as chemical or microbial decomposition of plants in reaction to disruption of the soil or elimination of the plant canopy, these fascinating findings might be explained. Another theory is that plants naturally produce endogenous karrikins that regulate seed development and that species from environments prone to fire have adapted to react to external karrikins as well. The idea that karrikins imitate naturally occurring plant chemicals like terpenoids, which regulate seed development, is a variation on this one. Whatever the reason, karrikins are now securely established as a significant family of naturally occurring plant growth regulators [1].

The merging of embryonic processes is greatly aided by plant hormones. Environmental variables frequently have causative impacts on a plant's metabolism and hormone dispersal by causing changes in those hormones. In addition to that, they control how well plants show their inherent genetic potential. The phytohormones' ability to regulate DNA expression at both the transcriptional and translational stages has been established. On the membrane surface, hormone-specific receptors and binding proteins have also been discovered.For the majority of grown plants, and particularly for crop plants, the use of growth inhibitors has become a crucial part of agro-technical processes. Plant growth hormones can currently be applied exogenously to fruit fields to reduce excessive fruit loss. Auxin and gibberellins are frequently used to reduce fruit loss and enhance produce flavor. Several agencies are in charge of removing some fruits from the ontogenic development from fruit establishment to fruit maturation and ultimate reach to consumer. We concentrate on the key roles that plant growth factors play in the creation of food in this review [2].

Plants produce triacontanol (TRIA), which is a constituent of the majority of organic matter. Femtomolar levels of new TRIA compounds have demonstrated efficacy. Small quantities of TRIA can be found in spongy tissue even though the bulk of TRIA in plants is attached to (and found in) the epidermis. Numerous metabolic and molecular processes are directly or tangentially regulated by exogenous doses of TRIA. Numerous studies have demonstrated that TRIA can boost agricultural yields, but in the United States, the findings have not been reliable enough to support its business application. TRIA, a derivative of TRIA or a secondary messenger, may travel quickly in plants after initial administration, according to several studies. The optimal ambient circumstances for treatment and changes in the concentrations of several compounds suggest that glucose metabolism may be implicated in the plants' reaction to TRIA. Additionally, after TRIA therapy, the activity of several enzymes involved in glucose digestion increases. Before aerial treatments, warm temps enhanced the plants' reaction to TRIA. Numerous substances have an adverse impact on how plants react to TRIA. Phthalate esters, which are frequently found in water and the study setting, are the most important. The conflicting findings that several scholars have observed in the classroom and outdoors could be explained by this pollution. With a speed not seen with other plant hormones or growth regulators, TRIA has induced numerous growth reactions in plants [3].

Recent molecular and genetic research has shown that peptide communication has a more significant impact on different facets of plant growth and development than previously thought. Many of these peptides are secreted and function as regional cues that facilitate cell-to-cell contact. The biggest family of receptor-like molecules in plants, membrane-localized receptor kinases, were discovered to be specific receptors for a number of peptides. These results highlight the significance of peptide signaling in the control of plant development, behaviors that were traditionally attributed to the joint action of what is known as "traditional plant hormones," tiny lipophilic substances. Here, we provide an overview of recent developments in our knowledge of physiologically active peptides found in plants, which are presently thought to represent a novel family of plant hormones [3].

Auxin, cytokinin, ethylene, gibberellin, and abscisic acid are examples of traditional phytohormones. Plant peptide hormones are also engaged in different facets of growth and development. This class of phytohormones is made up of short peptides that typically act as receptor kinase ligands to start a signaling chain that controls plant growth in reaction to internal or exterior environmental cues. The overview looks at the peptide phytohormones that have been discovered so far, including their structure, production characteristics, receptors, and function in plant development [4].

An essential family of communication molecules that mediates embryonic impulses between plant cells is peptide hormones. Specific external peptide ligands attach to membrane-bound receptors to facilitate cell-to-cell transmission. In this overview, we highlight newly discovered peptide hormones with a focus on their chemical shapes. We will discuss the specific metabolic functions of the CLE family of peptides in a variety of plant species, including Arabidopsis, agricultural species, and bryophyte models [5].

While other polyamines are present in smaller amounts in plant cells, the diamine putrescine, the triamine spermidine, and the tetramine spermine are present in all plant cells. Their chemical and metabolic and biosynthetic routes have been extensively studied. In addition to being attached to different proteins and tiny compounds like phenolic acids, they also exist in the unbound form of cations. Their concentration fluctuates between about micromolar and more than millimolar and is highly influenced by external factors, particularly stress. By almost every observed external stimulus, the activity of arginine decarboxylase, one of the main polyamine biosynthesis enzymes, is quickly and drastically raised in grains, resulting in 50-fold or higher rises in putrescine concentration within a few hours. Although the majority of recent research points to an adaptive, defensive function, the biochemical meaning of this rise is still unclear. Contrarily, it appears that polyamines generated by ornithine decarboxylase are necessary for cell division and DNA reproduction. Exogenous polyamine administration has an impact on morphogenetic and senescence patterning, implying but not demonstrating a regulating function for polyamines in these processes. There is increasing support for such a regulating role [6].

NITRIC OXIDE'S PHYSIOLOGICAL EFFECTS:

Nitric oxide production by the arterial endothelium keeps a bronchodilator tone that is vital for controlling blood flow and pressure levels. Nitric gas facilitates cell-cell signaling in the brain. Nitric oxide is also produced by numerous neurons that were originally categorized as non-adrenergic and non-cholinergic in the peripheral nervous system. This straightforward diffuse molecule thus serves a multitude of biochemical purposes.

THERAPEUTIC MANIPULATION POSSIBILITIES:

Nitric oxide sources can be given (for hypertension, cholesterol, gastric, and genitourinary diseases) or nitric oxide gas can be inhaled to counteract impaired nitric oxide generation. (in chronic pulmonary hypertension or adult respiratory distress syndrome). The greatest challenge is to create tactics that specifically target nitric oxide's harmful and deleterious effects without affecting its vital defensive functions [7].

It is now known that free radical and gas nitric oxide plays crucial metabolic functions. The three variants of nitric oxide synthase, one of which is inducible and capable of producing much higher levels of NO, are used to synthesize it enzymatically from the amino acid L-arginine in a variety of organs. In addition to preventing blood platelet activation, NO plays a crucial role in the endothelium-dependent control of blood flow and pressure. At least in some kinds of neurons, NO is recognized as a messenger. Along with other free radicals, NO plays a crucial role in the body's initial defenses against microorganisms. NO interacts closely with proteins that contain iron and attach to hemoglobin. Through this process, NO triggers the soluble guanylyl cyclase enzyme, which contains haem and is triggered a thousand times to create the signaling substance cyclic GMP. This has numerous biochemical effects to educate the pathways that spread the various metabolic effects of NO [8].

We have looked into whether curcumin, a substance with anti-inflammatory and antitumor action, can directly scavenge nitric oxide because it suppresses the production of nitric oxide synthase in stimulated macrophages and has been shown to be a powerful free radical scavenger. The quantity of nitrite produced by the interaction of air and the nitric oxide produced by sodium nitroprusside was decreased by curcumin. The methoxy and phenolic groups are not necessary for the antioxidant action of curcumin, according to other similar substances like demethoxycurcumin, bisdemethoxycurcumin, and diacetylcurcumin. The findings suggest that curcumin is a nitric oxide absorber. The curative effects of curcumin against these diseases may be at least partially explained by its free-radical quenching qualities, including those toward nitric oxide, given that this substance has been linked to cancer and inflammation [9].

Many facets of plant growth and development are regulated by stragolactone (SL) and karrikin (KAR) signaling through comparable processes that make use of cognate /-fold hydrolase-receptors and a shared F-box protein known as MORE AXILARY GROWTH2 (MAX2) in Arabidopsis or DWARF3 in rice. Although SUPPRESSOR OF MAX2-1 (SMAX1), a similar protein, is believed to be involved in the reaction to KAR in Arabidopsis, D3 facilitates the SL-dependent ubiquitination and proteolysis of DWARF53 (D53), a protein considered to be involved in the regulation of gene expression. The D53/SMAX1 multigene family presumably mediates a variety of reactions that affect plant growth and development. Numerous genes that are controlled by SL or KAR have been found through analysis of reactions to these substances. There is also evidence of crosstalk with other signaling systems, such as radiation, hormones, and abiotic stress. Here, we evaluate the best way to move forward in gaining a better grasp of the goals and operations of the SL and KAR signaling systems [10].

CONCLUSION

A range of traits and procedures, notably cell size and variety, fertilization, plant responses to food availability, and pathogen defense, have been reported to vary as a result of peptide hormone regulation of gene expression in plants. Nitric oxide (NO) is a straightforward, widely distributed signaling molecule that is crucial to practically every cellular function. Emerging data point to the possibility that NO functions as an endocrine molecule. Recent research points to NO as a hormone that, after being produced in tissues, is stabilized and transported to target cells as nitrite and/or S-nitrosothiols in the blood. As an innate plant growth regulator, triacontanol (TRIA) promotes a variety of metabolic processes that benefit plant development and growth. Also, by controlling the activity of the drought tolerance pathways, TRIA is crucial in reducing the effects of stress on agricultural plants. Karrikins (KARs), which can improve germinating seeds for a variety of plant species, have been discovered as chemicals produced from plant matter smoke. KARs, however, were shown to influence a variety of biological systems in addition to germinating seeds.

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CHAPTER 12

AN OVERVIEW OF THE USE OF PHYTOHORMONES IN HORTICULTURE, AGRICULTURE

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ABSTRACT:

In the plant different metabolic pathways substances generated small biological molecules known as phytohormones. The plant comprised a group of phytohormones, which regulated their biological and physiological function to maintain plant growth, development, and morphology. Biologically study the plant required to grow these plants in the *in vitro* condition. Apart from the biological study agriculture productivity also depends upon plant growth. There are several factors biotic and abiotic factors that influenced plant growth during *in vitro* cultivation. Apart from these factors, there are several others factors like salt concentration, water availability, and pathogenic. These occurrences have captivated the scientific community in recent years to prevent the disastrous impacts that climate change is having on agricultural productivity and get more food to meet the rising food requirements of the growing population. As a result, it is expected that finding different plant hormones and using them to enhance metabolic activity in plants will assist preserve plant life, life. To mitigate the negative effects of biotic and abiotic promote sustainable agriculture, this chapter focuses on defining the essential phytohormones involved in horticulture.

KEYWORDS:

Abiotic Stress, Abscisic Acid, Growth Regulator, Horticulture Crops, Seed Coat.

INTRODUCTION

Due to recent worldwide climate change and the fast increase in the human population, agriculture output is declining. To support future large populations, it will be necessary to enhance and increase the essential farming yields by almost 70% by the middle of the century. The growth of garden products is also negatively impacted by climate change. Since modernization and cities have increased climatic extremes, crop growth, and output are steadily declining. The yield of garden products is severely constrained by a number of biotic (like bug pests and illnesses) and abiotic stressors (like dehydration, salt, heavy metals, and temperature extremes). Plant reaction to various external duress circumstances is one of the most difficult parts for plant experts.

Major abiotic limitations affecting plant health at the development, production, and quality phases include a lack of water, an overabundance of minerals, and extreme temperatures. A new requirement for protecting against abiotic stressors is the creation, classification, and assessment of resistant genotypes. While some conventional methods have been used to create adaptable genotypes, they are time-consuming, labor-intensive, and unable to completely eradicate multiple stressors. As a result, suitable measures are being created to meet the global population's dietary requirements. Additionally, it is essential to create adequate and acceptable methods in the current period to resolve the issues with prejudice in agricultural products. Hence, the exogenous application of phytohormones (including salicylic acid, abscisic acid, ascorbic acid, melatonin, brassinosteroids, strigolactones, jasmonates, auxins, ethylene, cytokinins, and gibberellins) may be an accurate and concise option for the production of climate-resilient crops with higher yields and excellent quality[1]–[3]. SA has been regarded as one of the phytohormones that can help many agricultural products improve their ability to tolerate abiotic stress while still being environmentally benign. According to, SA is useful in many ways, even at very low concentrations, for controlling plant growth and reproductive phases in reaction to adverse situations. Due to SA, regulation of internal and exterior stimulation is promoted, which furthers the significant changes in agricultural products' growth processes.

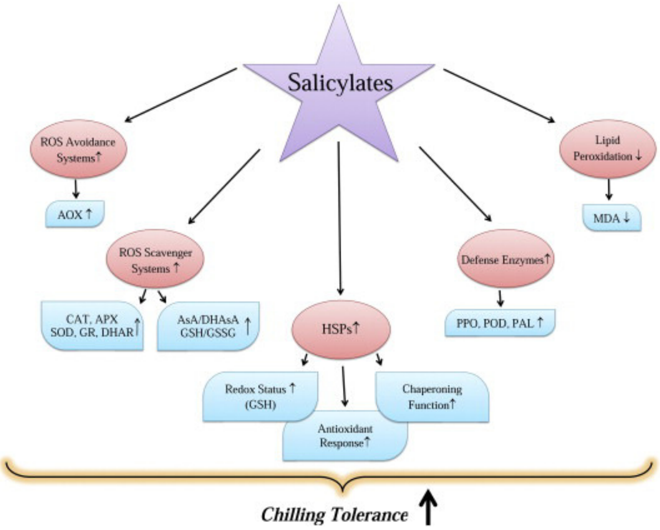
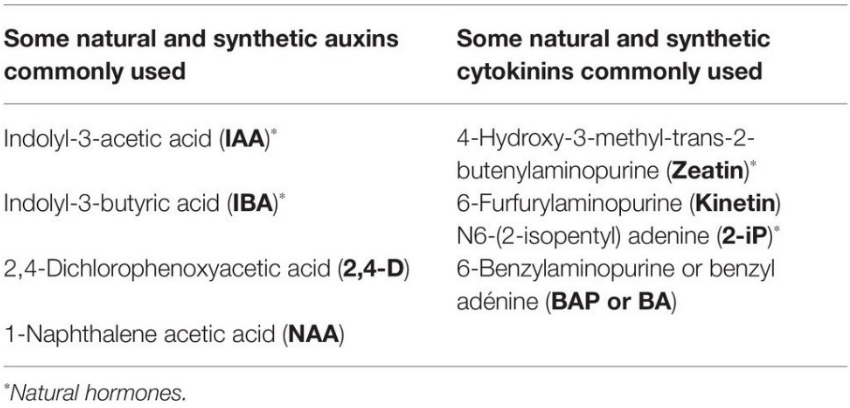


Figure 1: Salicylic acid in horticulture: Diagram showing the effect of salicylic acid on the plants (Science direct).

One of the communication molecules in agricultural products that are susceptible to abiotic stress is commonly recognized as SA. As a result, it has been believed that SA is suitable and useful for reducing the negative effects of abiotic stress. SA is advantageous for the excellent agricultural produce output as well. The additional use of SA against abiotic stress was found to control a variety of metabolic, pharmacological, photosynthesis pigments, and molecular processes. One of the potential phytohormones, SA is renowned for its exceptional capacity to deal with the difficulties brought on by abiotic stress (Figure.1). SA may increase the production of beneficial substances and trigger plant defense mechanisms in response to stressful situations. As a result, the use of SA as an additive is efficient and beneficial for the outstanding output of agricultural products thriving under abiotic stress.

Organic substances known as plant growth factors are produced in very small quantities by plants in reaction to particular triggers. These molecular mediators, also known as signal molecules, are essential for managing and modulating the plant's growth, development, fertility, and death. On the other hand, they manage every stage of plant growth, including fertilization, organ size management, disease defense, stress endurance, and sexual development. PGRs mediate growth, development, and nutrition distribution to help the plant adjust to shifting conditions. PGRs are broken down into three categories based on where they came from: manmade substances, microbiological origins, and vegetation. Phytoregulators are a word that is now applied to both manufactured and native organic PGRs. Based on their molecular compositions and outcomes, the following five major groups of PGRs can be distinguished: (i) auxins, (ii) cytokinins, (iii) gibberellins, (iv) abscisic acid, and (v) ethylene. In addition to these traditional plant hormones, more recent research has led to the discovery of PRGs like polyamines, analogs of diphenyl urea, salicylic acid, jasmonates, sterols, brassinosteroids, strigolactones, oligosaccharides, phosphoinositides, systemins, and florigen. Because they control numerous biochemical processes, auxin, and cytokinin classes are typically regarded as the most significant phytohormones in plant development regulation. These two hormones could be produced by PGPMs. The various auxin and cytokinin substances frequently used in plant micropropagation are listed in (Figure.2

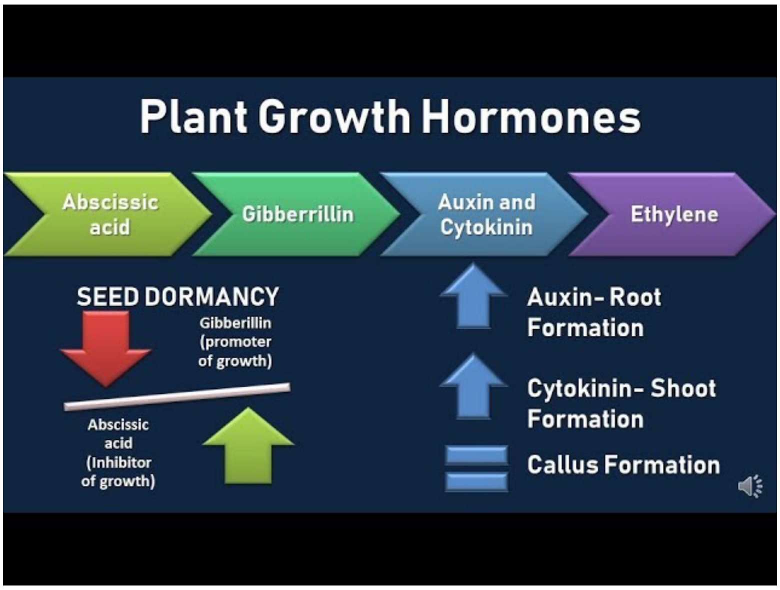


Some natural and synthetic auxins commonly used	Some natural and synthetic cytokinins commonly used
Indolyl-3-acetic acid (**IAA**)*	4-Hydroxy-3-methyl-trans-2-butenylaminopurine (**Zeatin**)*
Indolyl-3-butyric acid (**IBA**)*	6-Furfurylaminopurine (**Kinetin**) N6-(2-isopentyl) adenine (**2-iP**)*
2,4-Dichlorophenoxyacetic acid (**2,4-D**)	6-Benzylaminopurine or benzyl adénine (**BAP or BA**)
1-Naphthalene acetic acid (**NAA**)	

**Natural hormones.*

Figure 2: Phytohormones in micropropagation: Diagrammed showing the different phytohormones that play important role in a micropropagation (Frontiers).

Plant hormones work on various sections of the embryo to influence sprouting and storage. The high ABA:GA ratio of embryo stasis is contrasted with the high abscisic acid sensitivity and low GA sensitivity of the seed. A change in hormone production and breakdown toward a low ABA/GA ratio, along with a reduction in ABA sensitivity and a rise in GA sensitivity, must take place in order to break the seed out of this form of stasis and start seed sprouting.



Plant Growth Hormones

Figure 3: Seed dormancy: Diagram showing the role of the different phytohormones during the seed dormancy stage (Youtube).

ABA regulates GA egg development and embryo stasis. Seed coat hibernation includes the mechanical limitation of the seed coat. Because of this and a limited embryonic development potential, seeds essentially enter stasis. By boosting embryonic development potential and/or reducing the seed covering so that the seedling's radical can penetrate it, GA breaks this stasis. Both kinds of seed coats, including those made of living cells and those made of deceased cells, can be affected by hormones; however, seed coats made of living cells are acted upon after seed development, whereas seed coats made of dead cells can be affected by hormones at the time of seed coat formation. Testa or seed coat development traits, such as girth, are impacted by ABA, which also has an impact on the egg growth potential facilitated by GA (Figure.3). These circumstances and outcomes develop during germ development, frequently in reaction to external factors. Additionally, hormones regulate endosperm dormancy: The endosperm in the majority of seeds is made up of living tissue that can react to chemicals produced by the fetus. When it comes to the germination process or the sterility of the seed coat, the endosperm frequently functions as a deterrent to seed sprouting. Living cells react to and influence the ABA:GA ratio and facilitate cellular sensitivity; as a result, GA enhances the embryo's capacity for development and may encourage the thinning of the endosperm.

GA also impacts endosperm mechanisms that are both ABA-dependent and ABA-inhibitory. Producing trimming is a crucial procedure for generating produce of market grade and ensuring a steady output from year to year. Due to the larger size of the fruit that is still present after the harvest burden is reduced, this raises the worth of products as a whole. Additionally, the crimson hue has improved in some types. Biennial bearing, or the situation where plants yield amply one year and badly the next, is prone to occur in apple trees. The quantity of blossom in the subsequent season will rise as a result of a chemical reduction in the first season. (return or repeat bloom). When it comes to encouraging repeat flowering, hand thinning is less successful than chemical thinning. The final pruning reaction is influenced by the compounds and amounts a farmer selects, the scheduling of their application, and the ambient variables met before, during, and after application. Ethylene plays a role in the abscission process, which results in the falling of foliage, seeds, and blooms. Ethylene causes the blooms or fruit to descend from a plant when a flower has finished blossoming or when a fruit is mature and ready to be consumed. Consequently, the use of phytohormones in sustainable agriculture is becoming more and more common, especially in plant bioengineering. At the molecular, cellular, and systemic layers of the plant, phytohormones are substances that control and have an impact on a variety of facets of plant growth and development.

LITERATURE REVIEW

At the CSU Horticultural Research Farm in 2016, the impact of photosynthetically active radiation (PAR) on the natural phytohormone levels of a heterocystous N-fixing Anabaena sp. cyanobacterium was investigated. The 52-L Anabaena sp. colonies were cultivated in CO2-supplemented Allen and Arnon N-free growth medium both inside and outside of polyethylene-covered high towers for the two-factorial experiment. The intended vaccination rates were 91% and 84% of the highest outdoor PAR on day 1. Across two trials, LC-MS/MS analysis detected mean concentrations of 0.137 ± 0.062 (standard deviation) ng mg−1 dry weight (dw) abscisic acid (ABA), 0.189 ± 0.049 ng mg−1 dw indole-3-acetic acid (IAA), 0.134 ± 0.048 ng mg−1 dw indole acetamide (IAM), 0.116 ± 0.032 ng mg−1 dw indole carboxylic acid (ICA), and 0.022 ± 0.017 ng mg−1 dw trans-zeatin riboside (tZr). Salicylic acid (SA) was discovered in trials 1 and 2 at amounts of 1.066 and 0.262 ng mg/dw and 0.449 and 0.229 ng/dw, respectively. As compounds produced by cyanobacteria, ICA and SA have not been identified. Solar radiation was found to be a major variable in forecasting ABA, IAA, IAM, and SA amounts using regression models based on treatment factors and output parameters, probably due to light stress or energy supply. IAA, IAM, and SA amounts were found to be significantly predicted by the abundance of Anabaena sp. culture inoculations. The amounts of IAA and SA were similar to those that have been linked to improved plant development when used as cyanobacterial biomass[4], [5].

The worldwide output of garden products is now seriously threatened by the present state of climate change. A complex system to avoid stress is provided by phytohormones at various physical, physiological, metabolic, and molecular levels. In addition to controlling other cell wall healing processes, pH modulation, root hair development, ionic balance, chlorophyll content, synthesis, and leaf shape, phytohormone also regulates the abiotic stress-responsive signaling cascade. Other phytohormones, including auxin, cytokinin, ethylene, strigolactones, brassinosteroids, salicylic acid, abscisic acid, and jasmonic acid, have also lately been found to be crucial in the development of abiotic stress-tolerant legumes. Additionally, polyamines, carbohydrates, neurotransmitters, and strigolactones recently found phytohormone-like plant growth regulators are a successful method of reducing biotic and abiotic stress.

Recent research has uncovered the function of various plant growth regulators that resemble phytohormones as well as a network signaling mechanism that targets transcription factors and genes involved in stress. Understanding the intricate phytohormonal interactions that occur in crops under different abiotic stress circumstances will improve our understanding of the complementary and conflicting functions that stress-tolerant varieties can play. A review on how various phytohormones in agricultural products regulate gene expression to influence plant growth and development is difficult to come by. In this context, the function of phytohormone-like plant growth regulators and the related interaction between them in plant growth and development under abiotic stress conditions are the main topics of our review.

Abiotic stress circumstances that are too extreme significantly disrupt horticultural products. This is regarded as one of the main dangers to the population's ability to live healthful lifestyles. One of the numerous multipurpose phytohormones that are present in plants, salicylic acid (SA), is well known. Additionally, it is a significant bio-stimulator that controls the growth and developing phases of agricultural products. The addition of even trace quantities of SA has increased the yield of agricultural products. It effectively lessens oxidative damages brought on by excessive reactive oxygen species (ROS), possibly increased photosynthesis, chlorophyll pigments, and stomatal control.

According to physiological and metabolic processes, SA increases the actions of osmolytes, secondary metabolites, enzyme and non-enzymatic antioxidants, and signaling molecules in plant cell sections. Numerous genomic methods have also investigated how SA controls the metabolism of genes linked to stress as well as transcriptional monitoring, transcriptional apprehensions, genomic expression, and those that are concerned with stress. While many plant scientists have studied SA and how it works in plants, its role in improving abiotic stress resistance in agricultural products is still unknown and requires further study. The current study, therefore, concentrates on a thorough investigation of SA in physiological and metabolic processes in crops under abiotic stress. The available data is thorough and seeks to be more helpful for the creation of higher-yielding cultivars resistant to abiotic stress.

One of the industries that use farming tools extensively and broadly is horticulture. Horticultural crops may grow both in the open and closed spaces such as greenhouses and tunnel, and there are several practical applications such as propagation with cuttings and grafting, pruning, and soilless culture; plant growth regulators that have little or no use with other crops were used largely in horticultural crop production. In addition, these practices should be ingrained in gardening production to guarantee adequate plant growth and development as well as high crop output and quality. As a result, gardening crops require more input than other farming products, and environmental upkeep is also very important. For these reasons, various methods to boost input effectiveness are required, and plant growth-promoting rhizobacteria (PGPR) has proven to be a crucial instrument. PGPR can affect plant growth by production and release of secondary metabolites, lessening or preventing deleterious effects of phytopathogenic organisms in the rhizosphere and/or phyllosphere, and/or facilitating the availability and uptake of certain nutrients like N, P, and Fe from the root environment. In accordance with these action mechanisms, PGPR can be used for various purposes such as rooting of cutting, grafting union, fruit setting and thinning, lateral root formation, increasing tolerance against abiotic stress as well as growth, development, and biological control with root inoculation and/or spraying. This review's main emphasis is on these screening techniques and real-world uses of PGPR in agricultural crops.

Phytohormones have drawn a lot of interest because they are a common and crucial component of phytophysiology and can effectively control the growth and aging of farm goods. However, the processes by which phytohormones work after harvest are not fully known. An summary of prevalent phytohormones for prolonging the storage life of fruits and veggies is given in this study. On the basis of defense gene expression activation, susceptibility of senescence-related phytohormones suppression, antioxidant enzyme activity stimulation, and cell membrane integrity maintenance, the regulation principles are explored in depth. The applications of jasmonates, salicylic acids, cytokinins, gibberellins, polyamines, and brassinosteroids in preserving fruit and vegetables based on defense signaling network stimulation, senescence-related phytohormones expression or sensitivity repression, as well as antioxidant system enhancement and cell membrane integrity sustentation are introduced. In addition to discussing the difficulties and issues that need to be resolved, new ideas for extending longevity by utilizing phytohormones in conjunction with other therapies are also put forth. Despite the fact that phytohormones have shown to be successful at sustaining farm goods, more cutting-edge combo therapies should be created to support one another.

Through a steady supply of healthy stock plants, clonal multiplication is essential to the development and success of a multi-billion dollar worldwide gardening business. Understanding the biochemistry of in vitro plants continues to be a crucial part of the supply chain because it relies on the micropropagation process being improved constantly. We evaluated the influence of exogenously applied cytokinins (CKs, N6-benzyladenine□=□BA, isopentenyladenine□=□iP, meta-topolin□=□mT, 6-(3-hydroxybenzylamino)-9-(tetrahydropyran-2-yl)purine□=□mTTHP) in Murashige and Skoog (MS)-supplemented media on organogenic response and accumulation of endogenous CK and indole-3-acetic acid (IAA) metabolites. The 20 M mT therapy produced the greatest sprout growth (30 shoots/explant). However, the 10 mM mT therapy generated regenerants of the highest grade. In vitro plantlets of Amelanchier alnifolia rooted at the lowest CK concentrations, with 1 M mTTHP regenerants showing the greatest root growth (3 roots/explant). High amounts of natural bioactive CK intermediates (free bases, ribosides, and nucleotides) were found in mT and mTTHP-derived regenerants, similar to the organogenic response. These cultures also had relatively large levels of O-glucosides. In comparison to the control, all CK-treated plants had higher amounts of naturally free IAA. This may indicate that CKs have an impact on the production of IAA.

Plants naturally generate compounds called phytohormones that support vegetative and sexual growth as well as aging. Similar to other products, phytohormones have an impact on pineapple's blooming and fruit growth. This paper gives a general summary of how phytohormones relate to and affect pineapple blooming and fruit growth. Three parts are combined and cover the impacts of phytohormones: 1) Pineapple flower induction; 2) Pineapple flower commencement; and 3) Pineapple product growth. According to the results of numerous studies, phytohormones such as auxin, gibberellin, cytokinin, ethylene, and abscisic acid are involved in the start and growth of pineapple inflorescences. (ABA). The phytohormones auxin, gibberellin, and cytokinin are known to increase pineapple product growth and quality. Commercial pineapple producers can use these collections of data as guidance to develop low-cost technological inputs for pineapple production.

The family of plant growth factors known as cytokinins (CKs) is biologically varied and exhibits a broad range of effects on plant growth and development, which is why it is used in agriculture for agricultural control and enhancement. They have extremely complex cross-talk interactions with other phytohormones, signaling networks, and synchronized regulation effects that trigger and regulate a range of biological processes from the cellular to organismal levels. Before emphasizing the wide range of how fruit cultivars react to CK-based developments, we quickly describe the mechanism of action and basic molecular biological impacts of naturally occurring CKs in this overview.

We give a thorough overview of the study on the use of CKs in non-model agricultural species during various stages of product production and administration. By doing so, it is clear that the effects of CKs on fruit set, development, maturation, and ripening are not necessarily generic, even for cultivars within the same species, illustrating the magnitude of yet unknown intricate biochemical and genetic mechanisms regulating these processes in different fruit crops. Current approaches using genomic-to-metabolomic analysis are providing new insights into the planta mechanisms of CKs, pinpointing the underlying CK-derived actions that may serve as potential targets for improving crop-specific traits and the development of new solutions for the preharvest and postharvest management of fruit crops. When the material is accessible, CK molecular biology is addressed concerning its current and potential future consequences in the uses of CKs in crops with significant agricultural value[6]–[8].

CONCLUSION

The current era's erratic climate change is contributing to an increase in biotic and abiotic stressors. Biological pressure on horticultural crops can be lessened by the application of several management techniques. For the sustainable production of horticulture crops against climate-related extremes, phytohormone supplementation is of them. There are many plant hormones, which are beneficial and supportive and play a role in reducing plants' sensitivity to stress. Synthesis and expression of the different phytohormones have an exceptional capacity to deal with difficulties that arise as a result of biotic and abiotic stress. Used the plant phytohormones strategy to deal with these problems and assure the continuous manufacturing of agricultural products across the world.

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CHAPTER 13

IMPORTANCE OF PHYTOHORMONES FOR THE HUMAN HEALTH

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ABSTRACT:

Phytohormones like auxin, gibberellins, cytokinin, etc. play important role in plant growth and development. Apart from that some other hormones like abscisic acids and ethylene mainly control the adverse environmental effects and according to the environmental conditions inhibit plant growth. Cumulative effects of the different phytohormones regulated the all-plant development stages like root and shoot development, fruit development, and ripping, control the plant aging and senescence, etc. Now, these plant hormones are used for increasing the production and quality of crops. But some time due to the use of higher concentrations of phytohormones causes several serious issues for human health. In some studies, it has been found that phytohormones could be used in the treatment of various diseases. In this chapter, we briefly emphasized phytohormones and their effects on human health.

KEYWORDS:

Abscisic Acid, Cell Cycle, Human Health, Oxidative Stress, Plant Hormones.

INTRODUCTION

The signaling components or chemical combinations that makeup plant hormones are found in very small amounts in plants. These hormones have a major impact on how plants expand, separate, and develop. They also have an impact on a variety of processes, including stomatal development. Through the phenomenon known as phototropism, which causes plants to curve toward the light, Darwin and Francis (1880) first proposed the idea of plant hormones. Thiamann first used the word "phytohormones" to describe an organic compound found naturally in plants. The word "plant hormones" refers to hormones that exist naturally in plants, whereas "plant growth regulators" (PGRs) refer to compounds that were created artificially or synthetically. Plant growth regulators play a significant part in the developmental processes of plants, which are linked to their responses to a variety of biotic and abiotic stresses. Fruit growth and aging are also well known to be strongly correlated with plant hormones.

Hormones have a limited site of synthesis and a specific concentration that they transport to target tissue through the circulatory system and regulate a physiological response. PGRs regulate the different plant cell processes and are responsible for the full development and growth of plants. Plant hormone influences things like transcription, cellular division, and development. Auxins, gibberellins, cytokinins, ethylene, abscisic acid (ABA), jasmonate corrosive, brassinosteroids, salicylic corrosive (SA), and bioactive oligopeptides are some of the different kinds of plant hormones that have been discovered so far. Strigolactones have most recently been recognized as a novel class of plant hormones. Spices and herbs are made from plant-based products, which also provide vitamins and nutrients. The primary commercial plant produce is cereal, which is used to make a variety of bakery goods like cake, noodles, rusk, and more. Since plants are the source of the majority of foods, the use of manufactured hormones in plant-based foods is concerning and needs to be curbed

For billions of years, microbes have been actively coevolving with other organisms to influence the environment. The so-called "microbiota" of microbial communities serves a variety of purposes for interacting with species, directly influencing their fitness. For biologists, it has become extremely difficult to understand how the microbiota influences host fitness. On the one hand, plant hormones control physiology and influence the microbial habitat of the plant. On the other hand, pathogenic, commensal, and symbiotic microbes secrete and imitate plant hormones to change the microbial communities and hosts of which they are a part. Animals, including humans, generate and are sensitive to plant hormones, which is a little-known fact. Surprisingly, it is known that these hormones have an impact on cellular functions, inflammatory reactions, and glucose homeostasis. The well-being of people is significantly affected by this. Here, we suggest that plant hormones that are consumed or made by human gut bacteria affect health (Figure .1). We use examples of how human diseases like diabetes, inflammatory bowel disease (IBD), and cancers all of which are influenced by the gut microbiota to demonstrate this idea[1]–[3].

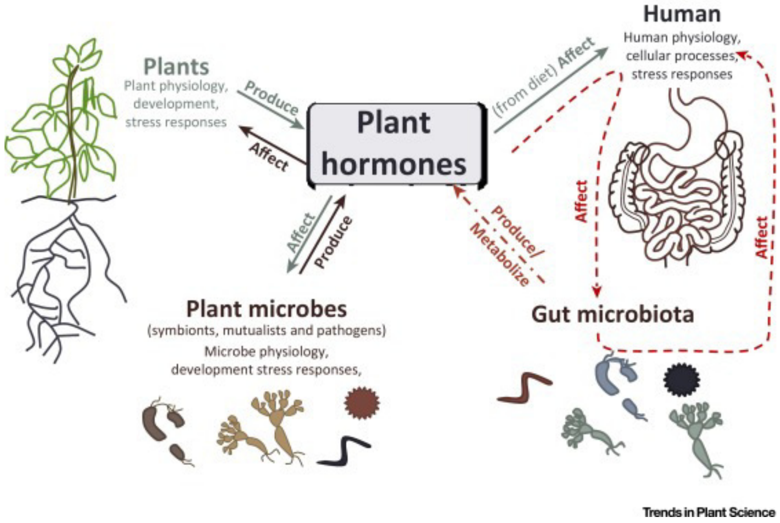

Figure 1: Plant hormones and human effects: Diagram showing the relationship between the phytohormones and humans (Cell).

The interaction between dietary choices and gut microbiota has been linked to a number of immune diseases. It is true that food affects the immune system's ability to fight off certain microbes and the release of microbial compounds. For instance, by directly altering the expression of important inflammatory factors, bacterial short-chain fatty acids reduce inflammation. In contrast, hydrogen sulfide produced by bacteria is believed to cause IBD and inflame intestinal tissues, further demonstrating how microbe-derived substances control human immunity. Gibberellic acids (GAs), a class of plant hormones made by microbes, have anti-inflammatory effects by reducing the production of proinflammatory interleukins. Therefore, a diet high in GA could reduce inflammation conditions. However, in this instance as well, it is unknown how these substances affect the gut microbiome or how GA-microbial production contributes to inflammatory disorders Auxin is also found in some parts of the mammalian body, mainly synthesized from an essential amino acid tryptophan which is consumed from different kinds of vegetables (soybean, broccoli, beans, onion, and leafy vegetables) and other animals products, such as milk, cheese, red meat, chickpea, pumpkin seed, almonds, and peanut. It was known from a few earlier studies that auxins can affect the way mammalian cells operate. Auxin may one day function as an antitumor drug, according to reports. According to some new scientific studies, in mammals, the suppression of SCF type ubiquitin ligase function (by suppressing SKP2 dependent CDK2 and CDK4 activity) results in G1 cell cycle arrest and causes a delay in cell cycle (S, G2, or M) progression in cells. For instance, inhibiting SKP2, the f-box protein of the SCF complex that regulates the proteolysis of CDK inhibitors like p27 and p21, results in G1 arrest in human ovarian cancer cells. With the aid of auxin, SKP2 suppression slows the G1 cell cycle's progression and lowers the proportion of cells in the S-phase (Figures 2 and 3).

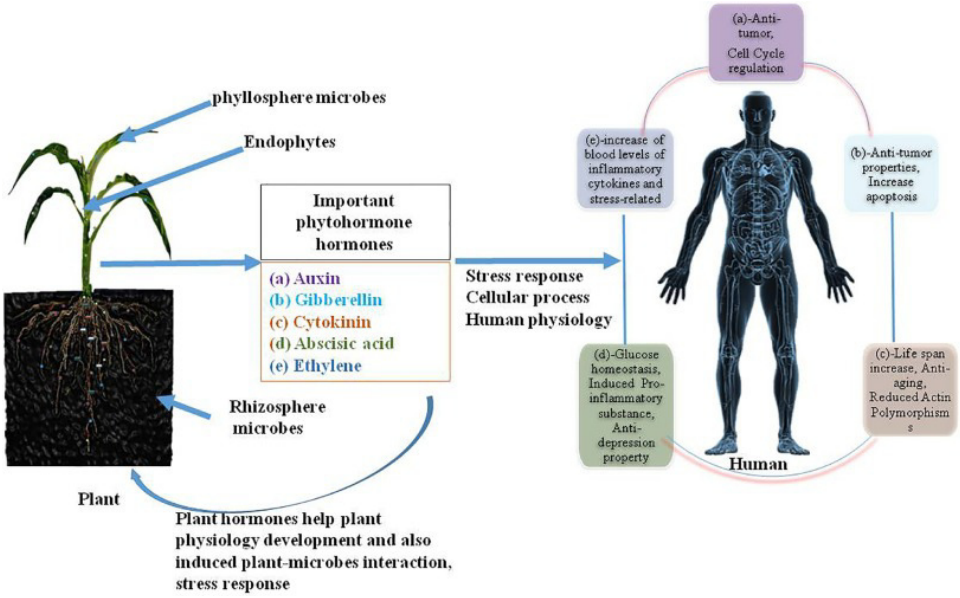

Figure 2: Phytohormones and human health: Diagram showing the effects of the phytohormones on the microbial environment in the human(Science direct).

The human organism gets gibberellic acid from a plant-based diet. (vegetables and fruits treated with gibberellic acid and some vegetables naturally produce gibberellic acids such as chilli and olive). The phytohormones in our diet can affect how humans metabolize food, but there is very little information on how GAs affect people. Inducing oxidative stress by producing reactive oxygen species (suppressing the function of antioxidant enzyme activities) and causing hepatotoxicity in adult male albino rats by lipid peroxidation in the liver cells, GAs has been described as a powerful pro-oxidant. In human lymphocyte culture, gibberellin A3 at various concentrations had a cytogenetic impact. Chromosome changes caused by gap deletion and break, sister chromatid swap, and DNA damage were all brought on by gibberellin A3. A gibberellin derivative (GA13315) was shown by Zhang et al. [64] to have anticancer properties against tumor cell lines both in vivo and in vitro. By elevating the ratio of the apoptosis-promoting protein bax to the bcl2 protein, GA13315 induced apoptosis in A549 cells (Figures 2 and 3).

Ethylene enters a person's body through the air and is a normal metabolic process. Ethylene is a component of human gut microflora and has the ability to make ethylene oxide, an IARC Group 1 known human genotoxic carcinogen. Human exhaled breath contains ethylene as well. found that ethylene is produced in humans with systemic inflammation. Reactive oxygen species [ROS] generate oxidative stress, which causes endogenous lipid peroxidation of unsaturated fatty acids and results in the formation of ethylene in conditions of systemic inflammation and infection (Figures 2 and 3). Oxidative stress is caused by a respiratory burst, which happens when pathogen-destroying blood cells come into contact with bacterial and fungal diseases. (monocytes and neutrophils).

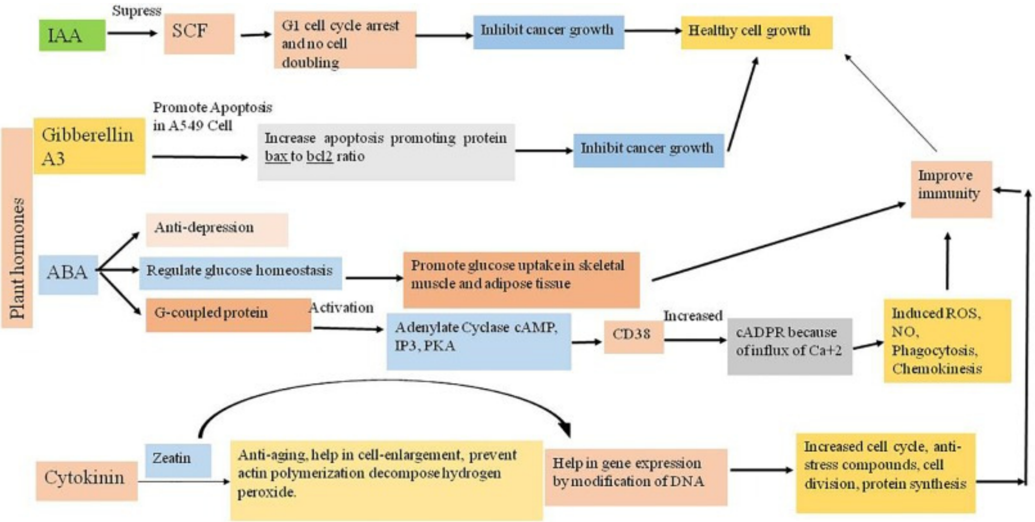

Figure 3: Effects of phytohormones: Diagram showing the biochemical effects of the phytohormones on human health (Science direct).

Due to this burst, a significant quantity of ROS is produced, which results in oxidative stress. They demonstrated that after being exposed to Fe3+ ions, fatty acids (docosahexaenoic acid and oleic acid) substantially produce ethylene, causing oxidative stress and lipid peroxidation in cells. The vitality of plants is largely maintained by microbes. Microorganisms cause the formation of various primary and secondary products that help plants combat various abiotic and biotic stresses in order to survive in various environmental circumstances. ACC is recognized as an ethylene phytohormone precursor. Endophytes that promote plant development have the capacity to express ACC deaminase, which shield plants from various abiotic and biotic stresses. Various creatures, besides plants, also contain cytokinin. Miller reported it in an autoclaved fish sperm at the time[4]–[6].

Cytokinin has an impact on a variety of physiological processes in animals. In Caenorhabditis worms, Voller found that cytokinins and their derivatives lengthened life expectancy. In vitro studies on human skin fibroblasts revealed gerontic-modulatory and anti-aging effects of zeatin, a well-known cytokinin plant growth factor. Long-term treatment with zeatin in human fibroblasts has been shown to maintain the health of the cells by decreasing intracellular waste, promoting cell growth, preventing actin polymerization, and improving the cells' capacity to break down hydrogen peroxide. According to reports, kinins are a byproduct of DNA's oxidative, secondary modification, and secondary reaction. They have an impact on a variety of biological processes, including gene translation, auxin action inhibition, calcium flux stimulation, cell cycle, and stress reduction. In animals, it even caused protein synthesis, cell differentiation, and cell division.Human fat tissue produces ABA under both low and high glucose conditions. Release of GLP-1 during a hyperglycemia situation causes cells and insulinoma cells to release ABA and insulin, promoting the uptake of glucose by skeletal muscles and adipocytes. A glucagon receptor called GLP1R triggers GLP-1 to cause pancreatic beta cells to secrete insulin. Additionally, it has been noted that ABA increases glucose uptake in murine adipocytes and rat myoblasts. Abiotic stress causes animal cells to produce ABA, which is also recognized as an endogenous pro-inflammatory substance. ABA causes a Ca2+ inflow within the neutrophil. Adenylate cyclase [AC], excessive cAMP production, a rise in IP3, PKA-mediated stimulation of CD38, and increased production of cADPR are all caused by the interaction between ABA and G-coupled proteins of the plasma membrane. The influx of Ca2+may be influenced by this process.

LITERATURE REVIEW

Plants are not aroused by human pheromones. However, according to recent research by Santina Bruzzone, Elena Zocchi (University of Genova, Genoa, Italy), and coworkers, plant hormones can be stimulating to people or at least to their immune cells. Abscisic acid (ABA), a plant hormone, is classified by the writers as a human cytokine.ABA causes stress-related reactions in plants, such as seed storage and stomatal closure. Zocchi earlier discovered that even very basic creatures like sponges use ABA-driven pathways to react to heat and light. She has discovered that ABA affects animals as well. Immune cells are frequently the first in people to be exposed to environmental stresses. The team's findings demonstrate that phagocytosing immune cells known as granulocytes produce ABA in reaction to high temperatures, such as those associated with a fever. By turning on chemokinesis, the ABA summons more granulocytes and perhaps other immune cell types. Additionally, it promotes the creation of nitric oxide, reactive oxygen species, and phagocytosis, all of which aid in the destruction of pathogens. (another cytokine). Similar to plants, granulocyte ABA reactions are activated by a biochemical pathway that causes intracellular calcium to rise. This pathway uses cyclic ADP-ribose. The ability to react to environmental cues through biochemical processes, according to Zocchi, is what makes life truly unique. Therefore, it comes as no wonder that it has been so well conserved

Abscisic acid (ABA), a phytohormone, is crucial for controlling tension and several pathological conditions in people. Stem cells, macrophages, and keratinocytes all naturally generate ABA, which can be consumed either exogenously or endogenously. Reactive oxygen species (ROS) generation, phagocytosis, and chemotaxis are all mediated by ABA. LANCL2 functions as an ABA receptor in mammals. ABA has the ability to either increase or decrease inflammation, depending on the signaling mechanism involved. ABA is essential for glucose tolerance, the therapy of atherosclerosis, and the dormancy of prostate cancer, malaria, type 2 diabetes, and dementia. A number of detection techniques, such as high-performance liquid chromatography (HPLC) and mass spectrometry, as well as chromatographic, spectroscopic, and colorimetric assays, have been created to detect ABA. In order to identify analytes in small concentrations, biosensors are frequently used.

Two different kinds of biosensors have been created for the sensing of ABA: LSPR and FRET sensors. FRET sensors rely on energy transfer between a donor and acceptor molecule, whereas LSPR sensors depend on light interacting with metal nanoppapers to identify analytes. While FRET sensors offer high specificity and adaptability, LSPR sensors offer high sensitivity, label-free detection, and the capacity to detect numerous targets at once. Recently, aptamers have been used in place of antibodies in biosensors to increase sensitivity and decrease expense. This review focuses on how ABA is used to treat different mammalian diseases and the various biosensors that can identify it.

The co-occurrence of various signs that start type 2 diabetes, cardiovascular diseases, and a number of comorbid diseases is what defines metabolic syndrome. It is challenging to develop universal therapeutic strategies that concurrently improve these pathological features due to the complex constellation of numerous comorbidities. The plant hormones auxin, cytokinins, salicylic acid, and abscisic acid have demonstrated potential anti-inflammatory and pro-metabolic effects that may alleviate a number of conditions associated with metabolic syndrome. It's intriguing to note that, in addition to plants, human cells and gut microbes also make these molecules endogenously, suggesting a part in the intricate interactions between nutrition, the gut microbiome, and inflammatory reactions linked to metabolic syndrome. Here, we describe how the gut microbiota and endogenous processes can produce bioactive phytohormones. These compounds then have an impact on metabolism and immune reactions. We go into more detail about how phytohormones can help to regulate the complications of the metabolic syndrome and suggest using them as nutraceuticals

From the feces of a healthy male adult, two anaerobic bacteria engaged in the conversion of the plant lignan secoisolariciresinol diglucoside were isolated. Strain SDG-Mt85-3Db, the first isolate, was a mesophilic, completely anaerobic, helically coiled rod. The closest cousins identified by 16S r RNA gene sequence analysis were Clostridium ramosum (96.6% similarity) and Clostridium cocleatum (96.7% similarity). The isolate did not thrive on maltose, melibiose, raffinose, rhamnose, or trehalose and lacked alpha-galactosidase and -glucosidase in contrast to these species. DNA-DNA hybridization tests supported the theory that strain SDG-Mt85-3Db represents a novel bacterium species of the Clostridium cluster XVIII. DNA from the SDG-Mt85-3Db strain had a G+C content (30.7 0.8 mol%) that was similar to that of Clostridium butyricum, the genus Clostridium's type species.

It is suggested that the strain SDG-Mt85-3Db (=DSM 17460T=CCUG 51486T) be given the designation Clostridium saccharogumia. The second isolate was a mesophilic, completely anaerobic, Gram-positive regular rod known as strain ED-Mt61/PYG-s6. According to analysis of the 16S rRNA gene sequence, its closest cousins were Ruminococcus productus (93.3%), Clostridium saccharolyticum (93.1%), and Clostridium amygdalinum (93.3%). The isolate's capacity to dehydrogenate enterodiol set it apart from these species. Alpha-arabinosidase and -galactosidase were also present, and its DNA had a higher G+C concentration (48.0 mol%). These results support the proposal to include strain ED-Mt61/PYG-s6 in a new genus, Lactonifactor, and a novel species, Lactonifactor longoviformis. DSM 17459T (=CCUG 51487T) is the strain's parent.

The soy phytoestrogen genistein may enhance vascular function, but it is uncertain how this happens. Nitric oxide (NO) produced by endothelial cells is a crucial modulator of atherogenesis and vascular tone. Previous research has demonstrated that estradiol can increase NO synthesis by directly stimulating the expression of endothelial NO synthase (eNOS) in vascular endothelial cells (EC). It is unclear, though, whether genistein has a comparable impact. Therefore, we looked into whether genistein directly controls NO synthesis in human umbilical vein EC and main human aortic EC (HAEC). (HUVEC). Genistein increased the expression of eNOS and consequently elevated NO synthesis in both HAEC and HUVEC at physiologically achievable concentrations in people who consume soy products, with 1–10 mol/L genistein causing the maximum effects. However, the effects of genistein on eNOS and NO were not mediated by activation of estrogen signaling or inhibition of tyrosine kinases, 2 known biological actions of genistein. Genistein (1–10 μmol/L) increased eNOS gene expression (1.8- to 2.6-fold of control) and significantly increased eNOS promoter activity of the human eNOS gene in HAEC and HUVEC, suggesting that genistein activates eNOS transcription. The biological significance of the in vitro results was confirmed when dietary supplementation of genistein to spontaneously hypertensive rodents restored aortic eNOS levels, improved aortic wall thickness, and reduced hypertension. According to our findings, genistein has unrelated to its known effects direct genomic effects on the vascular wall that increase eNOS expression and NO synthesis while lowering blood pressure[7], [8].

Sesquiterpenoid plant hormones known as strigolactones (SLs) play a part in how plants react to different biotic and abiotic stresses. They are sensed by both parasitic plants and helpful mycorrhizal fungi when released into the rhizosphere. SLs are possibly interesting agricultural targets because of their variety of roles. In fact, using SLs as agrochemicals can support sustainable agriculture through a variety of processes, such as modifying root architecture, encouraging ideal branching, boosting nutrient absorption, controlling parasitic weeds, reducing drought, and improving mycorrhization. Additionally, over the past few years, a number of studies have cast light on the influences that SLs have on human cells as well as their potential medical uses. For instance, it has been shown that SLs are crucial for the regulation of processes involved in apoptosis and inflammation. Further research into their effects on human cells and potential applications as anti-cancer and antimicrobial agents has been stimulated by the elucidation of the molecular processes underlying their action.

Auxins, cytokinins, gibberellins, and brassinosteroids are among the diverse molecular structures that make up phytohormones, a class of secondary metabolites. While they play active roles in growth or defense in higher plants, many phytohormones have not been thoroughly studied despite their potential to safeguard human health. In this research, we developed a target fishing approach on 53 selected naturally occurring phytohormones spanning various protein families involved in crucial cellular processes related to human metabolism and health maintenance/disease. Through the examination of how various phytohormones interact with particular targets, this in silico analysis approach seeks to identify the bioactivity of more than fifty phytohormones that may be relevant to human health. Twenty-eight human candidates were found through this analysis. Numerous phytohormones were bound by some targets, such as the proteins mitochondrial glutamate dehydrogenase (GLUD1) and nerve growth factor (NGF), emphasizing their role in amino acid metabolism and/or the preservation or survival of neurons. On the other hand, some phytohormones had particular interactions with certain proteins, such as the SPRY domain-containing SOCS box protein 2 (SPSB2) or the Inosine-5′-monophosphate dehydrogenase 1 (IMPDH1), both of which are essential for the human immune system. They were subsequently looked into using a molecular docking research strategy. According to the results of our bioprospecting research, many phytohormones may have positive effects on human health and may play a functional role in a variety of cellular functions, including immune response and cell cycle progression.

Numerous studies have been done on the impacts of plant hormones and how they affect plants' productivity, growth, and defense. However, little is known about their function in both people and animals. Recent research suggests that plant hormones function in mammalian systems as well and may be used to treat human diseases like cancer and diabetes as well as to promote healthy cell development. Plant hormones like indole-3-acetic acid (IAA) and gibberellins aid in apoptosis, and ABA and cytokinin regulate glucose balance, act as antidepressants, and act as antitumor and anti-cancer agents, respectively. The primary objective of this review is to investigate and compare the relationships between plant hormones and their significant functions in animals, microbes, and plants, as well as their interactions, with a focus primarily on human health. This review will examine the impacts of the most significant and well-recognized plant hormones, such as IAA, gibberellins, ABA, cytokinin, and ethylene, on both people and animals[9], [10].

CONCLUSION

Phytohormones are well known to regulate the growth and development of plants but little research has been performed in the area of phytohormones usage in humans. Some studies found that phytohormones can a key tools for the treatment of diseases like diabetes, cancer, and drugs. Cytokinin which has antioxidant properties can be used in anti-aging g cream and then used as an antioxidant. Some phytohormones' higher concentration also affects the human microbial environments. Which directly affects the biochemical pathway and the biological activities of the human systems. Some edible plants including their fruits and vegetables which are consumed by human being directly affects their health due to the concentration of these hormones used in the development and maturation of the plants.With the aid of biological technology, the genetic material in microorganisms that produce these chemicals can be independently, and the results can then be controlled. The following might be utilized to create medicines, cosmetics, and drugs for the treatment of different illnesses. In the future, omics data from a human microbiota investigation could be examined to address this unanswered, enigmatic issue.

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CHAPTER 14

A BRIEF OVERVIEW OF THE PHYTOHORMONE RESPONSES UNDER ABIOTIC STRESS

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ABSTRACT:

Numerous environmental factors that plants experience cause reactive oxygen species (ROS), which in turn impede regular plant growth and development. Apart from that some solutes accumulated in the plant environments for the protection of plants from oxidative damage. Under all these circumstances plant hormones which are mainly responsible for controlling these environmental stress and protecting environments for the maximal growth and development of the plants under these stress conditions. These phytohormones include cytokine, ethylene, jasmonate, salicylic acids, etc. In this chapter, we cover a brief discussion of these phytohormones and their response to abiotic stress.

KEYWORDS:

Abiotic Stresses, Abscisic Acid, Medical Aromatic, Plant Growth, Plant Development.

INTRODUCTION

Plants face a severe threat to their survival as a result of environmental changes brought on by anthropogenic activities or by abrupt seasonal weather changes. Plants must contend with these unfavorable environmental circumstances because they are sessile organisms. The best plant growth and development are hampered by a variety of environmental shifts, including water shortage or drought, water logging, high salinity, low or high temperature, heavy metals, and solar radiation. Consequently, this causes a worldwide decline in biomass and grain yields. Different abiotic stresses can co-occur in extreme settings. For instance, drought is frequently related to salt stress, and drought can be made worse by extremely high temperatures. The toxic effects of salt have a negative influence on root development and regulate water and nutrient uptake.

To combat these harmful stressors, plants have evolved effective sensing, signaling, and response mechanisms. One of the most conspicuous examples of these response mechanisms exerted by plants is represented by the PHs, which can be defined as cellular signal molecules that act as chemical messengers in plants under low concentrations, and have paramount functions in the regulation of the responses that plants show to abiotic stresses. In a complicated network of interconnected signaling pathways, physiological processes are modulated to respond rapidly to environmental stresses

Regulation of metabolic pathways, transport, and cellular compartmentations governs the balance of PHs. Recently, it has become common practice to study the integration of hormonal circuits into the molecular processes related to stress reactions using mutants of the hormone-biosynthetic pathways. Therefore, figuring out how plants can more effectively tolerate environmental stresses with little to no loss in productivity is a key study task. An overview of the stress tolerance processes in plants that are mediated by microbial phytohormones is shown in (Figure 1). This review seeks to clarify the potential mechanisms of phytohormone-mediated abiotic stress responses in plants by advancing knowledge of the effects of abiotic stresses on endogenous PHs concentrations and their function in plant physiology. In our rapidly changing world, this knowledge can be applied to innovative methods for creating crop cultivars that are climate-smart.

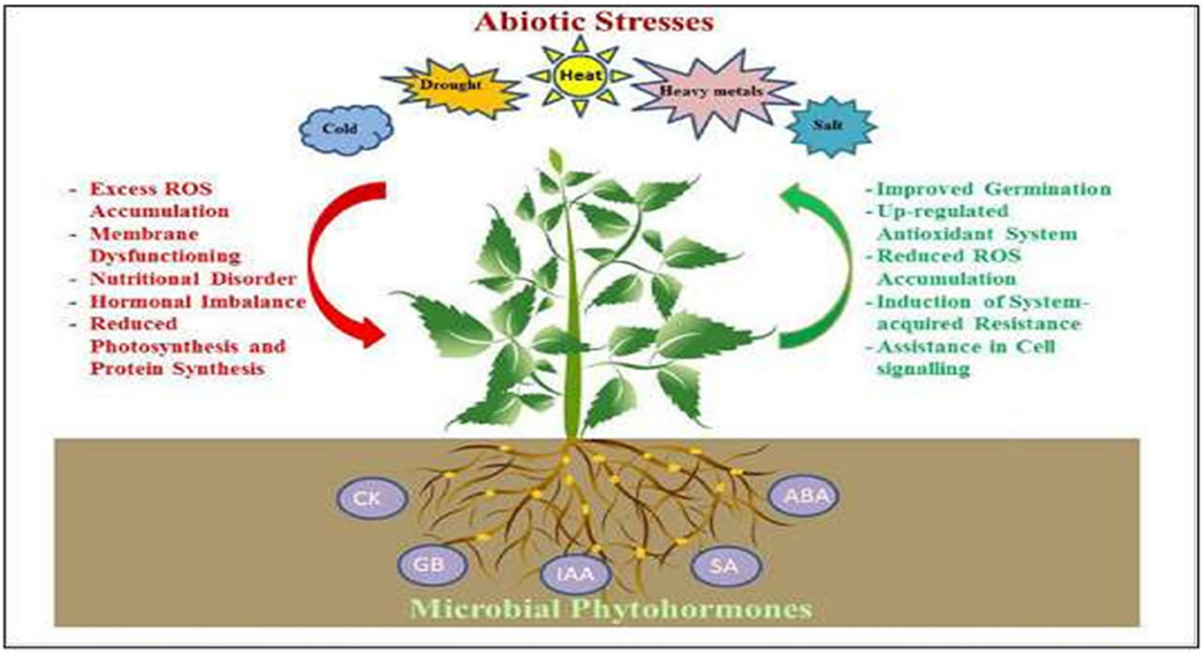

Figure 1: Stress tolerance by plant: Diagram showing the overview of the different mechanisms used by the plants against abiotic stress (Frontier).

In agriculture, drought stress, which is characterized as a naturally occurring water shortage, is a major factor in crop losses. This is because water is necessary for many important processes involved in plant growth. Recent years have made it more crucial than ever to discover a solution to drought stress. Future global warming will almost certainly result in a decrease in precipitation and a rise in drought.

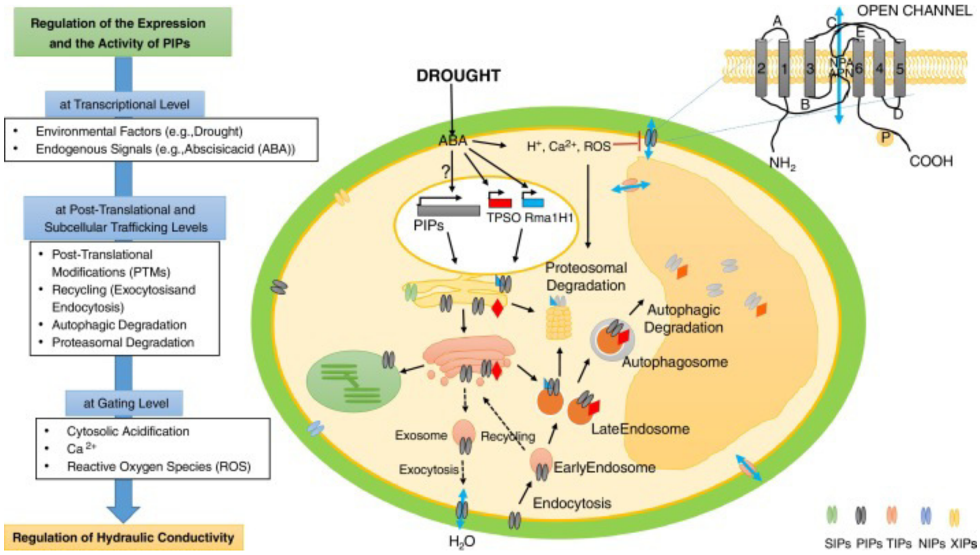

Figure 2: Drought response: Diagram showing the drought response mediated by the different phytohormones (Science direct).

In an effort to cope with drought stress, plants have developed a variety of processes and adaptations. The closing of stomata is one of the primary strategies used by plants to fight drought stress. Abscisic acid is a crucial hormone that controls stomatal opening and closure. (ABA). The binding of ABA to receptors results from its synthesis (Figure. 2). This binding then has an impact on how ion channels open, lowering turgor pressure and causing the stomata to shut. Recent research has demonstrated how drought-stressed plants' ABA levels rose. They demonstrated that under stressful conditions, plants generated more ABA in an effort to hold onto any water they may have in their leaves. Aquaporins (AQPs) are yet another crucial element in managing drought stress and controlling the absorption and export of water. (Figure.2). The membrane proteins known as AQPs are a crucial component of channels. The movement of water and other vital solutes is the primary function of these pathways. Numerous variables, including ABA, GA3, pH, and Ca2+, control AQP transcription and post-transcriptionally, and the precise concentrations of AQPs in particular plant parts, such as the roots or leaves, aid in attracting the greatest amount of water to the plant.

Future drought-resistant plant breeding will be made possible by better knowing the mechanisms of AQPs and the hormone ABA. The effectiveness of SA (106 M) foliar supplementation in two menthol mint cultivars, Kosi and Kushal, grown under Cd (50 M) stress conditions was evaluated in yet another study. Under Cd stress, both genotypes showed a decrease in growth, photosynthesis, and mineral nutrients with a concurrent rise in electrolyte leakage (EL), malondialdehyde (MDA), and hydrogen peroxide (H2O2) contents. However, under Cd stress, both genotypes also showed a distinct upregulation of proline content and the activities of antioxidant enzymes. In contrast, SA application at three distinct growth stages proved to be the most effective at reducing Cd toxicity, and this was true for both cultivars, out of three foliar-applied PGRs[1].

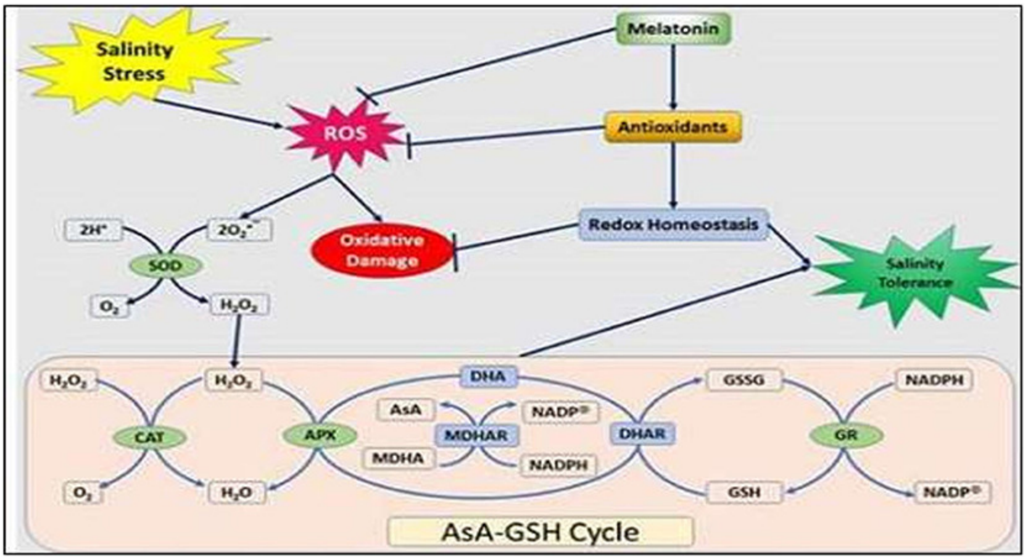

Figure 3: Ascorbate-glutamate cycle: Diagram showing the ascorbate-glutamate cycle and the role of the melatonin response in the drought (Frontier).

It is regarded as an antioxidant that plays a significant role in the regulation of ROS (Figure.3), reactive nitrogen species (RNS), and other free radicals as well as dangerous oxidative compounds found in plant cells. Additionally, plant melatonin plays a role in a variety of physiological processes like germination, development, rooting, and defense against biotic and abiotic stressors. The first plant melatonin receptor was recently discovered, which paved the way for this regulatory molecule to be recognized as a novel plant hormone. However, melatonin has also been suggested as a plant master regulator due to the variety of its effects.SLs affect how quantitatively nitrogen-fixing bacterium symbiosis develops in root nodules. The amount of SLs produced by plants is tightly controlled and regulated by the stresses that plants experience at different phases of development. The role of SLs in controlling various physiological and molecular processes during plant response to various abiotic stressors, including salinity, drought, nutrient starvation, temperature, and pathogenic assail, has been supported by numerous studies. SLs appear to actively engage in regulatory networks of plant stresses based on evidence of crosstalk between SLs and other PHs in responses to abiotic stresses [1].

In addition, ET controls a number of stress-related biochemical reactions in plants that are subjected to abiotic stressors like heat, drought, chilling, salinity, heavy metals, water logging, flooding, or submergence. In *Arabidopsis* and *Medicago truncatula*, for example, freezing and cold stress were closely related to elevated ET levels, and regulation of ET homeostasis is essential for sub-optimal temperature stress (chilling and freezing) tolerance. High ET levels aid in the ability of plants like Arabidopsis to withstand salt duress. By preserving Na+/K+ homeostasis and ROS generation, the ETIO1 (ethylene over producer) acts favorably in salt stress. Additionally, it alters how plants react to pathogen invasion, exterior mechanical damage, UV radiation, and nutrient deficiency. Many instances of ET biosynthesis and accumulation in reaction to damage or mechanical injury have been documented [1].

LITERATURE REVIEW

Being sessile, plants have a need for methods to escape unfavorable situations, which has led to the evolution of unusual and sophisticated responses to environmental stresses. Depending on the level of flexibility, plants respond to abiotic stress by changing in a variety of morphological, cellular, anatomical, and physiological ways. Small molecules called phytohormones play important roles in controlling plant growth and development as well as stress tolerance to help the plant survive and adapt to different habitats. Plants use their genetic mechanisms, as well as various adaptive and biological strategies, to congregate the challenges of salinity, temperature extremes, and osmotic stress for life and high production. In this effort, we review the possible roles of various phytohormones and rhizobacteria that promote plant growth in abiotic stresses and provide a research update on plant physiological and molecular responses to abiotic stresses. As a result of exposure to abiotic stresses, we focused on the regulatory networks of abscisic acid, indole acetic acid, cytokinins, gibberellic acid, salicylic acid, brassinosteroids, jasmonates, ethylene, and triazole. The discovery and validation of several important genes that improved crop tolerance to stress in the field serves as an example of current development. These results open up the possibility of modifying the hormone biosynthetic pathways for the transgenic plant generation with increased resistance to abiotic stress and increasing crop output in the ensuing decades [2].

Reactive oxygen species (ROS) are produced by stress on the environment in plants. As ROS build up inside of cells, proteins, chlorophyll, lipids, nucleic acids, carbs, etc. are oxidized. Cells have evolved intricate defense systems including enzymatic (superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione reductases (GR), monodehydroascorbate reductases (MSHAR), dehydroascorbate reductases (DHAR), glutathione peroxidase (GPX), guaicol peroxidase (GOPX) and glutathione-S- transferase (GST) and non-enzymatic systems such as ascorbic acid (ASH), glutathione (GSH), phenolic compounds, alkaloids, non-protein amino acids and α-tocopherol, which can scavenge the indigenously generated ROS. Numerous researchers have demonstrated how antioxidants influence plant stress tolerance. Plant stress endurance may be improved by antioxidant resistance mechanisms. To advance our comprehension of the function of the antioxidant system, different ROS-scavenging enzymes have been altered, overexpressed, or downregulated. Numerous plant hormones, including ethylene, salicylic acid (SA), jasmonic acid, brassinosteroids, abscisic acid (ABA), etc. are produced as a result of ROS. These phytohormones are necessary for plant growth, development, and defense mechanisms in reaction to environmental stresses. The current review sheds light on the function of ethylene and brassinosteroids during abiotic stress tolerance in plants [3], as well as the enzymatic and non-enzymatic antioxidants in plants that improve stress tolerance.

In the current period of climate change, abiotic stress factors like drought, flooding, cold, heat waves, ultraviolet radiations, oxidizing agents, and salinity are endangering plant growth and development, resulting in crop failure all over the world. Engineered plants with increased resistance to abiotic stresses would make it possible to adjust crops to changing climates while also increasing food production and promoting sustainable agricultural growth. Growth and development of plants involve a wide range of sophisticated genetic, hormonal, metabolic and environmental events which are tightly regulated by internal and external cues, such as phytohormones (including various biostimulants and different organic and inorganic elicitors), temperature, light irradiation, etc. Out of these, phytohormones such as jasmonates, gibberellins, abscisic acid, brassinosteroids, nitric oxide, salicylic acid, etc. have evolved to control vital functions in regulating various plant physiological and developmental processes, ranging from seed germination, photosynthesis, leaf senescence, pollen growth, to plant defense responses, and ameliorating various abiotic stresses. Such phytohormones are just beginning to play a part in helping plants adapt to changing climates. There aren't many reports accessible right now. In this chapter, we attempt to summarize recent studies that have provided insights of the plant environmental adaptability and the multidimensional role of different phytohormones viz. salicylic acid (SA), nitric oxide (NO) and hydrogen sulphite (H2S) in regulating various developmental processes and stress tolerance, taken together with the molecular mechanisms of phytohormone signalling [4].

Higher plants are negatively impacted by a variety of environmental stresses, which can be divided into two categories, biotic and abiotic, based on the source of stress. A wide variety of abiotic stressors include osmotic stress brought on by salinity, ionic, nutrient, or metal stresses, as well as others brought on by mechanical elements, light, or radiation. Since plants, unlike animals, are unable to avoid these environmental restrictions, they have evolved physiological, biochemical, or molecular defenses against stress over the course of evolution. Phytohormones such as auxin, cytokinin, abscisic acid, jasmonic acid, ethylene, salicylic acid, gibberellic acid, and few others, besides their functions during germination, growth, development, and flowering, play key roles and coordinate various signal transduction pathways in plants during responses to environmental stresses. These phytohormones regulate genes through intricate networks involving cis- or trans-acting elements in response to abiotic stressors. Phytohormones control a number of transcription factors, including ARF, AREB/ABF, DREB, MYC/MYB, NAC, and others. This work provides a brief summary of changes in gene expression, protein synthesis, modification, or degradation that are started by or connected to these transcription factors and their associated cis-acting elements. Additionally, the regulation of transcription or translation under abiotic stresses is described in terms of crosstalk between signal transduction pathways involving phytohormones [5].

Through their roots, plants continuously release a number of substances, including primary and secondary chemicals, into the rhizosphere. Growth factors, such as pH, nutrient availability, soil salinity, or temperature, can have an impact on root exudation. As plant material, two citrus genotypes with different tolerances to heat- and salt-stress conditions were in vitro grown. We assessed the proline and phytohormone concentration in root exudates from plants exposed to high temperatures or salt. Additionally, endogenous amounts of chloride, proline, and phytohormones as well as tissue damage and lipid peroxidation were found in the roots and shoots. When plants experienced salt or heat duress, more proline was released into the rhizosphere. The exudates from plants that were resistant to that specific stress condition had a greater concentration of this amino acid under each stress condition. However, under both unfavorable conditions, root exudation of the phytohormones salicylic acid, indole acetic acid, abscisic acid, and jasmonate acid usually increased. The findings support the existence of a previously unrecognized phytohormone exudation in citrus plants, which may play a significant part in rhizosphere communication. Additionally, both quantitatively and qualitatively, the exudation pattern is greatly modified by stress conditions as well as the varying susceptibility of each genotype to that particular stress [6].

Under abiotic stress conditions such as nutrient deprivation, intense light, extreme heat, high salinity, and the presence of heavy metals, microalgae can generate lipids and high-value byproducts. However, negative stresses may impede the formation and growth of microalgae as well as the buildup of metabolites. Phytohormones have become a hotly debated subject in microalgae study in recent years. Under abiotic stress, phytohormones could support the development of microalgae. Additionally, the interaction of plant hormones and abiotic stresses may enhance the capacity of microalgae to withstand abiotic stresses and further support the biosynthesis of metabolites. This review primarily focuses on the regulatory effects of exogenous phytohormones on the biosynthesis of metabolites by microalgae under adverse environmental conditions and discusses the mechanisms of phytohormone-mediated cell growth, stress tolerance and lipid biosynthesis in microalgae under abiotic stress conditions [7].

Reactive oxygen species-induced signals and the hormonal response in plants interact very effectively, causing the expression of genes or triggering proteins/enzymes that are probably involved in stress tolerance. Although abiotic stress reactions and the function of the antioxidant system have been thoroughly studied in the literature, it is unclear how hormones interact with one another and how this affects the antioxidant system. We made an effort to survey the literature on how hormones affect oxidative stress in plants. We believe that this area of study is one of the most exciting and promising in the field of abiotic stress studies because hormones have the ability to regulate a variety of responses. We are providing an overview of the more recent research on the interactions between oxidative molecules and antioxidant compounds and auxin (AUX), gibberellins (GA), cytokinins (CK), abscisic acid (ABA), and ethylene (ET). Even though it is known that a number of stress-responsive genes are hormone-responsive, and that AUX, GA, CK, ABA, and ET are involved in stress signaling, more research is still required to understand how and which hormones control abiotic stress responses [8].

The most significant barriers to sustainable farming practices in general and the cultivation of medicinal and aromatic plants in particular are abiotic pressures such as metal/metalloids, salinity stress, ultraviolet-B radiation and ozone, temperature extremes, and water stress. Abiotic stresses change the physiological, biochemical, and molecular network of the plants, which leads to abnormalities in the metabolic processes of the plant, such as growth, photosynthetic capacity, development, and yield. Plant stress physiologists are presently working on cutting edge research to engineer tolerance through the external supplementation of organic and inorganic signaling elicitors that modulate stress markers. Phytohormones are organic signaling elicitors that regulate growth and development in a variety of agricultural plants under a variety of abiotic stresses. Unraveling the mechanisms in medicinal and aromatic plants under abiotic stresses has received very little focus. In particular, the regulatory function of phytohormones, which mediates the control of key plant metabolic processes, is getting new insights into how to improve abiotic stress tolerance in medicinal and aromatic plants. The current chapter emphasizes the role of phytohormones during environmental stresses in medicinal and aromatic plants in view of various new updates. The possibility for phytohormone priming and foliar application to increase abiotic stress tolerance in medicinal and aromatic plants has received particular focus. Additionally, a few type specimens for some significant aromatic and medicinal plants have been emphasized. At the close, a conclusion based on the literature reviewed here demonstrates how phytohormones promote abiotic stress tolerance. The current review may clarify novel underpinning mechanisms for abiotic stress tolerance in medicinal and aromatic plants that are mediated by phytohormones [8].

CONCLUSION

The plant undergoes several abiotic stress in environmental conditions. This stress directly affects plant growth and development. Due to maintaining the stress conditions plants usually slow down their growth. Due to this plant development and the quality of the crop is reduced, which directly affects the overall crop production. Researchers are looking into the different signaling mechanisms and genes, which are mainly responsible for the plant's function for the control of abiotic stress. At the conclusion of this chapter, we summarized the importance of the different phytohormones for a response to abiotic stress.

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CHAPTER 15

A BRIEF OVERVIEW OF THE PHYTOHORMONES RESPONSE UNDER BIOTIC STRESS

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ABSTRACT:

Plant growth and development are mainly dependent upon the environmental condition and the collaborative effects of the phytohormones. Phytohormones maintained the plant's homeostasis for its maximum growth and protect it from any kind of stress. Apart from the environmental stress plant has to respond to the biotic response also. Many phytohormones, which are auxin, gibberellins, cytokinins, ethylene, jasmonate, and Abscisic acid are mainly a response to that biotic stress. In this chapter, we discuss a summary of the biotic stress and the plant response against that biotic stress with the help of phytohormones.

KEYWORDS:

Abscisic Acid, Biotic Stress, Plant Hormones, Salicylic Acid, Transcription Factor.

INTRODUCTION

When harmful microorganisms interact with a plant, a situation known as "biotic stress" results in the plant's inability to continue growing normally. (fungi, bacteria, viruses, viroids, phytoplasma, and nematodes). These microorganisms mainly develop on or within plant tissues, where they produce a variety of signs like chlorosis, stunting, rotting, or the development of localized lesions. Instead of infections caused by single pathogens, infections caused by fungi, bacteria, and viruses all at once are frequent and result in serious disease symptoms. The interplay between the pathogen and the plant results in a range of molecular, biochemical, and morphological responses and suggests that it activates a number of signaling pathways. As viral, fungal, and bacterial infections affect leaves, the amount of photosynthesis in all the main crops is reduced, which significantly reduces yield. About 28.2%, 37.4%, 31.2%, 40.3%, 26.3%, and 28.8% of the yield declines in the crops of wheat, rice, maize, potatoes, soybeans, and cotton can be attributed to biotic stresses. Additionally, crop losses brought on by plant diseases not only reduce crop output but also significantly jeopardize global food and nutritional security[1]–[3].

A plant needs to be able to distinguish between abiotic and biotic stresses in order to protect itself against biotic stress. The first step in a plant's reaction to a herbivore is the recognition of specific chemicals that are present in large quantities in the herbivores' saliva. These substances, also referred to as elicitors or herbivore-associated molecular patterns, cause a reaction in plants. (HAMPs). These HAMPs start the plant's defense system and enable it to minimize damage to other areas by activating signaling pathways throughout the entire plant. These HAMPs start the plant's defense system and enable it to minimize damage to other areas by activating signaling pathways throughout the entire plant. Phloem feeders, like aphids, do not significantly harm plants mechanically, but they are still considered pests and can significantly reduce food yields. When defending themselves against phloem feeders, plants have evolved a defense mechanism using the salicylic acid pathway, which is also used in infection stress. Plants target an insect's digestive system more directly. The plants use proteinase inhibitors to accomplish this. Once inside an insect's digestive tract, these proteinase inhibitors bind tightly and specifically to the active site of protein hydrolyzing enzymes like trypsin and chymotrypsin to block protein digestion. The most probable scenario is that plants developed this mechanism to defend themselves against insect attack.

Insect saliva contains elicitors that plants can sense. A signal transduction network is triggered after detection. Ca2+ ions are released into the cytoplasm in response to the presence of an elicitor. Target proteins like Calmodulin and other binding proteins are activated as a result of the rise in cytosolic content. Ca2+ dependent protein kinases activate downstream targets like phosphorylation and transcriptional activation of stimulus specific reactions. The IQD1 calmodulin-binding transcriptional regulator causes a suppressor of herbivore activity in Arabidopsis when it is overexpressed. Therefore, it is crucial to understand how calcium ions function in this signal transmission network.

Plants are exposed to a variety of biotic stressors (pathogens and herbivores) as they mature and develop, which has a greater impact on crop productivity. Plants that experience biotic stressors change in a variety of physiological, biochemical, molecular, and metabolic ways. Reactive oxygen species (ROS) production is one of the significant changes that is seen in reaction to pest and pathogen attack (Figure.1). (ROS). Although chloroplasts, mitochondria, and peroxisomes are the main locations where ROS are produced, endoplasmic reticulum, cell walls, cell membranes, and apoplast are additional locations where ROS are produced under stress. Free radicals (O2• and OH•) and nonradicals are both included in ROS. (H2O2, 1O2). Oxidative stress is brought on by a high level of ROS and results in lipid peroxidation, chlorophyll damage, redox disequilibrium, and the degradation of nucleic acids and proteins. Therefore, plants have evolved antioxidant mechanisms to lessen the harmful impacts of ROS. However, ROS also functions as a signaling molecule at low to moderate levels, interacting with other signaling molecules to trigger plant defense and tolerance mechanisms.

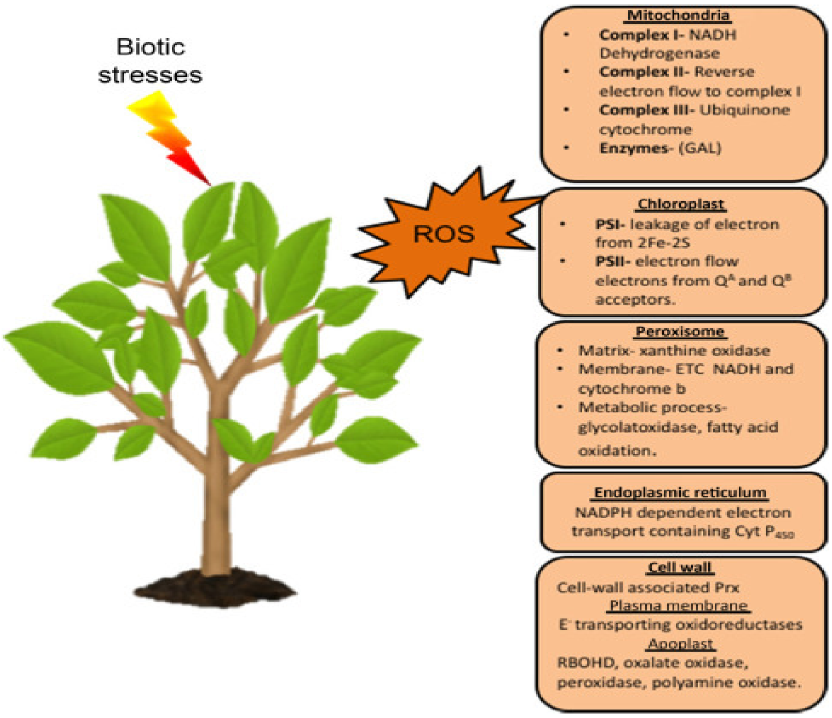

Figure.1: Biotic stress: Diagram showing the different biotic stress of the plant (Science direct).

Plants adjust the expression of numerous genes engaged in various pathways as a molecular response to various environmental stress conditions. Abscisic acid, ethylene, salicylic acid, and jasmonic acid are plant hormones that have been linked to both biotic and abiotic stress reactions. Auxin may also play a role in biotic and abiotic stress signaling pathways, according to some new studies. A substantial number of auxin-responsive genes are recently reported to be differentially expressed in rice under various abiotic stress conditions. This finding suggests a cross-talk between auxin and abiotic stress signaling. In this research, we examined the expression profiles of genes responsive to auxin (239 auxin-induced and 76 auxin-repressed) and members of auxin-related gene families (GH3, Aux/IAA, SAUR, and ARF) under different biotic stress conditions, as well as how these profiles overlapped with abiotic stress responses. Adenine derivatives, like CKs, are used as signaling molecules by many species besides plants.

The best molecules for interkingdom contact between plants and phytopathogens are thus CKs.Plants have evolved elaborate strategies to respond to attacks by other living organisms, which rely often on the action of different defense hormones, in particular, salicylic acid (SA) to defend against biotrophic and hemibiotrophic pathogens, and JA and ethylene (ET) to defend against necrotrophic pathogens and herbivores. Plants have developed a number of inducible defense mechanisms, including Induced Systemic Resistance (ISR) and Systemic Acquired Resistance, to reduce the expense of constitutive defense. For SAR, important regulators closely linked to the expression of pathogenesis-related genes (like PR1) in distal tissues including SA and SA conjugates, such as the volatile and phloem mobile methyl salicylate (MeSA). To influence defense reactions, CK action needs to be connected to these well-established defense pathways. An overview of current research on the functions of CK in the interactions between plants and pathogens will be given below, followed by an outline of the emerging picture of how this is realized[4]–[6].

SA, JA, and ET, which essentially control specific reactions to either (hemi)biotrophic or (necrotrophic) pathogens, are the foundational strands of phytohormonal defense signaling.. The conflict between JA and SA has a significant impact on this central backbone, and ET acts as another regulator SA and JA/ET play a crucial role in controlling plant immunity, making them important regulators of particular resistance mechanisms. While JA and ET are involved in induced systemic resistance (ISR), which is regarded as a partial resistance mechanism, SA is mainly responsible for mediating the so-called systemic acquired resistance (SAR). SAR is defined as a long-lasting and wide-spectrum effect that is triggered (also) in distal plant tissue and is characterized by the activation of particular PR genes. SAR can be induced by PTI or ETI.. Mutant lines with defects in SA synthesis and signal transmission, which lack SAR induction, demonstrate the significance of SA signaling for SAR. (Durrant and Dong, 2004). Instead of its direct activation, which is frequently found to be induced by advantageous rhizobacteria, ISR is mainly mediated via JA/ET and is described as priming for enhanced defense.

The phenolic phytohormone SA accumulates strongly in reaction to pathogen infection, but it also affects other physiological and developmental processes as well as the body's ability to respond to abiotic stress. In addition to being engaged with plant defenses against (hemi)biotrophic pathogens, SA signaling can also work in conjunction with MAPK signaling to increase resistance to aphids. The central transducer Nonexpressor of PR Genes1 (NPR1), which is triggered by changes in the cellular redox status by reducing NPR1 oligomers to active monomers, is a key component of defense signaling downstream of SA accumulation. These monomers interact with TGA transcription factors to trigger SA responsive genes like PR1 and WRKY transcription factors in the nucleus. According to Arabidopsis thaliana mutants sid2 and npr1, greater susceptibility to (hemi)biotrophic pathogens is evidence of the significance of functional SA accumulation and signaling for the defense against these pathogens. In addition to activating genes that are sensitive to SA, NPR1 also plays an indirect role in the antagonistic interaction between SA and JA by controlling genes that inhibit JA-dependent genes. Additionally, MPK4 and DELLA proteins, which are frequently referred to as growth repressors, are involved in the antagonistic relationship between SA and JA(/ET). In lab tests, NPR1 expression levels can be changed to enhance (partial) resistance to a variety of pathogens in transgenic plants. The specificity of the defensive reactions regulated by these hormones, which are primarily regulated by JA (along with ET) and necrotrophic pathogens in contrast to SA, explains the antagonistic relationship between JA and SA. However, involvement in developmental processes and abiotic stress reactions have been reported for this classical defense-related phytohormone as well. When conjugated to the amino acid isoleucine, the oxylipin JA exhibits the greatest activity and accumulates significantly in response to herbivory, pathogen infection, and wounding. As a component of the JA receptor complex, the F-box protein Coronatine Insensitive1 (COI1) is critically important for signaling downstream of JA buildup.

The degradation of the Jasmonate Zim-Domain (JAZ) proteins, which function as repressors of JA-responsive genes by binding to key transcription factors like MYC2, 3, and 4, is triggered by the binding of JA to this complex. Downstream of JAZs, in *A. thaliana*, the JA signaling pathways split into two different antagonistic branches that are either activated by necrotrophic pathogen infection or by herbivory and injury. Additionally dependent on ET, the pathogen defense signaling activates particular defense genes like Plant Defensin1.2 (PDF1.2) or THI2.1 (thionin) through the transcription factors ERF1 and ORA59. Vegetative Storage Protein2 (VSP2) is induced by signaling in reaction to herbivores through the activation of MYC transcription factors. The significance of JA for the defense against necrotrophs has been demonstrated, for instance, in the fad mutants of the plant *A. thaliana*, which cannot accumulate JA and are more vulnerable to the necrotroph *Pythium mastophorum*. But also for other interactions between plants and pathogens and plants and herbivores, important JA impacts in defense signaling are well researched.

LITERATURE REVIEW

Significant losses in crop yield are also caused by biotic stresses. Understanding the pathogen defense mechanisms of plants will aid in the development of breeding and biotechnological crop protection methods. The functions of Protein Phosphatase 2A (PP2A), a key element that regulates pathogenic responses in different plant species, are described by researchers. The connections between these multifunctional enzymes and the signaling system that regulates plant immunity, cell death, and more broadly primary and secondary metabolism are thoroughly explained by the authors. utilizing a sophisticated molecular and focused strategy. According to research, the stability of the AtWKRY46 transcription factor following PAMP elicitation in Arabidopsis is mediated by post-translational control of this transcription factor by a MAPK3-dependent phosphorylation. It is notable that model plants and cultivated species are both used to study plant molecular responses to biotic stress. The identification of plant immunity regulators in various economically significant crops is thus reported in this subject. Report on the identification and characterization of GmIFR, a new member of the isoflavone reductase gene family found in soybean that is controlled by phytohormones (SA, ET, and ABA) and is implicated in the plant's ability to fend off the oomycete Phytophthora sojae. A new defense protein, PR4-1, from the wild Chinese grape Vitis pseudoreticula has been discovered and characterized using a functionally transgenic approach that is quite comparable. In Vitis vinifera, it increased resistance to powdery mildew when overexpressed. In non-model species, gene expression in reaction to microbes is now frequently studied using the RNAseq methodology. A model showing the major molecular reactions and gum polysaccharide formation in peach tree (Prunus persica) infected by Lasiodiplodia theobromae, the fungus responsible for peach tree gummosis, is proposed in the report based on the analysis of the differentially expressed genes[4]–[6].

Environments with multiple, concurrent stressors are common places for plants to thrive. Less is known about the integrative signals and convergence points activated by plants in response to various (a)biotic stresses, and less is known about the complex and precisely tuned molecular mechanisms activated by plants in reaction to abiotic and biotic environmental variables. In order for plants to grow and respond to (a)biotic stresses, phytohormones are essential. One of these, an oxylipin, the plant hormone jasmonic acid, is one of the most significant communication molecules. Polyunsaturated fatty acids are oxygenated to produce oxylipins. Due to their physiological impacts and abundance in the plant, jasmonic acid and its volatile derivative methyl jasmonate have long been thought to be the bioactive forms. Recent research, however, unmistakably demonstrated that they are merely the precursors of the active forms that are typified by some amino acid conjugates. Jasmonates are created and momentarily accumulate in response to environmental or developmental cues. Upon perception, a complex system made up of particular repressor proteins that in turn regulate a number of transcription factors that control the expression of jasmonate responsive genes, fine-tunes the jasmonate signal transduction process. We go over the most recent findings regarding the function of jasmonates in plants' defenses against biotic and abiotic stressors. The intricate interactions between various phytohormones during stress communication will also be covered.

Numerous investigations up until a few years ago concentrated on the transcriptomic response to single stresses. However, a variety of biotic and abiotic stresses that can happen separately or in combination frequently limit tomato cultivation, and the reaction from the defensive mechanism can involve several genes. Therefore, we analyzed and compared the transcriptomic responses of resistant and susceptible genotypes to seven biotic stresses (Cladosporium fulvum, Phytophthora infestans, Pseudomonas syringae, Ralstonia solanacearum, Sclerotinia sclerotiorum, Tomato spotted wilt virus (TSWV) and Tuta absoluta) and five abiotic stresses (drought, salinity, low temperatures, and oxidative stress) to identify genes involved in response to multiple stressors. Using this method, we discovered genes involved in signaling, cell wall metabolism, TF and phytohormone encoding, as well as protection against biotic and abiotic stress. A total of 1474 DEGs were also discovered to be shared by biotic and abiotic stress. In the reaction to at least four distinct stresses, 67 DEGs were among those. We specifically discovered genes for RLKs, MAPKs, fasciclin-like arabinogalactans (FLAs), glycosyltransferases, auxin, ET, and JA pathway genes, as well as MYBs, bZIPs, WRKYs, and ERFs. To significantly increase plant tolerance in the field, it may be possible to further explore detected genes responsive to multiple stresses using biotechnological methods.

Abscisic acid (ABA), a phytohormone, is crucial for controlling tension and several pathological conditions in people. Stem cells, macrophages, and keratinocytes all naturally generate ABA, which can be consumed either exogenously or endogenously. Reactive oxygen species (ROS) generation, phagocytosis, and chemotaxis are all mediated by ABA. LANCL2 functions as an ABA receptor in mammals. ABA has the ability to either increase or decrease inflammation, depending on the signaling mechanism involved. ABA is essential for glucose tolerance, the therapy of atherosclerosis, the dormancy of prostate cancer, malaria, type 2 diabetes, and dementia. A number of detection techniques, such as high-performance liquid chromatography (HPLC) and mass spectrometry, as well as chromatographic, spectroscopic, and colorimetric assays, have been created to detect ABA. In order to identify analytes in small concentrations, biosensors are frequently used. Two different kinds of biosensors have been created for the sensing of ABA: LSPR and FRET sensors. FRET sensors rely on energy transfer between a donor and acceptor molecule, whereas LSPR sensors depend on light interacting with metal nanoppapers to identify analytes. While FRET sensors offer high specificity and adaptability, LSPR sensors offer high sensitivity, label-free detection, and the capacity to detect numerous targets at once. Recently, aptamers have been used in place of antibodies in biosensors to increase sensitivity and decrease expense. This review focuses on how ABA is used to treat different mammalian diseases and the various biosensors that can identify it.

Recent research suggests that melatonin plays a beneficial role in plant biotic stress tolerance among its many other roles in plant growth and stress tolerance. Melatonin, reactive oxygen species (ROS), and reactive nitrogen species (RNS), which are all produced immediately after a pathogenic invasion and are interdependent, are thought to create the integrative melatonin-ROS-RNS feedforward loop. Here, we talk about how the loop, which may be present in the mitochondria and chloroplasts, increases disease resistance at the earliest possible stage of pathogen ingress while also offering an on-site defense. We also review how melatonin interacts with phytohormone signaling pathways to mediate defense responses and discuss the evolutionary context from the beginnings of the melatonin receptor–mitogen-activated protein kinase (MAPK) cascade in unicellular green algae, followed by the occurrence of phytohormone pathways in land plants.

Plant hormones are essential for controlling how a plant develops. Auxins, gibberellins, cytokinins, abscisic acid, and volatile hormone ethylene are among the plant hormones that have lately been joined by jasmonic acid, salicylic acid, and brassinosteroids. Auxins, gibberellins, abscisic acid, cytokinins, and brassinosteroids are known to modulate the effects of plant hormones, while ethylene, jasmonic acid, and salicylic acid play important roles in the plant defense response in addition to their regulatory functions in plant development. The signaling networks of various hormones are integrated at different levels to enable crosstalk between them, which is necessary for an efficient reaction to biotic stresses. In this chapter, I'll examine how plant hormones control plant defense by signaling the defense reaction and interacting with one another through crosstalk.

These days, factors such as population expansion, rising temperatures worldwide, and the emergence of new crop diseases raise questions about the security of the world's food supply. The "go-to" method for eradicating phytopathogenic microorganisms, including *Magnaporthe oryzae*, which causes blast disease in rice and other cereals, Botrytis cinerea, which causes gray mildew in more than 500 plant species, and Puccinia spp., which causes rust in cereals, has been the use of agrochemicals. However, their excessive use has hurt ecosystems and human health (contaminating water and causing soil degradation); in addition, phytopathogens can adapt to them and become resistant to them. Plant growth-promoting microorganisms (PGPMs) is an environmentally friendly method of boosting crop production and quality while reducing biotic stresses. Likewise, PGPMs, such as Pseudomonas, Bacillus, and Trichoderma, can trigger a series of signals and reactions in the plant that lead to the induction of systemic resistance, a mechanism by which plants react to microorganism stimulation by activating their defense system, resulting in protection against future pathogen attack. This plant defense systems aid in reducing biotic stresses that imperil the safety of the world's food supply. Because of this, it is essential to study these processes at the molecular, transcriptomic, and metabolomic levels to understand how stresses impact globally significant crops[7]–[9].

Despite their immobility, plants have evolved sophisticated signaling pathways to sense environmental changes, initiate molecular and biochemical reactions, and produce phenotypic plasticity. Numerous scientific studies imply that plant hormones, particularly ethylene, can control the plasticity of phenotype in reaction to biotic and abiotic stresses. Following a biotic stress, ethylene acts as a signaling molecule in the plant defense system. Pathogen development, insect bite wounds, and insect herbivore attacks are some of the most prominent instances. The initial trigger in the biosynthesis of ethylene is the particular recognition of a number of molecules derived from wounds and pathogens. Multiple immune systems are activated and morphological structures change as a result of complex sensing and signal transduction processes. In symbiotic interactions with soil-born fungi, the gaseous phytohormone is also engaged in the process of plant-fungal interaction.

Worldwide crop growth is impacted by insect herbivores, which yearly result in significant yield losses. In addition to activating regulatory genes involved in plant defense that are responsive to stress, phytohormones are important signaling molecules that regulate a variety of physiological processes. Here, we give a comprehensive overview of the key functions of different phytohormones, including auxin, cytokinin, gibberellins, salicylic acid, ethylene, abscisic acid, and brassinosteroids, in regulating the various molecular interactions between plants and insect herbivores. The chapter begins with an overview of the early signaling response before concentrating on the function of various important phytohormones in protecting plants from herbivory and their interactions. In order to defend against harmful herbivores, we also explain the creation of secondary metabolites and other defense toxins mediated by phytohormones. For agricultural sustainability, it is now essential to apply the wealth of information found in well-established model plant-herbivore systems to less-studied food plants.

Rhizobacteria that stimulate plant development also reduce environmental stresses on plants, including salinity, flooding, heavy metals, drought, cold, soil compaction, mechanical impedance, and nutrient shortage. This chapter discusses the methods used by microbes to reduce plant stress. The creation of phytohormones like auxin, volatiles like hydrogen cyanide and ammonia, osmolytes like proline and sugars, exopolysaccharides, and the activation of antioxidant defense mechanisms in plants are some of the mechanisms. Stress causes plants to produce more ethylene, which causes senescence and plant mortality. Here, rhizobacteria that promote plant development encourage 1-aminocyclopropane-1-carboxylate deaminase activity, which indirectly lowers the concentration of ethylene.

Blueberries develop significant quantities of anthocyanin pigments derived from flavonoids in the berry skin during ripening, but not in the flesh. However, we discovered that infiltration with Agrobacterium and even sterile water triggered anthocyanin biosynthesis in the fruit flesh. We investigated the function of phytohormones and their associated gene expression patterns in contrast with skin-specific anthocyanin biosynthesis during fruit ripening because we hypothesized that this stress response was mediated by these hormones. Active abscisic acid (ABA) concentrations in ripening berries were highest at the start of anthocyanin biosynthesis, indicating that ABA plays a role in controlling anthocyanins at this stage of fruit ripening. While genes and metabolites linked to ABA catabolism and reversible conjugation were up to 10-fold higher in fruit skin and highly correlated with anthocyanins, active ABA concentrations were comparable between fruit tissues during berry development. As a result, more ABA was processed during fruit growth in the skin of the fruit, which probably had an effect on tissue-specific pigmentation. While ABA was actively catabolized and concentrations decreased in reaction to biotic stress, salicylic acid (SA) concentrations rose in fruit flesh and showed a strong correlation with anthocyanin biosynthesis, suggesting a role for SA in triggering stress-anthocyanin production. Application of SA and ABA revealed that both phytohormones boosted the expression of flavonoid genes and the accumulation of anthocyanins, demonstrating that alternate signals can control the biosynthesis of anthocyanins[10].

CONCLUSION

Hormones produced by plants are essential for controlling how a plant develops. Auxins, gibberellins, cytokinins, abscisic acid, and the gaseous substance ethylene are among the plant hormones that are currently joined by jasmonic acid, salicylic acid, and brassinosteroids. Auxins, gibberellins, abscisic acid, cytokinins, and brassinosteroids are known to modulate the effects of plant hormones, while ethylene, jasmonic acid, and salicylic acid play important roles in the plant defense response in addition to their regulatory functions in plant development. Various phytohormones formed across talk at the signaling level for regulating the biotic stress. Which is necessary for an efficient reaction to biotic stressors. In this chapter, we summarized the role of the phytohormones and their role in plant development during biotic stress.

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CHAPTER 16

PRESENCE OF PHYTOHORMONES IN ALGAE

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ABSTRACT:

Phytohormones are the chemical synthesis by plants in response to their growth and development. Some phytohormones are also synthesized by the microalgae species. These phytohormones are auxin, ABA, cytokinins, ethylene, and gibberellins. Phytohormones in the algae performed various functions for maintained their biological features for the algae. In this chapter, we discussed the overview of the phytohormones synthesis by the alga. We have also discussed the role of these phytohormones and they are used for industrial development. A new perspective on the development of phytohormones in plants may result from the dissection and manipulation of microalgae phytohormones systems, which may also open up new possibilities for producing microalgae feedstock for biofuels.

KEYWORDS:

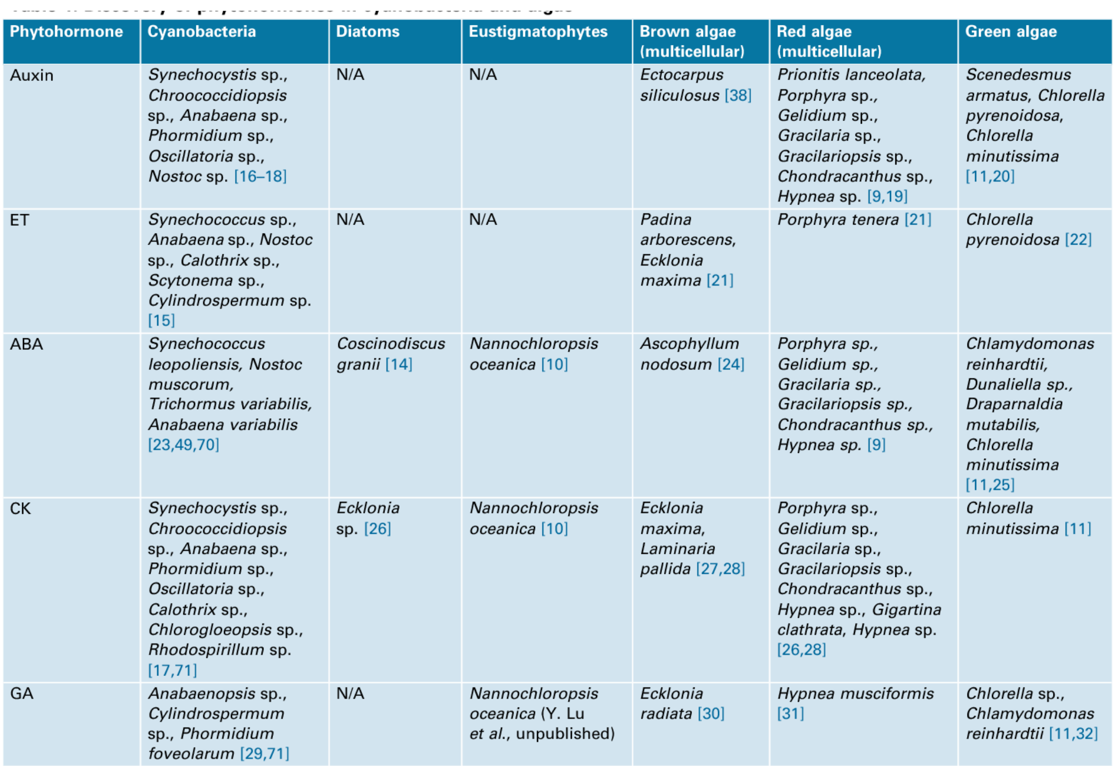
Abscisic Acid, Higher Plants, Phytohormones Algae, Physiological Effects, Phytohormones Function.

INTRODUCTION

A group of tiny molecules known as phytohormones function as chemical messengers to orchestrate cellular activities in higher plants. Phytohormones systems typically comprise signal transduction pathways that mediate the effects of phytohormones and biosynthesis pathways that generate phytohormones. The presence and function of phytohormones in microalgae are still poorly understood, despite theories that higher plant hormone systems descended from a primary metabolic system in microalgae. The potential use of microalgae as a feedstock for biofuel has recently increased the number of microalgal genomic research, which has made it possible to follow the biosynthetic and signaling pathways of phytohormones in the main microalgal lineages.

In this paper, we present a survey of the presence of phytohormone molecules in microalgae, including *Stramenopiles* (diatoms, brown algae, and eustigmatophytes), *Archaeplastida* (or Plantae, which includes red algae, glaucophytes, and green algae; the first land plants are descendants of ancient green algae, collectively referred to as the streptophyte algae, and cyanobacteria, which share a common ancestor with the endosymbiont that evolved into higher plant chloroplasts. The essential and bioactive forms of the five classical phytohormones, auxin, ABA, CKs, GAs, and ET, have been found in a variety of algal lineages, the physiological functions are still mainly unclear (Figure. 1). Moreover, despite the fact that they may contain various dominant species and biosynthetic intermediates, the phytohormone profiles of microalgae can mirror those of higher plants.

Currently, a lot of research has been done on plant hormones that control higher plants, but very little has been done on plant hormones' effects on microalgae. The genome of some microalgae has been discovered to contain traces of plant hormone synthesis and signal channels, making charophyte algae the closest living relatives of land plants. In this manner, it is possible that the single-celled microalgae are the source of the higher plants' phytohormone biosynthetic pathway, and that the effects of phytohormones on microalgae are comparable to those on higher plants. The study and application of microalgae phytohormones may offer fresh perspectives on how to enhance microalgae biofuels and high-value products' anti-stress properties in accordance with the properties of plant hormones in higher plants.



Phytohormone	Cyanobacteria	Diatoms	Eustigmatophytes	Brown algae (multicellular)	Red algae (multicellular)	Green algae
Auxin	*Synechocystis* sp., *Chroococcidiopsis* sp., *Anabaena* sp., *Phormidium* sp., *Oscillatoria* sp., *Nostoc* sp. [16–18]	N/A	N/A	*Ectocarpus siliculosus* [38]	*Prionitis lanceolata*, *Porphyra* sp., *Gelidium* sp., *Gracilaria* sp., *Gracilariopsis* sp., *Chondracanthus* sp., *Hypnea* sp. [9,19]	*Scenedesmus armatus*, *Chlorella pyrenoidosa*, *Chlorella minutissima* [11,20]
ET	*Synechococcus* sp., *Anabaena* sp., *Nostoc* sp., *Calothrix* sp., *Scytonema* sp., *Cylindrospermum* sp. [15]	N/A	N/A	*Padina arborescens*, *Ecklonia maxima* [21]	*Porphyra tenera* [21]	*Chlorella pyrenoidosa* [22]
ABA	*Synechococcus leopoliensis*, *Nostoc muscorum*, *Trichormus variabilis*, *Anabaena variabilis* [23,49,70]	*Coscinodiscus granii* [14]	*Nannochloropsis oceanica* [10]	*Ascophyllum nodosum* [24]	*Porphyra sp.*, *Gelidium sp.*, *Gracilaria sp.*, *Gracilariopsis sp.*, *Chondracanthus sp.*, *Hypnea sp.* [9]	*Chlamydomonas reinhardtii*, *Dunaliella sp.*, *Draparnaldia mutabilis*, *Chlorella minutissima* [11,25]
CK	*Synechocystis* sp., *Chroococcidiopsis* sp., *Anabaena* sp., *Phormidium* sp., *Oscillatoria* sp., *Calothrix* sp., *Chlorogloeopsis* sp., *Rhodospirillum* sp. [17,71]	*Ecklonia* sp. [26]	*Nannochloropsis oceanica* [10]	*Ecklonia maxima*, *Laminaria pallida* [27,28]	*Porphyra* sp., *Gelidium* sp., *Gracilaria* sp., *Gracilariopsis* sp., *Chondracanthus* sp., *Hypnea* sp., *Gigartina clathrata*, *Hypnea* sp. [26,28]	*Chlorella minutissima* [11]
GA	*Anabaenopsis* sp., *Cylindrospermum* sp., *Phormidium foveolarum* [29,71]	N/A	*Nannochloropsis oceanica* (Y. Lu *et al.*, unpublished)	*Ecklonia radiata* [30]	*Hypnea musciformis* [31]	*Chlorella* sp., *Chlamydomonas reinhardtii* [11,32]

Figure 1: Phytohormones in algae: Diagram showing the different phytohormones synthesized by the algae and cyanobacteria (Semantic scholar).

Similar to higher plants, cyanobacteria also use auxin for biological purposes. In plant cells, indole-3-acetic acid is the most crucial auxin. IAA, IBA, IPK, and IAM have been discovered in 46 microalgae belonging to Cyanophyta and Chlorophyta. Microalgae use auxin in a variety of ways for development and metabolism. Higher auxin concentrations can inhibit cell development, while lower auxin concentrations can stimulate growth, increase biomass, and promote the biosynthesis of highly valuable biomolecules.

Zeatin is the primary type of cytokinin, which is produced from purine. It has both cis and trans forms. It is primarily the cis component in microalgae. Inducing microalgal cell division, boosting the buildup of photosynthetic pigment, increasing photosynthetic efficiency, and promoting biomass accumulation are all possible with CK. Cytokinins are present in relatively low concentrations during the night and relatively large concentrations during the day. CKs have protective effects on the physiological functions of microalgae, particularly photosynthesis, under unfavorable environmental circumstances.

A sesquiterpene compound with 15 carbons called abscisic acid is primarily found in aging organs or tissues and functions physiologically by inhibiting cell development. ABA can also assist microalgae in entering a dormant state in challenging circumstances, dealing with pressure from the surroundings, and improving stress resistance. For instance, ABA can cause cells to enter the stationary phase and inhibit the development of algal cells in *Haematococcus pluvialis*.

Ethylene is an unsaturated hydrocarbon with two carbon atoms that can control the formation and growth of microalgae and is crucial to higher plants. There isn't much research on ethylene in microalgae, though. Although ethylene is thought to be a growth inhibitor, mounting evidence suggests that, in certain concentration ranges, it can also support growth and biosynthesis. In *Haematococcus pluvialis*, for instance, 0.05 mL/L ethylene greatly increased astaxanthin accumulation, whereas 0.1 mL/L ethylene can inhibit it. Proline and saturated fatty acid content will rise with the inclusion of ethephon (an ethylene release agent), but citric acid and unsaturated fatty acid content will fall.

According to the variations in double bonds and hydroxyl groups in its structure, gibberellin, a type of shell shortened compound, can be split into seven forms, such as GA1-7. By regulating carbon metabolism, gibberellin can take part in cell elongation and have an impact on the development and metabolism of microalgae cells. A brand-new plant hormone called brassinosteroid (BRS) has the ability to control cell division and elongation, enhance the antioxidant capability, encourage nutrient uptake, and synthesize proteins, nucleic acids, carbohydrates, and photosynthetic pigments needed for growth. Additionally, BRs are crucial for microalgae's ability to withstand abiotic stresses like heavy metals, extremes in temperature, and elevated salt levels. In order to encourage cell division and the production of metabolites, BRs can also work in conjunction with other plant hormones like auxin.

Plants can produce the phenolic molecule salicylic acid (SA). Its influence on the antioxidant system primarily reflects its regulatory effect on microalgae. By encouraging the production of H2O2 and increasing the expression of carotenoid-related genes, SA can encourage the accumulation of antioxidant compounds, which protects algal cells from abiotic stress. By influencing the transcription of associated enzymes, it can also encourage protein and carbohydrate degradation, leading to an increase in lipid buildup in microalgae.

When microalgae are under abiotic stress, jasmonic acids (JAs) primarily involve methyl jasmonate and jasmonic acid in signal transmission. Similar to SA, JAs can raise the expression of carotene-related genes in microalgae and promote the accumulation of antioxidant substances such as astaxanthin and β-carotene. In other words, microalgae phytohormones might be able to control how they grow, evolve, and use energy. One of the cornerstones of the "Green Revolution" in higher plants, which involved the introduction or improvement of agriculturally beneficial traits to attain ever-higher productivity of food crop cultivars, has been the manipulation of phytohormone systems.

Crop tolerance to a variety of abiotic stresses has been improved through the use of both genetic modification of endogenous phytohormones systems and the exogenous administration of phytohormones (alone or in combination with other plant growth regulators). (e.g., high levels of light, salinity, temperature extremes, drought, flooding, and lack of nutrients) As part of activities to tackle the energy crisis and global warming, oleaginous microalgae have been thought about as a potential feedstock for biofuels microalgal strains discovered in nature have a sufficient level of biomass productivity, oil content, and environmental tolerance to sustain cost-competitive production. considering the important regulatory roles played by phytohormones in higher plants, for instance, in germination, seed development, growth, vegetative growth and development, biomass manufacturing, dormancy, senescence, and in response to environmental factors, the discovery and dissecting of phytohormones systems in algae could help investigators to devise rational methods to select or genetically engineer algal species for useful industrial traits, such as increased biomass productivity and elevated tolerance to adverse the environment. Conditions (Figure 2). Such hormone-related elements, whose functions may or may not be comparable to those of those found in higher plants, could be possible targets for the development of microalgal feedstock.

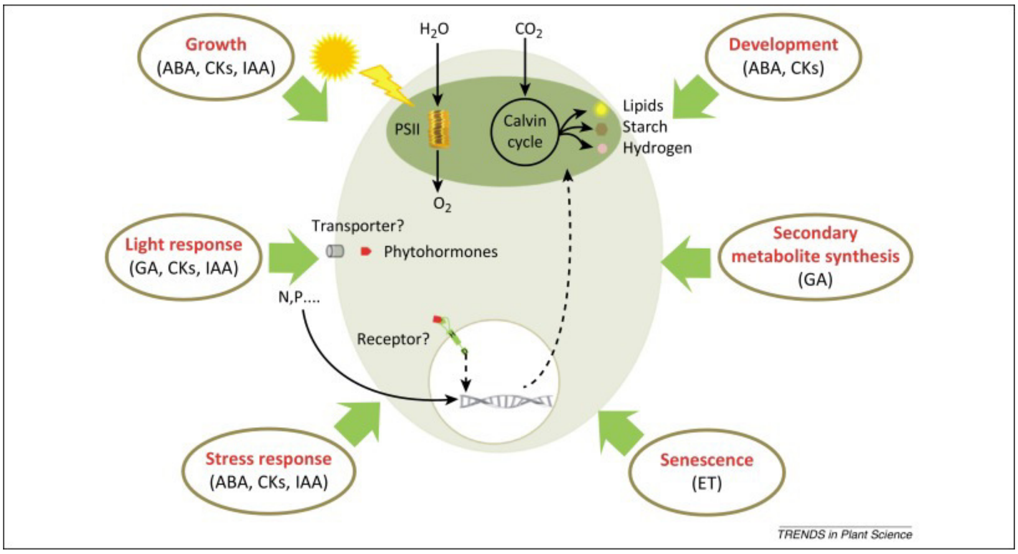


Figure 2: Effects of the phytohormones on the algae: Diagram showing the different effects of the phytohormones on the algae (Semantic scholar).

LITERATURE REVIEW

Algal growth and maturation are governed by the hormonal regulatory system, just like in the case of higher plants. Essentially all known phytohormones were identified in different algal taxa, and the range of their physiological activities was verified. However, we know very little about the enzymes that phytoplankton use to synthesize phytohormones. The information on the genes that produce these enzymes is still in its infancy. According to recent information on the proteomes of some algae, conserved regions and amino acid sequences that are similar to those of higher plant enzymes can be revealed [1].

Environmental pollution by heavy metals (HM) is a serious problem that is driving up demand for remediation methods. Algae-based remediation presents an economical, effective, and efficient alternative for HM elimination. Similar to plants, the hormonal system governs the growth and development of algae. Phytohormones are involved in HM tolerance and can thus control remediation ability, but the precise processes by which they work are still unknown. The goal of this study is to develop a thorough model of the contributions of phytohormones to algal performance under HM stress. We concentrate on the processes of HM biosorption, uptake, and intracellular storage, as well as the interactions between phytohormones and algal defense mechanisms when exposed to HM. We give instances of how algae have been successfully used in remediation and the post-processing of algal materials. Finally, we go over the benefits and dangers of algae remediation. Effective HM remediation strategies can be informed by a thorough knowledge of these processes [2].

A wide range of microalgal lineages has been discovered to contain phytohormones, including auxin, abscisic acid (ABA), cytokinin (CK), ethylene (ET), and gibberellins (GAs). Molecular evidence from the oleaginous microalga Nannochloropsis oceanica shows that endogenous ABA and CK are functional and that their physiological effects are comparable to those in higher plants, even though the functional role of microalgal endogenous phytohormones remains elusive. In this Opinion piece, we propose that modern higher plant phytohormone biosynthesis pathways descended from ancient microalgae, even though some of the microalgal phytohormone signaling pathways are still unknown. This idea is founded on genome-based metabolic reconstruction. A new perspective on the development of phytohormones in plants may result from the dissection and manipulation of microalgal phytohormone systems, which may also open up new possibilities for producing microalgal feedstock for biofuels [3].

Recently, it has been thought that using phytohormones could improve the lipid productivity of microalgae. To examine how auxin phytohormones affect microalgae and how they work, eight dosages were tried. Scenedesmus sp. SDEC-8 and Chlorella sorokiniana SDEC-18 saw increases in biomass concentration of 59.3% and 76.6%, respectively, while lipid content increased from 18.74% to 56.17% (SDEC-8) and from 19.69% to 55.76% (SDEC-18). (SDEC-18). The stimulants triggered proton pumps, causing H+ to be excreted, which led to a drop in pH and a favorable environment for growth. , etc. The inclusion of auxin increased the diameter of C. sorokiniana SDEC-18 by 3 m and changed the cellular structure of Scenedesmus sp. SDEC-8, enhancing the ability of the cells to elongate. For more information, visit the website.

An RP-HPLC-PDA method for the simultaneous analysis of 9 compounds deriving from the phytohormones class was developed and optimized, namely indoleacetic acid (IAA), indolebutyric acid (IBA), phenyleacetic acid (PAA), naphtyleacetic acid (NAA), trans-zeatin (TZ), kinetin (KA), isopentenyladenine (IA), 6-benzylaminopurine (6-BA) and abscisic acid (ABA). Using a mixture of Baltic algae, the SFE-CO2 extract was used to validate the technique. For plant hormones, the regression values ranged from 0.997 to 0.999. The values of the LOD and LOQ were 0.05-0.29 and 0.15-0.88 mg/L, respectively. The separation and identification of plant hormones in extracts obtained by SFE-CO2 (supercritical fluid extraction) from a mixture of Baltic algae, Cladophora glomerata and Spirulina sp., used a developed technique. The concentration of two of the tested chemicals in the extract of Baltic seaweed was 154,45 20,63 g/g for TZ and 362,47 13,00 g/g for PAA, whereas the concentration of PAA and IAA in the extract of Cladophora glomerata was 229,30 7,90 g/g and 23,91 0,80 g/g, respectively. (all values per g of extract). an an an ad an an an an an an an an an an an an a d by an e a g for the link an an e a. need an a need .

The present study was undertaken to test the influence of exogenously applied phytohormones: auxins (IAA, IBA, NAA, PAA), cytokinins (BA, CPPU, DPU, 2iP, Kin, TDZ, Z), gibberellin (GA3), jasmonic acid (JA) as well as polyamine - spermidine (Spd) upon the growth and metabolism of green microalga Chlorella vulgaris (Chlorophyceae) exposed to heavy metal (Cd, Cu, Pb) stress. Cd > Pb > Cu was the sequence in which heavy metals inhibited algal development, metabolite accumulation, and enzymatic and non-enzymatic antioxidant systems. Phytohormones that have been added exogenously alter the phytotoxicity of heavy metals. By preventing the biosorption of heavy metals, resuming algal development, and raising primary metabolite levels, auxins, cytokinins, gibberellin, and spermidine (Spd) can reduce the symptoms of stress. Additionally, by increasing the antioxidant capacity in cells developing under abiotic stress, these phytohormones and polyamines promote the activities of antioxidant enzymes (superoxide dismutase, ascorbate peroxidase, catalase), ascorbate accumulation, and glutathione production. Lipid peroxidation and hydrogen peroxide levels are indicators of oxidative stress, which was decreased by increased antioxidant enzyme activity. In comparison, JA increased the toxicity of heavy metals, which increased metal biosorption and ROS production. In reaction to JA and heavy metals, it was also discovered that cell number, chlorophyll, carotenoids, monosaccharides, soluble proteins, ascorbate, and glutathione content, as well as antioxidant enzyme activity, all decreased. Determining the stress markers (lipid peroxidation, hydrogen peroxide) and antioxidants' level as well as antioxidant enzyme activity in cells is important for understanding the metal-specific mechanisms of toxicity and that these associated novel endpoints may be useful metrics for accurately predicting toxicity. The evidence points to the importance of phytohormones and polyamines in C. vulgaris' ability to react to abiotic stressors and adapt to metal contamination of the aquatic environment [6].

We've analyzed and compiled information from the literature on biosynthesis, qualitative and quantitative diversity, participation in the regulation of physiological and biochemical processes, and the potential applications of microalgae cytokinins (CKs) and gibberellins (GA) in biotechnological developments. 37 types of CKs are found in 45 phytoplankton species from 5 divisions. It has been established that light conditions and the existence of an energy source in the culture medium have a significant impact on the qualitative composition and quantitative content of microalgae CKs. Microalgae CKs' primary biological actions include the promotion of cell division, activation of growth mechanisms, and enhanced photosynthetic activity. It is discovered that microalgae cytokinins have defensive qualities that shield cell divisions and the photosynthetic system from harm in stressful situations. It is still debatable how microalgal cytokinins are produced, and more research is required to understand how they combine with other phytohormone classes. Twenty hormone variants were found to exist in the 31 microalgae species that contained gibberellins. In a lag phase, microalgae GA shows reduced and stimulated cell growth and division, increased biomass, accumulated proteins and pigments, and reduced effects of heavy metals. These physiological effects are comparable to those of higher plants.

The lipid content of microalgae can be increased by nitrogen starvation, but due to poor biomass, this technique is not yet widely used. In this study a combination of phytohormones, indolebutyric acid (IBA) and naphthylacetic acid (NAA), was used to verify whether phytohormones can assist two microalgae, Scenedesmus SDEC-8, and Chlorella sorokiniana SDEC-18, to resist nitrogen depletion, and achieve satisfactory biomass and lipid productivity. Under nitrogen-depleted conditions and in the absence of phytohormones, the two algae grew slowly but amassed high lipid concentrations. However, the biomass concentration was preserved by the addition of phytohormones, which also produced lipid productivities that were nearly three times higher than those in BG11 (SDEC-8: 26.7 mg/L/d, SDEC-18: 25.9 mg/L/d). Phytohormones may be able to reduce the oxidative harm brought on by nitrogen depletion. In comparison to the strategy of nitrogen depletion alone, the study showed that phytohormone supplementation simultaneously improved lipid accumulation and kept microalgal growth while also optimizing the properties of biodiesel [8].

At concentrations comparable to those found in hydroponic effluent, the physiological effects of the phytohormones abscisic acid (ABA), 24-epibrassinolide (EBL), brassinolide (BL), and 3-indoleacetic acid (IAA) on the microalga Scenedesmus quadricauda were examined. The growth of S. quadricauda cells, the generation of biomass, as well as intracellular concentrations of chlorophyll-a, carotenoid, and lipids biosynthesis, were all positively stimulated by all tested phytohormones. EBL and IAA were the most effective inducers of carotenoid and chlorophyll-a biosynthesis, and IAA, ABA, EBL, and BL had the greatest effects on fatty acid biosynthesis.

The types of phytohormones and the precise concentrations examined had an impact on both the amounts of fatty acids and their profiles. The impacts, whether favorable or unfavorable, of all the tested phytohormones on S. quadricauda cell size were dose-dependent. To our understanding, this is the first paper that compares the effects of four phytohormones, including two different types of brassinosteroids, on a wide variety of physiological parameters in S. quadricauda [9].

CONCLUSION

Microalgal phytohormones systems may be dissected and manipulated to provide a novel perspective on phytohormones. Understanding the largely unicellular hormonal systems in eukaryotic microalgae could reveal more about the variety and development of intercellular signaling pathways in eukaryotes. In the endocrine system of multicellular organisms, one type of cell usually produces the signal molecule that is interpreted by other cell types. Despite evidence suggesting that excreted hormones play such intercellular signaling functions in several protozoa and microalgae, it is unclear how communications are mediated in unicellular eukaryotes. In summary, the lately started excitement for algae biofuel may result in stimulating novel understanding regarding metabolism as well as regulating systems of chemicals in the enormous and evolutionary distinct algae world, as well as provide new perceives of the phytohormones change in organisms and extensive fresh possibilities for algae biotechnology. The development of hormones in plants offers fresh possibilities for producing microalgae feedstock for biofuels.

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CHAPTER 17

SYNTHESIS OF PHYTOHORMONES BY PLANT-ASSOCIATED BACTERIA

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ABSTRACT:

This chapter discussed the overview of the phytohormones synthesized in association with the microorganism. Phytohormones that are involved in playing a role in bacterial association are mainly auxin, cytokinins, and gibberellins. Some microorganisms which are living in the plant are the rhizosphere, endophytic and nitrogen-fixing bacteria. Numerous microorganisms are capable of creating phytohormones, and it is possible to improve the microbial synthesis of indole-3-acetic acid, which can be used to produce it rather than extracting it from plants or synthesizing it chemically. This capacity for microbes to concurrently produce plant-based hormones and additional naturally present substances in antibacterial, and additional different consequences allows the development of complicated polyfunctional bacteria plans in different natural characteristics over utilize within agricultural output to promote growth development as well as an insect control.

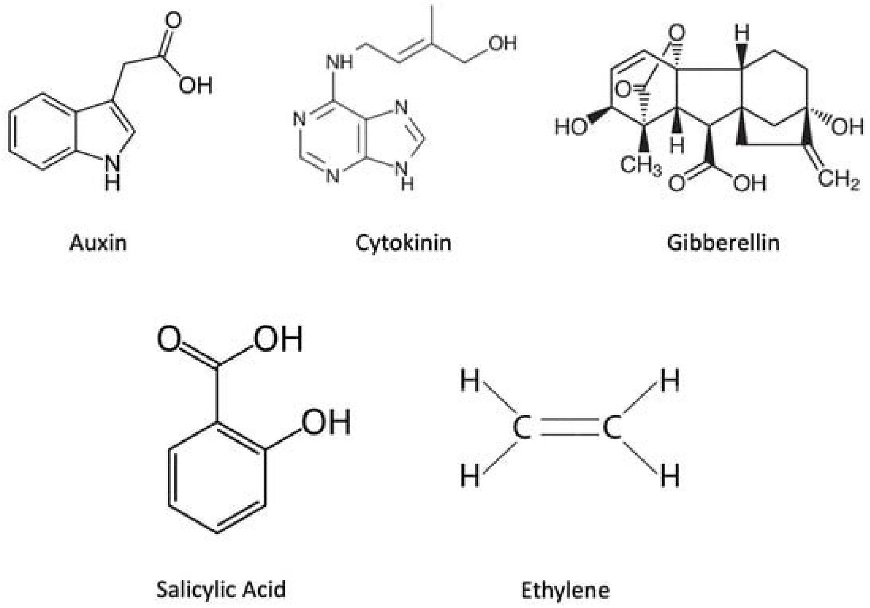
KEYWORDS:

Auxins Cytokinins, Biotic Factor, Plant Health, Plant Growth, Plant Development.

INTRODUCTION

The metabolic processes of plants are regulated by a variety of phytohormones, such as auxin, gibberellin, abscisic acid, salicylic acid, jasmonate, brassinosteroids, and gibberellin. It's interesting to observe that several of these phytohormones, including auxin, ethylene, gibberellin, salicylic acid, and cytokinin, can be produced or broken down by a variety of plant growth-promoting bacteria (PGPB) (Figure 1). Additionally, many PGPBs produce a wide range of different volatile organic compounds. (VOCs). Some of these VOCs influence plant growth directly, while others change how the aforementioned phytohormones are expressed. Plants and the PGPB encode phytohormones, which control how plants grow and evolve and help them adapt to environmental changes. (Both biotic and abiotic). Different phytohormones function by allowing or suppressing the expression of other plant genes, which support the plant's ability to respond to various environmental stresses. Furthermore, plants can maintain the highest amounts of various phytohormones by using the phytohormones-degrading activity found in many soil bacteria [1].

The majority of the knowledge that is currently available regarding the exact mode of action of various phytohormones was obtained in laboratory settings by administering purified hormones to plants and observing how these hormones affected the growth and development of the plants. However, it can be difficult to gauge the precise quantity of additional phytohormones that have been integrated into a plant and its intended target tissue. (added either as a purified chemical or as phytohormones produced by a PGPB). (s). The concentration and activity of a particular phytohormone may also have an impact on the production or breakdown of other phytohormones within a plant's tissues. Because the majority of PGPB can synthesize or alter the concentrations of a variety of phytohormones, it is frequently challenging to connect a plant's physiological response to a PGPB to a specific phytohormone. In order to study the effects of the mutant PGPB strains on plant growth and development in comparison to the wild-type strain, it is best to create mutants of the PGPB that lack or produce excessive amounts of a particular phytohormone[1]. Plant growth regulators are frequently used as agents for regulating plant growth and development, methods for increasing agricultural yield, and stimulants for seed and tuber germination. They are also frequently used to speed up the formation of roots and fruit ripening. Growth promoters control dormancy and speed up root development. (in plants where root age presents problems or does not occur under normal circumstances). Viral infections and diseases caused by phytopathogenic fungi are treated with phytohormones.



Auxin Cytokinin Gibberellin

Salicylic Acid Ethylene

Figure 1: Phytohormones: Diagram showing the chemical structure of the different phytohormones (MDPI).

Phytohormones must always be used when a whole plant is grown from an in vitro plant tissue culture. PGP Effect on Important Agronomic Crops: The observed PGP (plant growth promotion) effect includes modifications of the root morphology after inoculation with Azospirillum, such as a dramatic increase of length and density of roots hairs, increase in root branching and root surface area, which led to enhanced uptake of water and minerals. The bacterial production of phytohormones like IAA, gibberellins, and kinetin is thought to be the root source of all these effects. Employing low-IAA suppliers of Azidirillum inoculation affects the plant, either encouraging or discouraging root growth, depending on the concentration. In many legumes, microorganisms that produce plant hormones are sown: Microbial phytohormones have beneficial effects on plant embryos, seedlings, etc. when they are handled with cultures and/or suspensions of producer microorganisms. using rhizobacteria from the soil to treat seeds Azospirillum, Bejerinckia, Rhizobium, Agrobacterium, Bacillus, Pseudomonas, Mycobacterim, Arthrobacter, Methylovorus, and Flavobacterium greatly stimulate the germination capability and germination of seeds, which also increases the growth and crop yield of mature plants. With an increase in growth rate, both the capacity of the bacteria to colonize the plant and the number of phytohormones generated increase. Wheat (Triticum aestivum L.) growth and crop yield were substantially increased by rhizobacteria strains that produced trace amounts of auxins. Inoculation with cytokinin-producing methylobacteria of transgenic tobacco plants characterized by altered morphology (rootlessness) restored root formation and the effects of the microorganism culture on seed germination and plant development were similar to those of the phytohormones or the culture liquid of methylobacteria. Treatment of dwarf rice with Azospirillum lipoferum and A. brasilense, which is unable to synthesize gibberellins, resulted in a discernible stimulation of plant growth. This impact was brought on by the bacteria's ability to transform exogenous GA20 (gibberellins 20) into the biologically active GA1. Furthermore, the production of gibberellins for use in agriculture is primarily dependent on the industrial-scale cultivation of the fungus Fusarium moniliforme, whose optimal stage (Gibberella fujikoroi) produces significant amounts of different gibberellins. Plants that are rare, beautiful, or important industrially can have their seed treated with bacteria to make it impervious to germination.

As a result, auxin-producing bacteria from the genera Pseudomonas, Bacillus, Xanthomonas, Rhodococcus, and Micrococcus strongly stimulate the symbiotic germination of tropical orchid seeds and hasten their development when grown in a greenhouse. It should be taken into account that the beneficial effects of bacterial treatment depend on a variety of factors, including the activity of the strain, the concentration of the cells, the number of phytohormones in the culture liquid, the quantity of the dry preparation of the stimulating microorganism, the duration of the treatment, the species of the plant, the state of the indigenous microflora at the time of seeding, the characteristics of the soil and the general conditions of the agro technological complex. The introduction of bacterial inoculums will be more successful if the bacterial strains are separated from mature plants of the same species' rhizosphere or rhizoplane. It is not frequent that stimulation of plant growth and development by PGPR (plant growth promoting rhizobacteria) strains of bacteria is underlain not only by phytohormone formation, but also by their capacity for nitrogen fixation, improvement of plant nutrition (water and mineral) and prevention or suppression of phytopathogen growth; the latter effect is due to excretion by PGPR strains of bactericidal and fungicidal substances[2]. Promotion of sugar cane: Up to 80% of the total N added to some sugar cane types is accounted for by BNF. (biological nitrogen fixation). It's a good idea to get a second opinion before making any decisions.

Under N-sufficient growth circumstances, plants inoculated with Gluconacetobacter diazotrophicus—either the wild type or a nifD mutant—grow 20% more than non-inoculated plants. These results suggest that Gluconacetobacter diazotrophicus could benefit sugarcane by transferring fixed bacterial nitrogen and by generating phytohormones. According to ACC-deaminase, there was an increase in root length. One of the ethylene's roles is to stop the growth of roots. It has been shown through experiments using canola roots inoculated with E. cloacae that the ACC-deaminase contributes to preventing the ethylene impact. By reducing plant ethylene levels, the bacterium enzyme ACC-deaminase stimulates plant growth. In addition to causing morphological changes, Osmo protection (the creation of osmolytes), and biofilm formation, drought also triggers microbial reactions. Overall, drought reduces microbial biomass by affecting soil heterogeneity, limiting nutrient mobility and availability, and increasing soil oxygen. Due to their thicker cell walls, monoderm bacterial lineages like Actinobacteria, Chloroflexi, and Firmicutes are well known to be more resistant to desiccation. Plant metabolism is what promotes their enrichment during dry times. Plant substances produced by drought, such as sugar, amino acids, and particularly G3P, are used in bacterial metabolism and serve as precursors to peptidoglycan biosynthesis in the creation of cell walls, which increases the capacity of monoderm taxa to increase host fitness. Uneven seasonal rainfall is a characteristic of semiarid habitats, including the caatinga biome. Recent studies have revealed the potential of native caatinga plant-associated bacteria as inoculants to encourage plant development in drought-prone environments. The microbes in caatinga may have evolved to withstand high temperatures, have desiccation tolerance genes, produce pigment to block UV light, produce thermostable enzymes, and produce intracellular osmolytes. A potential method to find a subset of particular microbial taxa and functions to increase plant drought tolerance is to investigate microbiome functions to comprehend how ecological processes work during long-term drought systems. To comprehend the relationships between environmental variables, however, whole microbiome community profiling, core microbiome assessments (composition and function), and characterizations of plant root exudates under moisture limitations will be required. The evolution of ecological systems that will be sustainable in our future global climate depends on identifying the microbiome functions that allow plants to control drought stress. Plant-growth-promoting rhizobacteria (PGPR), mycorrhizal fungi, and viruses are the plant-associated species that have been the focus of the most research (Figure 2).

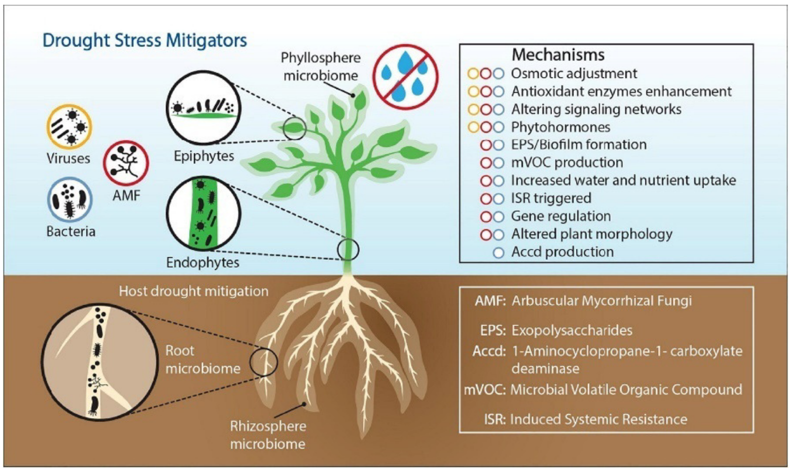


Figure 2: Over of the microorganism association with the plant: Diagramed showing the role of the different microorganism association to plant in the stress condition (Frontier).

LITERATURE REVIEW

Several phases of plant growth and development, including cell elongation, cell division, tissue differentiation, and apical supremacy, are regulated by the plant hormones auxins and cytokinins. A lot of research has been done on biosynthesis and fundamental mechanisms of action of auxins and cytokinins. Auxins and cytokinins can be made by microbes as well as plants. The role of phytohormone biosynthesis by microorganisms is not fully elucidated: in several cases of pathogenic fungi and bacteria these compounds are involved in pathogenesis on plants; auxin and cytokinin production may also be involved in root growth stimulation by beneficial bacteria and associative symbiosis. Pseudomonas, Agrobacterium, Rhizobium, Bradyrhizobium, and Azospirillum have well-studied genetic mechanisms for auxin biosynthesis and regulation, and a number of their physiological impacts have been linked to the production of bacterial phytohormones. Indole-3-acetic acid is produced by the indole-3-acetamide pathway, which is used by the pathogenic microbes Pseudomonas and Agrobacterium. They do, however, also have the chromosomally encoded indole-3-pyruvic acid system. Additionally, they possess genes that can hydrolyze conjugated types of auxins and cytokinins or conjugate free auxins. Near the auxin and cytokinin biosynthetic genes in Agrobacterium are a number of additional genes that control how sensitive the changed plant tissue is to auxins and cytokinins. Indole-3-pyruvic acid is used by the symbiotic bacteria Rhizobium and Bradyrhizobium to produce indole-3-acetic acid. Genetic determinants for the indole-3-acetamide pathway have also been found, but their function has not yet been proven. Both the indole-3-pyruvic acid and the indole-3-acetamide pathways are found in the plant growth-promoting bacteria Azospirillum, just like in Agrobacterium and Pseudomonas, though in Azospirillum the indole-3-pyruvic acid pathway is of primary importance. A tryptophan-independent indole-3-acetic acid route in Azospirillum has also been suggested by biochemical evidence [2].

On plants, secreted metabolites facilitate interactions between microbial communities and their host. The combined impact of various organisms and their various metabolites on plant health hasn't yet been completely understood. A review of the multifactorial interactions at the molecular and organismal levels that result in the biological regulation of plant diseases is presented here. In order to do this, we go into great detail about the ecological importance of three distinct classes of secondary metabolites and talk about how they might aid in biological control. Because auxin, acetoin, and phenazines are three very distinct but significant types of secondary metabolites, their functions are specifically examined. We also discuss the identification of novel genes and phenotypes associated with plant health enhancement as a result of research on the global regulation of bacterial secondary metabolism. We conclude by outlining three directions for future study that will aid in fusing these nuanced and disparate findings into a more cohesive synthesis of bacterially driven biocontrol of plant diseases [3].

Indole-3-acetic acid (IAA), ethylene (ET), and salicylic acid (SA) are significant phytohormones that control plant growth and development as well as relationships with microbes. Plant growth-promoting bacteria (PGPB) are naturally found in association with plants and promote plant development through a number of mechanisms, including the capacity to control the levels of these phytohormones in planta. Furthermore, the prevalence of phytohormone degradation pathways among symbiotic and other soil- and plant-associated bacteria suggests that the capacity to control phytohormone concentrations is crucial for bacterial colonization and plant development promotion. Therefore, obtaining phytohormone-degrading bacteria is essential for the creation of innovative approaches intended to boost plant growth and defense.

In this paper, we report an optimized targeted methodology and the consequent isolation of novel soil- and plant-associated bacteria, including rhizospheric, endophytic and phyllospheric strains, with the ability to degrade the phytohormones, SA, and IAA, as well as the ET precursor, 1-aminocyclopropane-1-carboxylic acid (ACC). By using an optimized targeted methodology, we rapidly isolated diverse soil- and plant-associated bacteria presenting phytohormone-degrading abilities from several plants, plant tissues, and environments, without the need for prior extensive and laborious isolation and maintenance of large numbers of isolates. Research on PGPB is made easier by developed methods, particularly in developing nations. Here, we also disclose the discovery of bacterial strains that can simultaneously metabolize three phytohormones for the first time. (SA, IAA, and ACC). At the end of the day, the targeted methodology outlined here and the novel phytohormone-degrading bacteria discovered as a result of this work may prove to be helpful resources for upcoming plant-microbe interaction studies as well as the creation of fresh inoculant formulations for biotechnology and agriculture [4].

In terms of the habitats they live in, their phylogeny, and the effects they have on the health of plants and the environment, bacteria that associate with plants are varied. Bacterial habitats are unique in the spermosphere, rhizosphere, phyllosphere, vascular tissue, and endophytic areas. Although the phylogenetic diversity of bacteria in these environments spans both the bacterial and archaeal domains, only four bacterial phyla the Cyanobacteria, Proteobacteria, Firmicutes, and Actinobacteria are known to be phytopathogens or phytosymbionts. The majority of commensal prokaryotes that are associated with plants are located mostly on plant surfaces and have no discernible impact on plant growth or physiology. Mutualistic bacteria include the legume symbionts, Frankia, and cyanobacterial symbionts, which form nitrogen-fixing symbioses, as well as associative nitrogen-fixing bacteria and plant growth-promoting rhizobacteria, which can enhance plant growth directly by increasing nutrient availability or producing plant growth-enhancing products, and indirectly by biologically controlling plant diseases. The symptoms that phytopathogenic bacteria produce are as varied as their invasion tactics, methods of pathogenesis, cultivability, and even genome structure and fluidity. The ice nucleating bacteria, the bacteria that overproduce plant growth regulators, and the harmful rhizobacteria, which can aid in weed management, are additional organisms that can adversely affect plant health. Plant-associated bacteria have an impact on the health of the ecosystem by helping to remove pollutants from the soil, decompose organic matter, and aggregate soil. Recent developments in microbial ecology, genomic sequencing, and functional genomics are fundamentally altering how we study these organisms and the questions we can ask about their biology and relationships with plants [5].

The area of soil that plants roots physically, chemically, and biologically effect is known as the rhizosphere, and it is incredibly diverse and active in terms of microbes. This microbial activity promotes nutrient uptake by the plant and provides resistance to a wide variety of plant pathogens, making it crucial for plant nutrition and health. The majority of microbial species in the rhizosphere are bacteria, and plant growth-promoting rhizobacteria (PGPR) promote plant development through a variety of mechanisms. This part provides an overview of the methods used by PGPR to have a positive impact on the colonized plants. The ability of PGPR to enhance plant nutrition and phytohormone production accounts for the majority of their direct impacts on plant growth. As an alternative, helpful rhizospheric bacteria can also benefit plants by defending them against pathogens, primarily by triggering systemic resistance and producing exoenzymes and a variety of antagonistic compounds. Here, particular focus has been placed on the biosynthesis and biochemical functions of polyketides, non-ribosomal peptides, and bioactive volatiles by PGPR. And finally, there is a discussion of the potential application of PGPR-based products as sustainable agricultural practices [6].

Growing plant cells release large amounts of the one-carbon alcohol methanol as a result of their wall-associated pectin metabolism. The Methylobacterium genus, which produces pink-pigmented microbes that live on the surfaces of leaves (epiphytes), can develop using this volatile C1-compound as their only source of carbon and energy. The findings of experiments using gametophytes of bryophytes (a moss and two species of liverwort) and germ-free (gnotobiotic) sporophytes of angiosperms (sunflower, maize) are compiled in this paper. The evidence indicates that methylobacteria does not promote the growth of these angiosperms, but they do significantly promote organ development in moss protonemata and in liverwort thalli. A model of plant-microbe interaction (symbiosis) is suggested in which the methanol-consuming bacteria are viewed as the gametophyte's co-evolved partners that control its growth, survival, and reproduction. This is because methylobacteria produce and secrete cytokinins and auxin. (fitness). The diploid sporophytes of higher embryophytes, which are perfectly adapted to life on land and appear to generate enough endogenous phytohormones, are exempt from this symbiosis because they are not moisture-dependent "living fossil" plants [7].

A group of free-living bacteria known as plant growth-promoting rhizobacteria (PGPR) colonize the rhizosphere and aid root development. Numerous groups of bacteria were found to be PGPR, with Bacillus and Pseudomonas species predominating. The production of phytohormones, solubilization of inorganic phosphates, increased iron nutrition via iron-chelating siderophores, and volatile compounds that influence plant signaling pathways are all direct effects of PGPR on plant growth. Additionally, by antibiosis, competition for space and nutrients, and induction of systemic resistance in plants against a broad spectrum of root and foliar pathogens, PGPR reduce the populations of root pathogens and other deleterious microorganisms in the rhizosphere, thus benefiting plant growth. Root colonization is a limiting element for the effectiveness of PGPR and is influenced by a variety of biotic and abiotic factors

In order to monitor the introduced PGPR in the rhizosphere, as well as to ascertain their metabolic state and the impact they have on the indigenous rhizosphere microbial communities, numerous reporter genes and nucleic acid-based methods have been developed. The viability and effectiveness of the PGPR formulations decide how widely they are adopted by end users. With particular emphasis on the mechanisms underlying their action, the variables influencing their effectiveness, and the potential for improvement, we address the significance of PGPR in sustainable agriculture [8].

CONCLUSION

Chemicals known as plant hormones are produced by plants to control their development and growth. Traditional approaches like inheritance, molecular science, biology, and molecular biology have made it easier to study the development of phytohormones. In this study, plant-associated bacteria control and significantly affect the growth and development of the plants. In reaction to external environmental conditions, various bacterial groups connected to plants secrete phytohormones. At this chapter's end, we outlined the various microorganisms' functions and how they contribute to the production of phytohormones.

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CHAPTER 18

PLANT FRUITS DEVELOP AND GROW VIA PHYTOHORMONES

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ABSTRACT:

Plant hormones are a crucial component of the plant that controls its development and growth. In addition, plant hormones are crucial for the development and development of the crop in plants. The coordinated actions of the various phytohormones and their signaling cascades result in plant fruit ripping. The growth and development of the fruits go through several phases. Fruit development includes the start of fruit set, growth, maturation, and ripening. Fruit formation happens after fertilization and is controlled by auxin and gibberellic acid signaling. The interplay between auxin and GAs as well as other phytohormones is controlled by auxin-responsive. Fruit development requires cell expansion and division, with the former procedure being demonstrated to be affected by auxin signaling. Research indicates that auxin and GAs cooperate with the input from other hormones to synergistically regulate cell growth, despite the fact that the regulation of cell growth is less well understood. Fruit matures, a transitory stage that hastens to ripen, when auxin and GA levels fall and abscisic acid and ethylene levels rise simultaneously. The summary of fruit ripening and maturation in the presence of phytohormones was covered in this chapter.

KEYWORDS:

Abscisic Acid, Fruit Ripening, Fruit Growth, Fruit Development, Plant Growth.

INTRODUCTION

The plant hormone auxin is a crucial regulator of numerous plant growth processes when it functions in concert with other plant hormones. Early fruit development in horticultural plants is particularly dependent on hormonal control of cell division and expansion. According to Joseph Gaertner's definition of fruit from a developed ovary in 1788, a fruit is a structure that contains seeds. Accessory fruits, which contain additional pieces of flower tissue, are frequently present with fruits. Only a tiny portion of the floral organ typically the gynoecium—develops into fruit during the flower's development. After the flower has opened, fertilization causes this tissue to enlarge, first through the activity of auxin. The biosynthesis of additional plant hormones, such as gibberellin (GA), can be aided by the auxin signal. The interaction of auxin with these additional hormones then regulates fruit growth and maturation. In many plant species, auxin and GA encourage cell division and enlargement during plant development. Fruits from various horticultural crops are not anatomically identical organs because of the diversity in the structure of floral organs or morphological characteristics[1]–[3].

The same plant hormones auxin and GA, however, regulate the development of these anatomically distinct fruit tissues, and it is intriguing that only fruit tissues in floral organs have strong competence for enlargement in response to these plant hormones. As a result, plant hormones like auxin and GA play a significant role in regulating how big the fruits of various plant types grow. Where does auxin, which encourages fruit development, originate (which tissues). Are the important actors in these plant hormones' signaling cascades conserved in anatomically distinct fruits. How are auxin and GA functions linked during the early stages of fruit development? In this review, we discuss how auxin and GA act coordinately to initiate fruit development and to promote fruit growth, focusing on the model plant Arabidopsis thaliana and two horticultural plants, tomato (*Solanum lycopersicum*) and strawberry (Fragaria vesca), as excellent examples of molecular genetic studies on fruit development. We address the possible mechanism suggested by expression analysis in grapes Which may play a key role in the development of parthenocarpic fruit, which is particularly important in the production of grapes.

Angiosperms are the only organisms with the elegant evolutionary strategy of fruit growth, which protects developing seeds and aids in seed dispersal. After two fertilizations, fruits develop from the ovary's development and enlargement and, on rare occasions, from auxiliary tissues, as in the case of the apple (*Malus domestica*) or strawberry (*Fragaria ananassa*). A rich diversity of fruit morphologies, generally categorized as dry or fleshy, exists across species and within families, and recent evidence suggests that dry morphotypes like the siliques of Arabidopsis thaliana are ancestral to the softer, flavorful tissue exhibited by fruits typically cultivated in orchards. Some phylogenies show the evolution of dry fruit varieties from fleshy fruit ancestors. The fact that dry fruit types senesce rather than ripen and acquire a lignified pericarp encasing their seeds that either stays fused shut (indehiscent phenotype) or mechanically shatters around an abscission zone is a crucial difference between dry fruit types and fleshy fruit types.

While fleshy fruits like tomatoes (*Solanum lycopersicum*) engage in numerous cellular modifications that collectively make them aromatic and delectable, increasing their ability to draw frugivores, dry fruits depend on abiotic methods to sow their seeds. These changes include the accumulation of starch during early development, cell wall remodeling to facilitate softening, changes in color as chloroplasts are degraded or de-differentiated into chromoplasts, and the fine-tuning of starch hydrolysis and the tricarboxylic acid (TCA) cycle to increase sweetness and modulate tissue acidity. A tomato (a berry), peach (Prunus persica) (a drupe), or strawberry are just a few examples of fleshy fruits that exhibit an impressive diversity of forms and flavors due to the presence or extent of such changes. (an aggregate fruit). Moreover, fleshy fruits are divided into climacteric and non-climacteric groups, with the former being distinguished by a rise in respiration and a sharp sensitivity to elevated ethylene. Although numerous observations indicate that they may either be more sensitive to ethylene or simply show less extreme hormone production and responses, non-climacteric fruits are less dependent on elevated ethylene for ripening.

A surprising amount of similarity has been found in the regulation of cellular events causing ripening and senescence between fleshy fruits and dry fruits, respectively, despite their remarkable phenotypic differences. A transcriptomic analysis comparing Arabidopsis siliques and tomato berries revealed that both species experience similar biological processes and parallel programs of cytological change following fruit maturation, even though minimal overlap exists between either species in terms of the number of genes being expressed. After the fruit set, both dry and fleshy fruiting species need to go through stages of cell division and expansion. This enables the measurement of fruit size before maturation and senescence/ripening. It was discovered that orthologous SHATTERPROOF MADS-box genes are essential for replum development and shattering in Arabidopsis as well as for fruit fleshiness and ripening in tomatoes in an intriguing example of functional characterization of homologous transcription factors. For seeds to disperse in dry and fleshy fruits, respectively, both of these mechanisms are required. Transient concentrations of phytohormones play an important role in the extensive regulation of the phases of cell development and death experienced by both fleshy and dry species. It has been repeatedly shown that growth-promoting substances like auxins and gibberellic acids (GAs) are essential because exogenous applications of both phytohormones can start fruit set and development even in the lack of fertilization. (parthenocarpy). Arabidopsis siliques also react to the presence of ethylene, which is crucial for controlling the ripening of tomatoes and other climacteric crops. Given the critical role of fleshy fruit in the human diet and the need for a deeper understanding of fruit biology in the face of evolving pest populations and a changing climate, the content of this review aims to present and highlight recent insights and open questions relevant to phytohormones-mediated fruit set, growth, and ripening, It has long been understood that ethylene is a key factor in fruit ripening, but it has only recently come to light that other molecules and/or processes may interact with ethylene and have an effect on the fruit's physiology and desirable qualities. A map of intricate interactions that control fruit quality and shelf life has been discovered through the molecular dissection of fruit growth and ripening processes (Figure.1). Studies on mutants that affected ripening, nutritional qualities, or photomorphogenesis have thus demonstrated the significance of ethylene biosynthesis and perception in addition to a link with light sensitive elements in bringing about the desired changes[4]–[6].

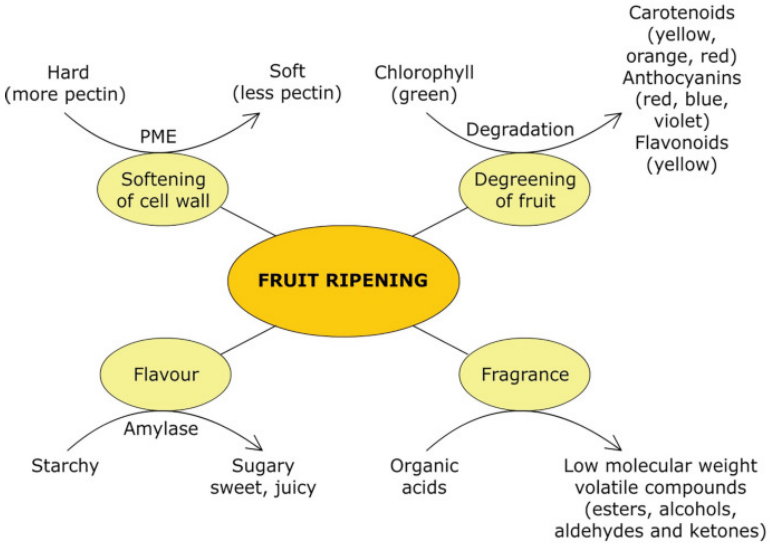

Figure 1: Fruits developments and ripping: Diagramed showing the overview of the development and ripping of the fruit (Springer link).

Auxin, cytokinin, gibberellins, ABA, jasmonates, and brassinosteroids are additional phytohormones that are important for fruit growth and ripening in addition to ethylene. Polyamines have recently come to light as important growth regulators of fruit flavor and shelf life. Breeding and molecular genetics techniques are revealing a great deal about particular genetic factors that are essential for enhancing the shelf life and biotic and abiotic signal response of fruits. It is becoming clear that additional efforts are required to fully understand the role of epigenetic factors in these processes, even though the study is still being done to address such significant challenges. It has been shown that protein glycosylation, specifically those enzymes that change the N-glycosylation of enzymes, affects fruit texture and shelf life. Thus, introduced difficulties include determining the order of authorities or a specific pattern of events that regulate desirable attributes and then using genetic assistance to alter critical and beneficial handles without any unfavorable impact on the plant, the environment in which it is grown, or the consumer. It is imperative to create and evaluate transgenic plants in the field that are especially well-suited to flourish in environmentally sound, long-term agricultural systems that rely little on chemical input and synergetically (positively) affect plant metabolism.

LITERATURE REVIEW

Phytohormones play a crucial role in controlling the growth and maturation of produce. By emphasizing fleshy fruit and highlighting new research in the model crop tomato (*Solanum lycopersicum*) and other species, this review advances our knowledge of the relationship between hormone signaling and fruit development. Fruit set initiation, growth, maturation, and ripening are all parts of fruit formation. After fertilization, fruit establishment occurs and is regulated by auxin and gibberellic acid (GA) signaling. Auxin-responsive Aux/IAA and ARF proteins modulate the interaction between auxin and GAs as well as other phytohormones. Cell expansion and division are required for fruit development, with the former process being shown to be influenced by auxin signaling. Although the regulation of cell growth is less well known, evidence suggests that auxin and GAs work in concert with input from other hormones to synergistically regulate cell growth. When auxin and GA levels decline with a concomitant increase in abscisic acid (ABA) and ethylene, fruit maturation, a transitional phase that precipitates ripening, takes place. In climacteric fruits, ethylene is involved in the ripening process, whereas ABA is typically linked to non-climacteric fruit development. Recent research suggests that both ripening physiologies require different amounts of both hormones, indicating that rather than relying solely on one, common regulators should be rebalanced and given specific roles. Numerous recent discoveries pertaining to the molecular basis of hormonal activity and crosstalk are discussed, while we also note that many questions remain such as the molecular basis of additional hormonal activities, the role of epigenome changes, and how prior discoveries translate to the plethora of angiosperm species.

The expansion of an ovary (carpel) or accessory tissue is frequently used by plant species that produce fruit as a means of seed dissemination. The tissues of the fruit follow a typical pattern of cell division and cell expansion as the seed(s) form, aiding in the fruit's growth. Once the seed is completely formed, the fruit reaches maturity and the surrounding tissue either dries out or ripens, aiding in the seed's dispersal. Plant hormones play a crucial part in the synchronization of signals between the growing seed and the surrounding fruit tissue(s), controlling each stage of fruit development, as they do with many other developmental processes in plants. After pollination, auxin, cytokinin, and/or gibberellin work together to depress development and activate cell division in order to produce fruit. After fruit set, the fruit's growth is aided by a time of cell expansion and endoreduplication, which is probably controlled by the same hormones as during fruit set. Fruit is ready to experience ripening once the seeds have reached maturity. During this time, there is a significant change in the relative hormone levels of the fruit, with an overall decrease in auxin, gibberellin, and cytokinin and a concurrent rise in abscisic acid and ethylene. Despite the fact that the function of hormones in fruit set and ripening is well understood, little is known about the functions of other hormones during development, maturation, and some specific ripening components[7]–[9].

Cherry tomato seeds (Lycopersicon esculentum Mill.) cv. Small Fry hormonal extracts At various phases of fruit development and maturation, auxin, gibberellin, cytokinin, and growth inhibitor activities were bioassessed. In comparison to the more mature fruits, the levels of endogenous growth promoters were generally much greater in the early developing fruits. The first two weeks of development saw the highest amounts of free cytokinin before a sharp decline. However, following treatment with alkaline phosphatase, cytokinin activity in the ribotide fraction decreased during the first three weeks of development and then rose quickly over the next four weeks. Early development saw a rise in auxin levels, which peaked in fruits that were three weeks old after anthesis. Gibberellin levels were significantly lower than those of auxins and cytokinins during the first two weeks of development, but they then rose to a climax in the fourth week following anthesis. The acidic fraction of the fruit extracts contained a substance that inhibited growth and had an Rf comparable to that of abscisic acid. This inhibitor grew steadily throughout the fruit's growth and development, peaking at five weeks, which is also when the fruit reaches the green mature stage.

The roles of plant hormones in the regulation of different facets of plant development have been thoroughly investigated. But over the past ten years, significant new discoveries have been made regarding their role in the growth and ripening of both dry and fleshy fruits. According to emerging research, a complex network of multiple plant hormones is involved in regulating different aspects of fruit development. This indicates that the relative functions of plant hormones are not limited to a specific stage. Despite the fact that some topics have received a great deal of attention, there are still many unanswered questions regarding the regulation of hormonal networks and the interactions between various hormones during fruit growth, maturation, and other ripening processes. In order to comprehend their mechanism of action in fleshy fruits, we assess the new information on their relative roles during tomato fruit development in this section. Relevant data on hormonal crosstalk during fruit development in other species are also addressed for a better understanding. We anticipate that having such thorough information will make it easier to create fresh plans for manipulating fruit ripening.

Abscisic acid (ABA) is a plant growth regulator well-known for its roles in biotic and abiotic stress adaptation, seed development, seed dormancy, and leaf and bud abscission. Multiple regulatory mechanisms that regulate ABA biosynthesis, signal transduction, and transport are in charge of controlling ABA activity. The ABA signaling molecule is transported from the stalk (the site of synthesis) to the fruit (the site of action), where ABA receptors interpret data as fruit maturation gets started and is strongly encouraged. The phloem of developing fruits exports the most ABA during seed formation and the start of fruit growth. ABA builds up in ripening fruit as a result of a substantial decrease in ABA export from the phloem in the later stages of fruit ripening. ABA regulates fruit development, ripening, and senescence, and the mechanisms underlying these processes are still being discovered. Both climacteric and non-climacteric fruits exhibit interplay between ABA and ethylene during the ripening process. Although it is obvious that ABA controls ethylene biosynthesis and signaling during fruit ripening, the molecular process governing how ABA and ethylene interact has not yet been identified. In order to comprehend the function of ABA in fruit ripening, more in-depth research is required to clarify the mechanisms underlying reaction and biosynthetic processes, signal transmission, and recognition of ABA receptors in fruits. Commercial uses of ABA signaling can be used to improve fruit yield and quality through genetic modifications. The mechanism of ABA biosynthesis, its translocation, and signaling pathways are all covered in this review, along with new research on the role of ABA in fruit development and ripening.

The development, reproduction, and senescence of a plant's primary organs leaves, flowers, and fruits—occur during the complex juvenile/maturity transition. Growth and senescence of leaves, flowers, and fruits involve several genetic networks where the phytohormone ethylene plays a key role, together with other hormones, integrating different signals and allowing the onset of conditions favorable for stage progression, reproductive success and organ longevity. The perception of ethylene, its level, and the hormonal interactions all directly or tangentially affect how long plants live. The emphasis of the current review was on ethylene's function in the growth and senescence of leaves, flowers, and fruits, with a particular focus on the intricate networks of ethylene crosstalk with other hormones. Additionally, areas where more research is needed have been emphasized, expanding our knowledge of the role of ethylene during growth and senescence and fostering future study aimed at enhancing the qualitative and quantitative traits of crops.

To improve crops in a sustainable manner and provide high-quality nutrition and output for a populace that is constantly growing, agriculture must overcome many obstacles. Phytohormones participate in a variety of life cycle events. Plant hormones are crucial regulatory biochemicals that affect a plant's growth and economic output under a variety of conditions, including duress. When given to plants or seeds, plant growth regulators (PGRs), which are biological and chemical hormone analogs, can stimulate, inhibit, or influence physiological features, improvements, and stress responses. By preserving a striking equilibrium between sources and sinks, PGRs are used in agriculture to increase crop yield and quality and overcome biotic and abiotic stresses. PGRs have been associated with root induction, blooming control, sex expression, maturity, plant aging, and modulation of environmental stress. By favorably affecting the regulation of the ascorbate-glutathione cycle, transpiration rate, cell division, and nitrogen metabolism and assimilation activities, exogenous phytohormone administration, such as auxins, cytokinins, and gibberellins, can support plant growth activity. To increase plant growth and output in unfavorable environmental conditions, PGRs are frequently used in agriculture, horticulture, and viticulture.

Citrus fruit growth and development are altered by the huanglongbing (HLB) infection, resulting in tiny, crooked, and unappealing fruit with undeveloped or aborted seeds. Fruit with symptoms typically develop later and abscise earlier. Because (1) a lack of carbohydrates has been associated with fruit growth arrest and ultimate abscission and (2) hormonal signals at least partly control fruit set and development, we investigated carbohydrate and phytohormone changes in HLB-affected fruit to explain symptom development. 'Valencia' sweet orange trees [Citrus sinensis (L.) Osbeck] were used to gather symptomatic fruit (S), asymptomatic fruit (AS) from symptomatic trees, and healthy fruit (H) from asymptomatic trees. PCR testing was used to determine whether or not the trees were contaminated with the HLB pathogen. Compared to AS or H, mature S were lighter, had a lower °Brix, were smaller, had more lost seeds, and were greener.

Compared to H and AS, mature S flavedo had reduced starch and sucrose contents. Indole-3-acetic acid (IAA) and abscisic acid (ABA) contents in flavedo removed from the stylar end, middle section, or stem end of fruit were typically higher in S flavedo than in AS and H. S and AS harvested 7 and 12 months after full bloom produced considerably less ethylene than H. In comparison to AS and H, the ABA content of flavedo from the center of S was four times higher. When compared to the normal-sized area of the same fruit on the other side, the flavedo removed from the large shoulder of misshapen S had a considerably higher IAA content. The size of the hypodermal cells in S flavedo also increased in accordance with this rise. Overall, these findings point to an unbalanced carbohydrate and phytohormone status in fruit from HLB-infected trees and indicate that such changes may play a role in the emergence of fruit symptoms.

After 4 hours of incubation, isopentenyl adenosine (IPA), mixtures of IPA and indoleacetic acid, and mixtures of IPA, indoleacetic acid, and gibberellic acid substantially decreased the amount of ethylene produced by tissue slices from preclimacteric, climacteric, and postclimacteric apples. Slices of apple (Pyrus malus L.) produced more ethylene in preclimacteric tissues than climacteric peak tissues, with little change in postclimacteric tissues. In tissues from preclimacteric apples, indoleacetic acid reduced ethylene production; however, it increased ethylene production in late climacteric rise, climacteric, and postclimacteric tissue sections. Preclimacteric peak tissue was less affected by gibberellic acid's suppression of ethylene synthesis than were late climacteric rise, climacteric peak, and postclimacteric tissues. In the pre- and postclimacteric tissue of tomatoes (Lycopersicon esculentum) and avocados, IPA also reduced ethylene generation. (Persea gratissima). IPA would appear to retard aging in ripening fruit, just as other cytokinins would appear to do in senescent leaf tissue, if ethylene production in tissue slices of ripening fruits is an indicator of aging.

In the cranberry varieties "Ben Lear" and "Stevens," proanthocyanidins, flavonols, and anthocyanins were measured in fruit during fruit development and ripening. Proanthocyanidin and total flavonol concentrations were highest in flower ovaries and the early phases of fruit development. Proanthocyanidin levels dropped sharply during ovary growth and development and then marginally rose during fruit ripening. Flavonol levels decreased less noticeably as fruit ripened compared to levels in the early phases of fruit set and the flowering stage. After fruit development stopped, anthocyanin synthesis began, and it peaked during fruit ripening. The flavonoid biosynthetic pathway channeled resources primarily towards anthocyanins in 'Ben Lear' and towards both anthocyanins and proanthocyanidins in 'Stevens' during fruit ripening. The major flavonol glycosides quercetin-3-galactoside and quercetin-3-arabinofuranoside showed comparable patterns of change over the course of fruit development in both varieties. varying amounts of quercetin-3-arabinopyranoside, quercetin-3-rhamnoside, quercetin-3-(6″-benzoyl)-galactoside, methoxyquercetin pentoside, and quercetin-3-(6″-coumaroyl)-galactoside accumulated at varying rates in the different varieties. The partitioning of the precursor pool in the biosynthetic pathway of flavonoids in cranberry fruit is influenced by both type and phenological stage[10]–[12].

CONCLUSION

Plants generate signal molecules known as plant hormones (or phytohormones), which are found in incredibly low concentrations. All facets of plant growth and development, including embryogenesis, the control of organ size, disease protection, stress tolerance, and reproductive development, are governed by plant hormones. It is now widely accepted that seeds are a rich source of hormones, especially auxins, GA, and cytokinin, which are important for stimulating the development of nearby tissues and even affecting the size of the fruit. Numerous facets of fruit development, such as fruit set and growth, ripening, and abscission, are regulated by auxin. However, it is still unclear how auxin controls these processes through what pathways. The hormone auxin is crucial for the growth and evolution of plants. It's a good idea to have a backup plan in case something goes wrong. In climacteric fruits, ethylene has long been thought to be the primary maturation regulator. In this chapter, we summarized the effects of the phytohormones on plant fruit development and maturation. We also discussed that the phytohormones like auxin and gibberellins, which are frequently used to produce parthenocarpic fruits and to improve fruit yield, can cause fruit set to occur even in the absence of reproduction.

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CHAPTER 19

PHYTOHORMONES IN THE PRESENCE OF THE VIRUS INFECTION AND DISEASE

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ABSTRACT:

The majority of biochemical processes in plant systems are regulated by phytohormones. Additionally regulated by phytohormones are abiotic stress and microbial defense. The activities of the plant are significantly impacted by even small changes in the expression and signaling of the phytohormones. Changes and accumulations of the various kinds of phytohormones for the response occur during pathogen and virus infection. Only recently have researchers begun to understand the mechanisms by which viruses modify the levels of phytohormones and the impacts these changes have on plant physiology. Till now the research suggests that a pattern of virus-directed manipulation of plant hormones responses is emerging, to neutralize defence mechanisms and alter the cellular environment to encourage replication and spread. This chapter explains the overview of the impact of viruses on plant hormone systems as well as the impact of altering phytohormones that on virus metabolism.

KEYWORDS:

Auxin Signaling, Jasmonic Acid, Plant Growth, Plant Virus, Viral Infection.

INTRODUCTION

Plants commonly encounter pathogens like viruses, bacteria, fungi, oomycetes, nematodes, and insects during their growth and development [1]. Most plants lack the specialized and mobile immune response cells needed to combat invasive diseases, making it difficult for them to avoid these harmful influences by shifting their spatial position. In the lengthy and ongoing conflict with viruses, plants have evolved a variety of highly effective defense mechanisms for their survival and procreation. Phytohormones control the majority of plant physiological processes, including organogenesis, apoptosis, and cell development and reproduction, despite having simple molecular structures and low cellular concentrations. Phytohormones are also involved in the defense of plants against viruses (Figure. 1), and salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) have all been widely studied in the interactions between plants and viruses.

Additionally, the roles of auxins, gibberellic acid, cytokinins, and brassinosteroids (BRs) in plant defense are progressively coming into clearer focus. The simultaneous production of hormones that work together or against each other and the activation of defense mechanisms are symptoms of hormonal pathway disruption caused by viral infection. Such changes frequently result in symptoms and are closely linked to viral transmission, reproduction, and systemic illness. In order to develop novel biotechnological, genetic, and breeding methods for crop protection and improvement, it is important to have a thorough knowledge of the roles played by hormones in plant-virus pathosystems. Here, we go over the various phytohormones' roles in plant-virus interactions' regulatory processes. We also pay attention to how various hormone communication systems interact with one another to optimize defense responses [1].

An oxygenated fatty acid called JA (oxylipin) helps the body fight necrotrophic pathogens and insect invasion. JA controls induced systemic resistance (ISR), which is caused by non-pathogenic microbes like rhizobacteria, along with Et. According to research, rhizobacterium-mediated induction of JA lessens Col-0's symptoms of CMV infection. Later research, but in a phase-specific manner, validated the beneficial roles of JA incompatible interactions. For instance, PCD was caused early in the course of infection by co-infection with PVY and PVX or by infection with PVY carrying HC-Pro from a potyvirus (PPV). Both studies demonstrated that COI1, a gene involved in the JA signaling pathway, can be knocked down to speed up the development of symptoms and viral titer accumulation in the early phases of infection. However, as infection progressed, symptoms were comparable in WT and knock-down lines. Early JA treatment of the PVY-PVX double infection increased resistance; however, later treatment increased susceptibility, likely due to JA's antagonistic impact on SA. Similar investigations, such as those on CaMV in *A. thaliana* and Panicum mosaic virus and its satellite virus in the monocot plant, have demonstrated that JA-responsive genes are modulated at the early stages of infection. Recent studies have demonstrated that treating *N. benthamiana* plants with JA or SA increases their systemic resilience to TMV, and that pretreatment with JA followed by SA increases that resistance even more. The early stages of the SA pathway may be modulated by JA, but it is unclear how JA controls SA biosynthesis and resilience in cooperative interactions [2].

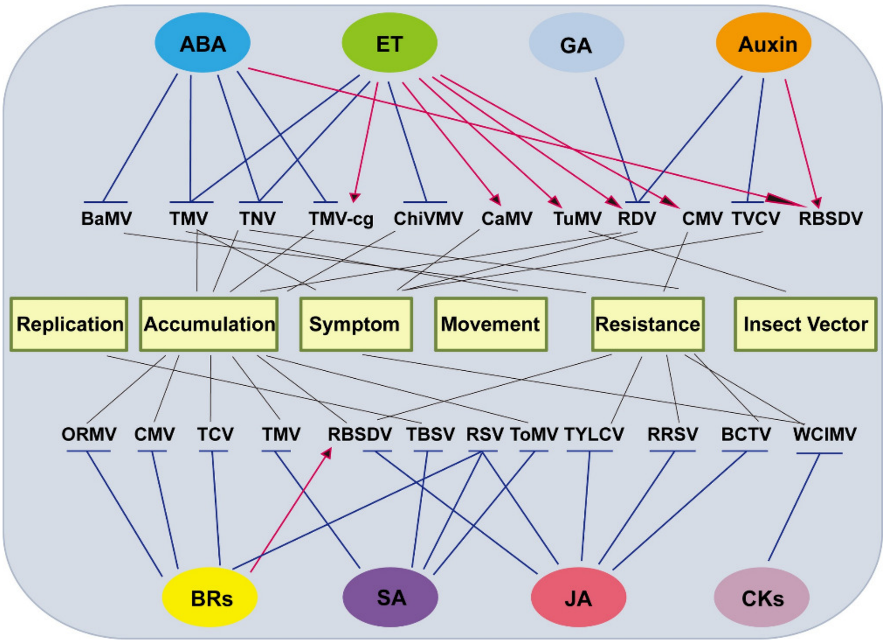

Figure 1: Phytohormones and virus: Role of the phytohormones in virus infection (Journal plos).

Auxin sustains apical dominance, which is important for plant growth and development. Mutants in the Aux signaling pathway or responsive factors show an aberrant growth phenotype. Stunting, leaf curl, and loss of apical supremacy are just a few of the abnormal phenotypes caused by many viral infections. These traits are similar to those of mutants with hampered Aux biosynthesis and/or signaling. For instance, the signs of tomato shoestring mosaic disease, which is brought on by CMV and ToMV infections, are similar to those of WIRY mutants. Later research revealed that WIRY genes contribute to siRNA synthesis. Trans-acting (ta)-siRNAs, which control the Aux response factors ARF3 and ARF4, were found in lower concentrations in WIRY mutants while their target ARF levels were higher. These results imply that the wiry phenotype is caused by an inability to adversely regulate

ARF3 and ARF4.The phytohormone ABA plays a variety of roles in plant processes, such as controlling stomatal aperture and launching adaptive reactions in response to different biotic and abiotic stresses. Although ABA's role in plant pathogen responses has been widely studied, its function in virus infection is poorly understood. There is limited understanding of how ABA contributes to the intricate interactions between virus infection and host-plant defense systems. Through the suppression of the JA pathway and the accumulation of ROS in plants, one study demonstrated how ABA can adversely regulate rice defense against rice black streaked dwarf virus (RBSDV) infection. The RNAi pathway and callose deposition at plasmodesmata (PD), two of the molecular mechanisms underlying ABA-mediated plant-virus interactions, are the subject of several bioassay-based reports.

Numerous studies have shown that ET contributes to the emergence of virus symptoms. Using a device for synchronous lesion formation caused by temperature, Additionally, lesion formation was greatly reduced by inhibitors of ET biosynthesis or action. The role of the CaMV P6 protein, which is involved in virus replication and RNAi suppression, is another piece of data that connects ET to the emergence of viral symptoms. CaMV infection is less likely to occur in Arabidopsis mutants that inhibit the phenotype brought on by the transgenic expression of CaMV P6, and they exhibit decreased ET sensitivity. The researchers came to the conclusion that P6 interacts with elements of the ET signaling system and that P6 transgenic plants have higher CaMV resistance. Some reports, however, asserted that the capacity of transgenic tobacco plants to develop local lesions after TMV infection was unaffected and that the HR response of Arabidopsis to turnip crinkle virus (TCV) was not reliant on ET. Therefore, it is still unclear how ET contributes to the growth of necrotic tumors and needs to be explained.

GA encourages stem elongation, stimulates seed germination, and controls blooming. By preventing DELLA proteins, which are detrimental regulators of plant development, this hormone encourages plant growth. GA appears to play a harmful function in plant defense. Loss-of-function variants of DELLA make plants more resistant to biotrophs like Pst DC3000, but they are more vulnerable to necrotrophic infection. By partly altering the balance between SAand JA/Et-mediated signaling pathways, GA may help defenses against biotrophs or necrotrophs. Ent-kaurene oxidase associates with the P2 outer capsid protein of Rice dwarf virus, a crucial component in the biosynthesis of gibberellins. (RDV). RDV-infected rice plants showed a dwarf phenotype and lower amounts of ent-kaurene oxidase and GA1, but GA3 supplementation exogenously reversed these defects. It needs to be demonstrated empirically whether the interaction between P2 and ent-kaurene oxidase-type proteins promotes viral replication by interfering with the biosynthesis of phytoalexins. Similar to this, TuMV infection of Chinese broccoli without heads reduced GA accumulation [2].

LITERATURE REVIEW

Nearly every element of plant biology, including development and pathogen defense, depends on phytohormones. Changes in phytohormone accumulation and signaling during viral infection have frequently been linked to disruptions in the plant's normal developmental physiology. Evidence describing the mechanisms by which viruses alter phytohormone levels and the effects these modifications have on plant physiology and virus biology has only lately come to light. According to these studies, a pattern of virus-directed manipulation of plant hormone responses to neutralize defense mechanisms and change the cellular environment to promote replication and spread is developing. In this review, we look at how viruses affect plant hormone systems and how manipulating phytohormones affects viral biology [3].

No known natural sources of resistance to the plum pox virus (PPV, sharka), which limits the output of peaches, have been identified. However, recent research has shown that grafting the "Garrigues" almond cultivar onto the "GF305" peach infected with Dideron-type (PPV-D) isolates gradually lowers disease symptoms and viral accumulation. Additionally, it has been discovered that grafting "Garrigues" onto "GF305" before PPV-D inoculation fully prevents virus infection, demonstrating that resistance is constitutive rather than brought on by the virus. We examined the growth-related phytohormones cytokinin trans-zeatin (tZ) and the gibberellins GA3 and GA4 as well as the stress-related phytohormones ethylene acid precursor in order to understand the phytohormone signaling of this process. Salicylic acid (SA), 1-aminocyclopropane-1-carboxylic acid (ACC), ABA, and jasmonic acid (JA). The prevalence of chlorosis symptoms was associated with the imbalances in GA3 and ABA that the PPV inoculation caused in peaches. However, grafting a "Garrigues" almond onto a "GF305" peach that had been infected with PPV had the opposite impact, decreasing the GA3 and ABA contents while also getting rid of the symptoms. Our findings demonstrated the importance of SA's role in the resistance that was produced in the peach and its additional impact on the concentrations of tZ and JA. The systemic acquired resistance (SAR) and the induced systemic resistance (ISR), which are based on other reactions causing necrosis, appear to be distinct from this SA-induced resistance based on the reduction in symptoms. To confirm these findings against the more aggressive Marcus-type (PPV-M) isolates, however, additional research is required [4].

Plant reactions to biotic and abiotic stresses are tuned by hormones. They affect numerous intricate networks through which they control how different inputs are responded to. Salicylic acid (SA), jasmonic acid (JA), ethylene (Et), and abscisic acid are the four hormones that mainly control plant defense against pathogens. (ABA). Viral infections cause hormonal disruption in vulnerable plants, which appears as the simultaneous induction of several antagonistic hormones. But in resistant lines, these antagonistic hormones might show some sequential buildup. Small interfering RNA (siRNA) antiviral machinery and/or the SA signaling cascade are typically activated to prevent viral spread. These two systems have been the subject of numerous investigations using various model viruses. However, the functions of other hormones besides SA, particularly those with hostile characteristics like ABA, have been overlooked. The small RNA system, which controls numerous processes (including the siRNA antiviral machinery and the microRNA system) at the transcriptional or post-transcriptional level, is thought to be controlled by hormones, according to mounting evidence. As a result, interactions between the SA and ABA pathways, which are antagonistic, alter plant reactions on various levels. In this review, we summarize current research on the various functions of hormones in controlling plant-virus interactions, which is assisting us in understanding how hormones fine-tune viral and plant systems [2].

In order to examine the potential of engineered nanomaterials (ENMs) for fostering crop development and resistance to viral infection, tobacco (Nicotiana benthamiana) and Turnip mosaic virus (TuMV) were used as a model system. For 21 days, the leaf surface of tobacco was foliar-sprayed with a 5 mL ENM solution containing either two carbon-based nanomaterials (NMs) (MWCNTs or C60) or two metal-based nanomaterials (NP Fe2O3 or TiO2). After being inoculated with TuMV that was GFP-tagged, fully formed young leaves were grown for 5 days. The shoot biomass was raised by about 50% after exposure to both metal- and carbon-based NMs. TEM images showed that exposure to NMs had no effect on the integrity of the cells; NP Fe2O3 and TiO2 accumulated predominantly in the chloroplasts. According to fluorescence images of TuMV abundance on leaf surfaces and fluorescence intensity measurements on freshly emerged leaves, NMs greatly inhibited viral proliferation. The methods by which NMs suppressed viral infection may also be explained by approximately 15–60% reductions in the relative quantity of TuMV coat proteins. A 40% increase in phytohormone levels further supports the idea that NMs are crucial for promoting plant development and activating defense mechanisms. These results advance our knowledge of the environmentally friendly use of ENMs in agriculture [5].

Auxin, a phytohormone, is essential for controlling numerous plant growth and development processes. Auxin signaling can be disrupted by microbial infection, leading to flaws in these processes, but the underlying pathways are unclear. A temporary co-receptor complex made up of the proteins auxin/indole-3-acetic acid (Aux/IAA) and transport inhibitor response 1/auxin signaling F-box (TIR1/AFB) detects auxin as the first step in auxin signaling. Auxin attachment to the co-receptor causes the Aux/IAA proteins to be ubiquitinated and degraded by the 26S proteasome, which sets off a chain of events that includes the expression of auxin-responsive genes. Here, we report that the deadly rice pathogen Rice dwarf virus (RDV) produces dwarfing, an increase in the number of tillers, and short crown roots in infected rice as a result of decreased sensitivity to auxin signaling. OsIAA10 is bound by the RDV capsid protein P2, which prevents OsIAA10 from interacting with OsTIR1 and prevents 26S proteasome-mediated OsIAA10 breakdown. However, knockdown of OsIAA10 improves rice's resistance to RDV infection. Transgenic rice plants overexpressing wild-type or a dominant-negative (degradation-resistant) mutant of OsIAA10 phenocopy RDV symptoms are more prone to RDV infection. According to our research, a crucial stage in the start of auxin signaling can be reprogrammed by viral proteins, which promotes viral infection and pathogenesis [6].

The impact of plant hormones on the replication of white clover mosaic potexvirus (WClMV) inPhaseolus vulgarisL.cv. Top Crop was examined. Hormones were wick-fed to plants, and an ELISA to detect virus titre was used to determine the impact on virus replication. While dihydrozeatin, 1-aminocyclopropane-1-carboxylic acid (ACC), salicylic acid, and jasmonic acid all prevented viral replication, abscisic acid, indole-3-acetic acid, and gibberellic acid did not. Treatment with hormones did not stop the virus from spreading throughout the body, but dihydrozeatin, ACC, salicylic acid, and jasmonic acid did decrease the virus titre in the systemic leaves. In hormone-treated plants, pathogenesis-related (PR) proteins from groups 2 and 3 were found, but only after viral challenge. Although it is rare that PR-proteins will directly interact with viruses, an imbalance in hormones brought on by a virus may cause PR-protein expression. Resistance to WClMV was independent of systemic acquired resistance, as evidenced by the lack of both elicited PR-1 proteins and a hypersensitive response [7].

Due to their ability to infect a variety of plant hosts globally, geminiviruses are now an emerging agroeconomic threat on a global scale. These viruses' connections to extremely effective insect vectors like whiteflies and satellite molecules further enhance their devastating effects. For the purpose of preventing the spread of these destructive pathogens, plants produce a potent antiviral immune reaction. Plants use phytohormones, which play an important role in mounting this defense against these biotrophs. These defense hormones not only prevent the spread of geminiviruses but also hinder viral transfer by impairing the efficiency of the insects that carry them. However, a few multitasking virulence factors that easily alter host cellular machinery to evade the phytohormone-mediated manifestation of the immune response have co-evolved with geminiviruses. Additionally, these obligate parasites use plant development hormones to create an environment in the cell that is conducive to virus replication. In this overview, we present the state of knowledge regarding the functions and control of phytohormones during the pathogenesis of geminiviruses [8].

MARK (mitogen-activated protein kinase) cascades are essential for plant growth and response to the environment. Previous studies have primarily concentrated on the MAPKs in groups A and B, and group C has received little attention. In this research, we isolated and characterized GhMPK7, a new group C MAPK gene from cotton. GhMPK7 transcript was found to be induced by pathogen infection as well as several signal molecules linked to defense. This was revealed by RNA blot analysis. Transgenic Nicotina benthamiana overexpressing GhMPK7 exhibited notable resistance to the virus PVY and the fungus Colletotrichum nicotianae, and the transcript levels of genes in the SA pathway were highly and quickly induced. By increasing the expression of genes linked to oxidative stress, the transgenic N. benthamiana also demonstrated decreased ROS-mediated injuries. Contrary to wild-type plants, the transgenic plants grew more quickly and germinated sooner. At the vegetative stage, the apical meristem contained GhMPK7-driven -glucuronidase activity, which was boosted by signal molecule and phytohormone therapies. These findings imply that GhMPK7 is involved in the control of plant growth and development as well as SA-regulated broad-spectrum resistance to pathogen infection [9].

Gibberellin (GA), a phytohormone, is an essential plant signaling molecule that controls plant development and protection from abiotic and biotic stresses. The molecular process of a viral infection-mediated response in plants is still unknown as of this writing. The SCFSLY1/GID2 complex's F-box protein, which is a part of the DELLA protein family, is able to identify DELLA as a GA signaling repressor. The ubiquitin-26S proteasome breaks down the identified DELLA, which activates GA signaling. Here, we describe symptoms of dwarfing and abnormal flower development in N. benthamiana plants infected with ageratum leaf curl Sichuan virus (ALCScV). The ALCScV infection substantially changed the expression of genes linked to the GA pathway and reduced the amount of endogenous GA in N. benthamiana. Additionally, the C4 protein produced by ALCScV interacts with the DELLA protein NbGAI and blocks its association with NbGID2 in order to stop NbGAI from degrading and thereby inhibit the GA signaling pathway. Exogenous GA3 therapy or NbGAI silencing both substantially reduce viral buildup and disease symptoms in N. benthamiana plants. Experiments using the C4 protein encoded by the tobacco curly stalk virus produced the same outcomes. (TbCSV). As a result, we suggest a new mechanism by which geminivirus C4 proteins regulate viral infection and the emergence of disease symptoms by interfering with the GA signalling pathway.

CONCLUSION

Virus infection in plants leads to various changes in the plant singling, metabolic pathways, and alternation at the transcription and translation levels. Details study is needed to understand the overall mechanism of the virus affection on plant hormones' secretion and their response. Future study is needed to understand the cellular organization changes during viral infections and the role of phytohormones. Identifying the roles of hormones in plant-virus interactions and the interactions between hormone pathways in the future will aid in figuring out the molecular processes by which plants fend off infection. In this chapter, we have summarized the overview of the plant phytohormones signaling, biochemical pathway, and their response towards the viral infection.

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CHAPTER 20

PLANT STOMATAL OPENING AND LEAF GROWTH ARE INFLUENCED BY PHYTOHORMONES

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ABSTRACT:

The various sets of phytohormones fully control a plant's life cycle. The auxin, gibberellins, ABA, cytokinins, and ethylene are examples of these phytohormones. In addition, additional phytohormones such as strigolactones, jasmonate, salicylic acid, and brassinosteroids controlled plant growth and development under stressful circumstances. To minimize water loss, plant stress is primarily controlled by shutting and opening plant stomata and altering leaf development. Given that effective utilization of water and photosynthesis are two processes that are crucial for plant growth, stomatal development is tightly controlled by a variety of signals. In this chapter, we provided an overview of leaf development as well as details on how these signals are incorporated into the primary stomatal development route.

KEYWORDS:

Abscisic Acid, Guard Cells, Leaf Development, Mycorrhizal Plant, Stomatal Development.

INTRODUCTION

Small organic molecules known as phytohormones serve as crucial development regulators for plants. Phytohormones influence plant growth and stress tolerance, cell division, elongation, and differentiation, as well as germination, rooting, flowering, fruiting, sex determination, dormancy, and organ shedding at very low concentrations. Numerous aspects of development are frequently regulated by a single variety of phytohormones, and several phytohormones can work together to control a single developmental process. Autins, cytokinins (CKs), gibberellins (GAs), abscisic acid (ABA), and ethylene (ETH) as well as brassinosteroids (BRs), jasmonate (JA), and salicylic acid have all been thoroughly investigated. (SA). Peptide phytohormones and stragolactones (SLs) are receiving more and more notice.

Other plant growth regulators, like polyamines (PAs) and karrikins (KARs), are straightforward, small organic compounds whose biosynthesis or receptors have not yet been completely elucidated, leaving their status as genuine phytohormones up for debate [1]. Autain functions in every stage of leaf development, whereas GAs and CKs control cell division, proliferation, senescence, and complexity. ABA encourages stress resistance and avoidance mechanisms in plants even at the earliest phases of their development, assisting them in surviving stressful situations.6 Auxin, GAs, and CKs are thus typically thought to support differentiation because they start developmental processes and control how final organ morphology is realized. ABA and ETH, on the other hand, inhibit plant development and favor maturation and aging. The following is a list of some of the most common questions that I get asked about the upcoming e-learning course.

Initiation of leaf primordia, the establishment of leaf polarity, and leaf morphology can be used as artificial markers to separate the early phases of leaf development into these three stages. In-depth research into the regulatory mechanisms underpinning these three processes has shown that endogenous (genetic) and exogenous (environmental) factors both play a role in controlling leaf development. A summary of the relevant phytohormones and their signaling pathways during leaf development is presented in Figure 1, including the temporal and spatial hierarchy of phytohormones activity during leaf development (Figure 1A), the initiation of leaf primordia (Figure 1B), the establishment of leaf polarity (Figure 1C), and the regulation of leaf morphology (Figure 1D). We go over the signaling pathways and potential phytohormones in each step of early leaf development in this section.

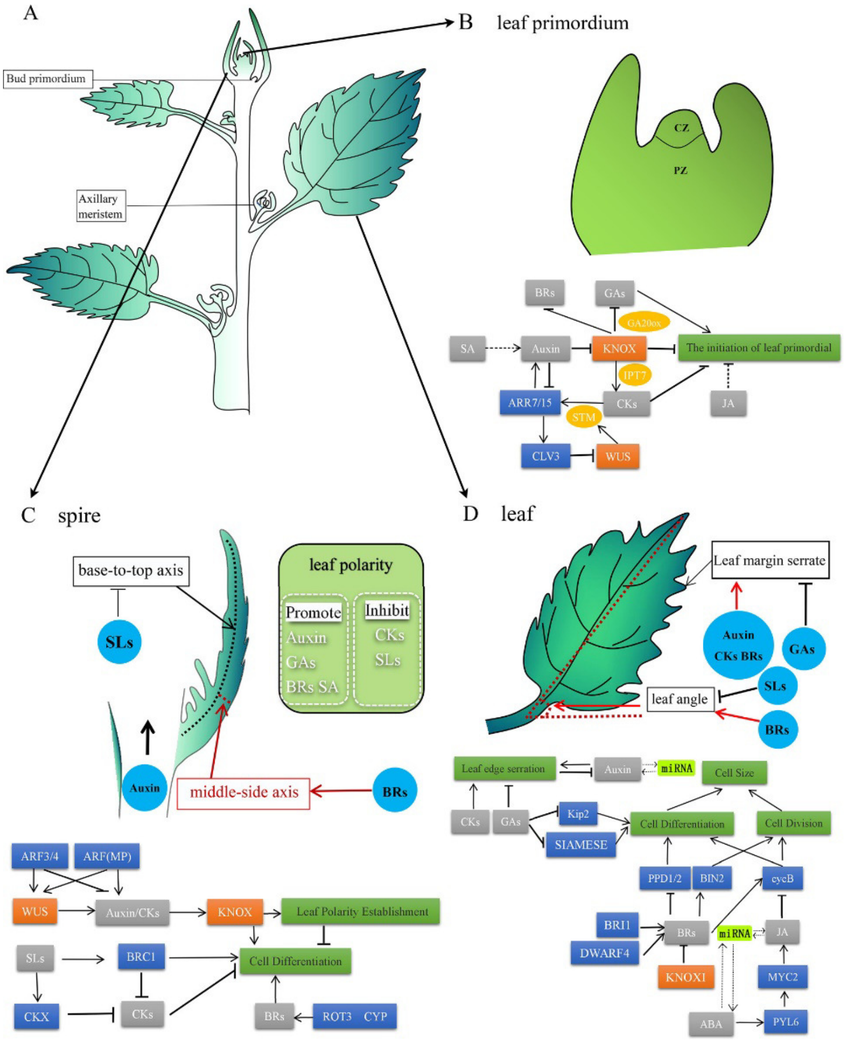

Figure.1: Phytohormones and plant development: Diagram showing the different phases and the role of the phytohormones in plant leaf development (ACS publication.)

Stomata are microscopic pores on the epidermis of above-ground plant tissues that allow oxygen, carbon dioxide, and water to travel between the interior of the plant and its surroundings. Stomata are therefore essential for effective photosynthesis as well as for the global cycles of carbon and water. Stomata enable the uptake of CO2 required for photosynthesis when they open, but this action also speeds up water evaporation through stomatal pores. Plants developed sophisticated mechanisms to control stomata in coordination with different stimuli in order to overcome this conundrum. To best balance photosynthesis and transpiration in the near term, stomatal aperture is modified. In the long run, plants control stomatal development by adjusting the number of stomata in response to internal and external cues. Stomata are created in the model plant Arabidopsis using a stereotypical process of cell division and differentiation that begins with a subgroup of protodermal cells known as meristemoid mother cells. (MMCs). A small meristemoid and a big stomatal lineage ground cell are produced by the asymmetrical division of MMCs that initiates the stomata lineage. (SLGC; Figure. 1a). A late meristemoid surrounded by SLGCs is created by the meristemoid, a precursor stem cell, renewing itself through one to three cycles of asymmetric division in an inward spiral. When the late meristemoid differentiates into a guard mother cell (GMC), it will divide once symmetrically to produce two guard cells encircling a pore (Figure. 2a). Additionally, the most recent SLGC might acquire MMC cell fate and split asymmetrically to produce a satellite stoma. (Figure. 2a). The sequential actions of several basic helix-loop-helix (bHLH) transcription factors, including SPEECHLESS (SPCH), MUTE, and FAMA in conjunction with their partner bHLH proteins SCREAM (SCRM, also known as ICE1) and SCRM2, are what regulate the aforementioned cell-state changes.

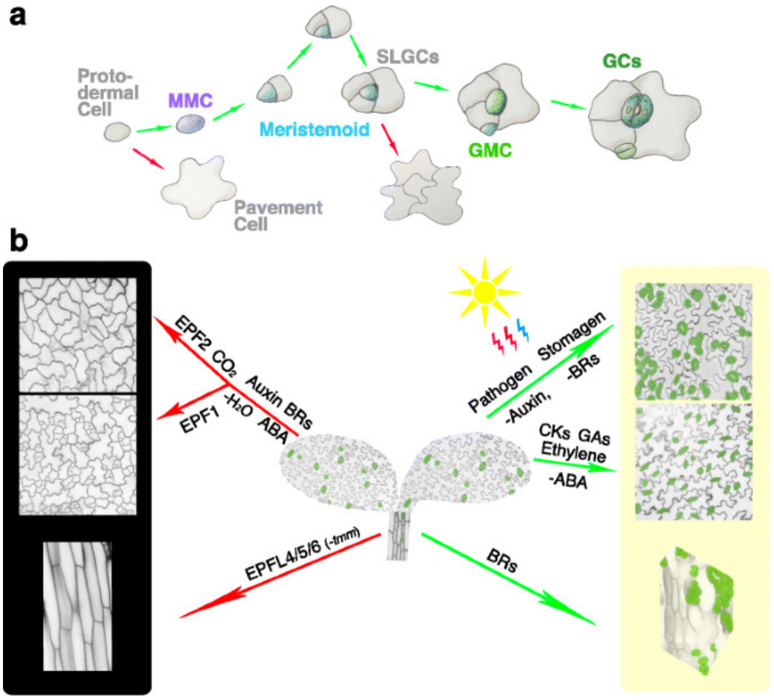

Figure 2: Phytohormones and the Stomata: Diagram showing the role of the phytohormones in the stomatal opening (bmcbiol).

The entrance asymmetric division of a meristemoid depends on SPCH. A thorough examination of the SPCH weak loss-of-function allele showed that it also plays a role in amplifying asymmetric division. On the other hand, SPCH's near relative MUTE is necessary to stop asymmetric division and encourage differentiation, which includes symmetric division. FAMA mediates the final stage of stomatal formation by preventing extra symmetric divisions in GMCs and fostering GC identity. Although different species have different developmental programs for stomatal formation, the bHLH transcription factors described above serve as the fundamental unit in all land plants. For optimal stomatal operation, stomatal patterning and density are two essential characteristics. The one-cell spacing guideline is strictly adhered to during stomatal development.

That indicates that stomata are not created in close proximity to one another, but rather with at least one non-stoma cell present to ensure that the orifice is properly opened and closed. Therefore, cell-cell contact is crucial for stomatal patterning. Tomatal patterning and density are influenced by a variety of signals, including secreted peptides from the family of EPIDERMAL PATTERNING FACTORS (EPFs), plant hormones, and external cues (Figure.

1b). By controlling the stability of the stomatal bHLH proteins in Arabidopsis, a well-known mitogen-activated protein kinase (MAPK) cascade made up of YODA (YDA), MKK4/5/7/9, and MPK3/6 processes these upstream signals.

LITERATURE REVIEW

Information on plant growth regulators, biomembranes, and cell compartments of stressed and unstressed leaves is given in a biophysical and biochemical manner. Incorporating these data into a physiological source-sink network enables the estimation of phytohormone concentrations at any given moment in each compartment using biophysical and biochemical laws.

The deduced outcomes and conclusions are addressed, including

(i) All known phytohormones vary in terms of the enumerated physicochemical properties (such as p Ka, partition coefficient octanol: water, and membrane conductance of neutral and charged phytohormone species).

(ii) The distribution and redistribution pattern of ABA as found in experiments can be adequately explained by the information provided.

(iii) If synthesis and degradation are missing, only cytokinins and the ethylene precursor amino-cyclopropane-carboxylic acid are evenly distributed between cell compartments. The bulk concentration of these growth factors in plant tissue homogenates only estimates concentrations in all compartments under these circumstances.

(iv) Even though synthesis and degradation are missing, there are uneven compartmental concentrations for other growth regulators based on pH, membrane potential, and anion conductance of biomembranes,

(v) Abscisic acid is the only phytohormone whose distribution follows the anion-trap process for weak acids almost exactly as it should. Measurements and calculated predicted values agree,

(vi) It is anticipated that C3 and CAM plants will redistribute ABA in the same way under diurnal illumination conditions. The influence of the extreme vacuolar pH change is small because of the low ABA percentage in CAM mesophyll vacuoles (maximum 2.7 % of the total ABA mass per unit leaf area),

(vii) Under drought stress, complex compartmental pH shifts in leaves induce a complicated redistribution of ABA amongst compartments, A 2- to 3-fold ABA accumulation in guard cell walls is enough to cause stomata to close

(viii) The ultimate accumulation of ABA in guard cell walls is up to 16.1 times greater than the initial value.

(ix) The minimal delay before the stomata begin to close is 1 to 5 minutes, and it is influenced by the level of stress and the ABA sensitivity of the guard cells. The plasmalemma, not the thylakoids, is the main target membrane of "stress".

(x) The epidermis cells may contain the efficient "stress sensor," which activates the suggested signal chain and ultimately causes stomatal closing. Only synergistically can mesophyll cells promote stomatal closure.

(xi) Drought stress has a significant but gradual direct biophysical effect on the ABA concentration in guard cell walls (increase in transpiration until stomata shut).

(xii) If guard cell sensitivity to ABA stays constant, a stress signal from the root system in the shape of an elevated ABA concentration is capable of controlling the stomatal conductance. Only within 1 or 2 weeks does the total ABA content per unit leaf area begins to decrease. (aftereffect),

(xiii) Other phytohormones do not redistribute after variations in compartmental pH or do so only moderately. Only ABA is primarily capable of acting as a "stress messenger" for stomata for biophysical reasons, and evolution seems to have chosen it [2].

Stomatal gas exchange and zeatin riboside levels (as determined by ELISA) of flax (*Linum usitatissimum L.*) were investigated concerning an observed growth response of these plants to vesicular-arbuscular mycorrhizal infection, which was shown not to be related to increased nitrogen, phosphorus or potassium contents of plants. Additionally, xylem application trials were used to examine how zeatin and abscisic acid affected the stomatal gas exchange responses of non-mycorrhizal plants. Highly infected plants showed higher rates of transpiration and CO2 absorption in contrast to non-mycorrhizal plants, whereas stomatal density was unaffected and the shoot water potential () remained the same or even decreased. These results suggested that increased stomatal opening was not mainly brought on by an increase in the shoots' water supply. At the conclusion of the experiments, mycorrhizal plants' leaves had reduced respiration rates than non-mycorrhizal plants.

Zeatin riboside levels in roots temporarily decreased during the early stages of the mycorrhizal infection when compared to non-mycorrhizal plants, whereas levels in shoots temporarily rose. However, transplanted roots showed noticeably more zeatin riboside than those of non-mycorrhizal plants once the symbiosis had developed. Higher amounts of zeatin riboside in the corresponding organs were present before the shoots and roots began to grow significantly in response to mycorrhizal infection. Abscisic acid alone reduced transpiration and CO2 absorption rates, whereas zeatin alone had no effect on stomatal gas exchange in the vascular system of non-mycorrhizal flax. Zeatin treatment, however, improved transpiration and CO2 assimilation rates and partly reversed the effects of abscisic acid-mediated effects, demonstrating an analogy to mycorrhizal infection. These findings support the hypothesis that increased internal cytokinin levels contribute to better photosynthesis and mycorrhizal flax growth [3].

A gaseous environmental hazard called ozone (O3) can harm vegetation by entering leaves through stomatal pores. Through the production of reactive oxygen species (ROS) like hydrogen peroxide (H2O2), which can directly contribute to stomatal closing or opening in plants, it can cause oxidative stress. Abscisic acid (ABA), ethylene (ET), salicylic acid (SA), and jasmonic acid (JA) are a few phytohormones that are involved in the control of stomatal function in plants.

However, there has been little research on the effects of ozone on the ability of these phytohormones to control the stomatal guard cells, and the purpose of this paper is to investigate and comprehend the effects of ozone on stomatal regulation through phytohormone signaling in guard cells. By taking into account a number of physiological processes connected to stomatal regulation following an ozone response, we updated the body of knowledge in this review. We should be better able to comprehend how ozone stress affects stomatal regulation, mitogen-activated protein kinase (MAPK) activity, and phytohormone signaling as a result of the data that has been gathered. We summarize the results, identify any voids in the literature, and then offer some suggestions for future ozone stress in plant research [4].

Both stresses and phytohormones have an impact on nearly all plant life processes, either directly or tangentially. However, aside from abscisic acid, the function of phytohormones in plants' reaction to water stress is still not completely understood. This review aims to provide a response to the issue of whether abscisic acid and other phytohormone interactions may play a role in controlling stomatal opening during water stress and subsequent rehydration. First, it explains how the composition of each endogenous phytohormone changes in response to water stress. The impacts of applied phytohormones on stomatal opening, transpiration, and photosynthetic rates in various plant species are then covered. Finally, it concentrates on using other phytohormones to reduce or stimulate abscisic acid-induced stomatal closure [5].

Phytohormones are important for controlling the abilities of plant species to overcome stress conditions and influence some aspects of stomatal control, preventing excessive water loss. In an evergreen woody species (*Cynophalla flexuosa*), this research examines the relationship between foliar phytohormone levels, water status, and stomatal conductance over the course of the dry and rainy seasons and the changeover between them. Abscisic acid (ABA), jasmonic acid (JA), salicylic acid (SA), and trans-zeatin concentrations in the leaves were quantified, along with stomatal conductance (gs), xylem branch water potential (x), and (tZ). In comparison to soil water balance, stomatal conductance was more susceptible to atmospheric factors like VPD.

The correlation between gs and x, however, suggests that these direct measures of water availability were a suitable substitute for gs in C. flexuosa. Additionally, ABA leaf concentration had no impact on gs, but ABA and tZ interplay was critical to this species' phenological behavior. In contrast to ABA, cytokinins postpone leaf senescence, which is important for evergreen species. JA displayed a substantial interaction with ABA as well, maintaining high foliar levels throughout the rainy season. The content of ABA fluctuated throughout the year, and to gs, its interaction with other phytohormones like tZ and JA was more significant than the concentration itself. The interaction between ABA, tZ, and JA likely contributed to the regulation of stomatal behavior in this species [6] even though ABA did not directly impact stomatal conductance in C. flexuosa.

Here, we focus on how the root and shoot environments affect the balance of hormones throughout the plant, especially when faced with stresses like soil drying, and we link hormone ratios and relative abundances to the mechanisms affecting plant performance and yield when faced with both mild and more severe stresses. We discuss evidence (i) that abscisic acid (ABA) and ethylene act antagonistically on grain-filling rate amongst other yield-impacting processes; (ii) that ABA's effectiveness as an agent of stomatal closure can be modulated by coincident ethylene or cytokinin accumulation; and (iii) that enhanced cytokinin production can increase growth and yield by improving foliar stay-green indices under stress, and by improving processes that impact grain-filling and number, and that this can be the result of altered relative abundances of cytokinin and ABA (and other hormones). In order to enhance plant performance and yield, we discuss evidence and novel processes that suggest these phenomena are/could be amenable to genetic and management manipulation. We explore the possibility that a range of ABA-ethylene and ABA-cytokinin relative abundances could represent targets for breeding/managing for yield resilience under a spectrum of stress levels between severe and mild, and could circumvent some of the pitfalls so far encountered in the massive research effort towards breeding for increases in the complex trait of yield [7].

Abscisic acid (ABA), a hormone produced by plants in response to water scarcity, shrinks the stomatal pores on the surface of leaves, reducing transpirational water loss. It has been proposed that extracellular ABA binds to a receptor found in the plasma membrane of guard cells to begin the inhibition of stomatal opening and encouragement of stomatal closure by ABA. However, in this study, we use three different experimental strategies to show that ABA can control stomatal apertures from within guard cells. (i) In Commelina communis L., the amount of [3H]ABA-measured ABA uptake is proportional to the amount of ABA that inhibits stomatal opening and encourages stomatal closure. (ii) Commelina guard cells' cytoplasm is directly microinjected with ABA, which causes stomatal closing to occur quickly. (iii) When ABA is applied using patch-clamp methods to the cytosol of Vicia faba L. guard-cell protoplasts, the resultant inhibition of inward K+ currents is strong enough to prevent stomatal opening. These findings show that phytohormone action occurs intracellularly and suggest that the hunt for hormone receptor proteins should be expanded to incorporate intracellular compartments [8].

Growing levels of atmospheric carbon dioxide ([CO2]) have a substantial impact on plant development, growth, and biomass. The two main factors that promote plant development at elevated [CO2] levels have been found as increased photosynthesis rate and decreased stomatal conductance. Variations in stomatal conductance and photosynthesis, however, cannot completely account for the dynamic shifts in plant growth. The post-photosynthetic secondary metabolic processes, such as carbon and nitrogen metabolism, cell cycle activities, and hormonal control, are always involved in the stimulation of photosynthesis at [CO2]. Even though there is growing evidence that e[CO2] plays a part in modulating secondary metabolism in plants, the majority of studies have concentrated on photosynthesis and stomatal conductance in response to e[CO2]. In this review, we concentrate on changes in other cellular mechanisms and growth processes at [CO2] in relation to plant growth and development after briefly discussing the effects of e[CO2] on photosynthesis and stomatal conductance. In order to increase crop productivity in a CO2 rich environment, information gaps in comprehending plant growth responses to [CO2] have been found [9].

CONCLUSION

The primary regulator of the general function of plant biology is a hormone found in plants. Different phytohormones are engaged in the various biological processes that occur in plants. Auxin and cytokinin signaling controls plant stomata opening, whereas ABA, jasmonic acid, and salicylic acids positively control stomatal closing. The stomatal opening was also controlled by ethylene but under unfavorable circumstances. The ABA and the jasmonic acids share an analogous pathway for the stomatal closer in reaction to the bacterial pathogens, according to research on the phytohormones signaling pathway. Hormones such as JA, auxin, cytokinin, ethylene, BRs, and gibberellins, in addition to ABA, controlled plant growth in plants. In the chapter synopsis, we concluded that plant hormones are the controllers of all functions.

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CHAPTER 21

PHYTOHORMONES SIGNALING DURING THE SEED GERMINATION

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ABSTRACT:

For plants to survive and spread, their spores are crucial. In addition, several other variables influence how the seed grows and develops. The biotic and abiotic variables have the greatest impact on seed germination. The physiology of the plant was kept by phytohormones, which controlled both normal and unfavorable conditions in the seed's development. The essential enzyme for seed maturation and growth is abscisic acid. It has been determined up to this point how the ABA signaling pathway controlled seed growth and maturation. In this chapter, we talked about how seeds germinate and how phytohormones play a part in that process.

KEYWORDS:

Abscisic Acid, Plant Growth, Seed Development, Seed Germination, Seed Dormancy.

INTRODUCTION

The seed is the beginning of the plant's growth, followed by the seedling, the vegetative phase, and the reproductive phase. For reproduction, seed generation is crucial. And diffusion of numerous plant species that have completely developed embryos that can survive during seed maturation and seedling establishment for the start of the following generation. Zygotic embryogenesis and seed maturation are two crucial stages of seed growth. Complex, overlapping developmental processes that begin at the end of embryogenesis and conclude when seeds are physiologically independent of the parent plant cause seeds to mature. It contains the less well-known maturation drying phase as well as a phase of seed storage reserve deposition. Additionally, as seeds mature, they develop a variety of physiological characteristics, such as dormancy and robust, uniform germination, which result in the establishment of a healthy seedling in the field to complete the life cycle[1]–[3].

Although seed germination and dormancy are crucial stages in the higher plant life cycle and significant crop yield traits, both of these processes are affected by environmental and developmental cues. A crucial factor in preventing the viable seed from germinating during the challenging and arid growth season is seed dormancy. A low seed dormancy level or non-dormant seed increases the risk of seed death and directs the seed to germinate under unfavorable growth conditions, while a high seed dormancy level stops or reduces the seed germination under favorable growth conditions which ultimately reduces the length of the growing season or crop yield. As a result, healthy seed dormancy is a crucial component of plant fitness and aids in adaptation to a broad range of environmental factors. Additionally, it is a genetic trait influenced by both environmental and inherited variables. Seed dormancy begins to increase along with the seed's later development and maturation and achieves a higher level in dry mature seeds known as primary dormancy.

Secondary dormancy, on the other hand, is the induction of dormancy in non-dormant seeds as a result of adverse environmental factors for germination, such as light and temperature. All higher plants go through germination, which is a crucial process that can affect how traits evolve and become expressed throughout a plant's existence. Seed germination begins when an inactive seed absorbs water, and it is completed when an embryonic component, such as a radicle, emerges from the seed coat. The completion of germination is defined as the emergence of a radicle by rupturing the seed coat; however, this procedure relies on the embryo's ability to absorb water and the activation of a number of physiological processes. Specific environmental conditions must be met for germination to occur, and as a result, the sensitivity of the seed to its surroundings varies over time. Therefore, for a dormant seed to effectively germinate, environmental cues like temperature, water, and sunshine work in conjunction with endogenous hormonal signals.

During seed maturation, particularly at the mid-and late phases when seeds absorb more nitrogen, the number of protein storage found in seeds, such as globulins and prolamins, increases. Storage proteins are released as a consequence of the activation of enzymes like proteinase. Additionally, the radicle and stalk of seedlings contain storage proteins. The release of storage proteins does not occur simultaneously throughout the seed's various regions. During the mobilization of proteins, the enzymes carboxypeptidase and aminopeptidase are also triggered. Among the most important parameters controlling the process of seed dormancy are changed at molecular levels, including protein and hormonal alterations, and the balance between ABA and gibberellins. Seed dormancy is influenced by variables like related genes, chromatin-related elements, and non-enzymatic processes.

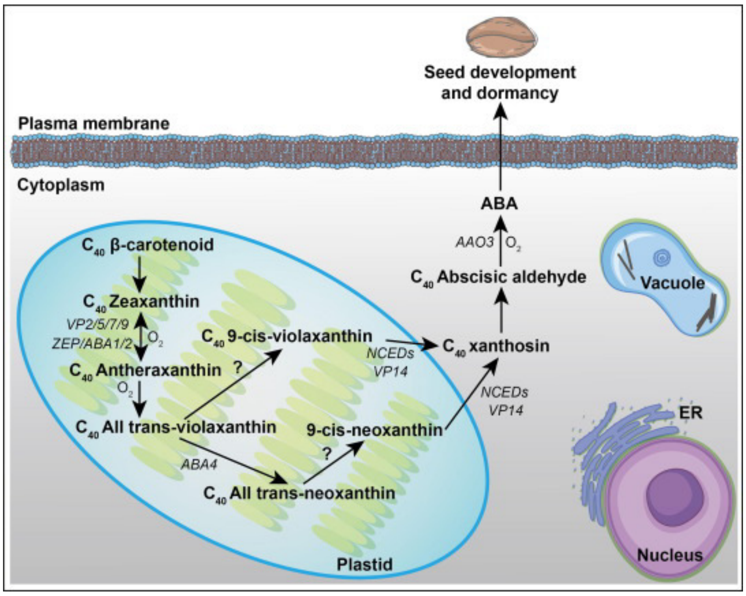

Figure 1: Seed development: Diagram showing the role of ABA biosynthesis in seed development and seed dormancy (Science direct).

The maturing genes, hormonal and epigenetic regulating genes, and the genes that control emergence from dormancy are among the genes that control dormancy. As a seed develops, the embryo body is formed through cell division and differentiation, which produces embryonic parts. This stage includes embryo growth and weight changes, organ development, nutrient storage, and seed maturation. It is followed by the development of desiccation tolerance and dormancy. As seeds mature, the cell cycle is inhibited, seed moisture decreases, ABA levels rise, storage reservoirs are created, and dormancy is formed. In tobacco and Arabidopsis, maternal ABA is crucial for embryo growth and seed maturation. But, ABA is also de novo produced in embryos and testa during embryo development, as well as accumulates during seed maturation, facilitates late seed development procedures, synthesis of preservation proteins to Prevent seed abortion, induces primary dormancy, and allows successful development as well as a successive seedling enterprise. De novo synthesis of active ABA, therefore, has a greater impact on seed growth and subsequent germination. Zeaxanthin, violaxanthin, and neoxanthin are a few examples of xanthophylls from which active ABA is derived indirectly. Three types of genes are responsible for the successive steps of ABA biosynthesis as ZEAXANTHIN EPOXIDATION (ZEP), OXIDATIVE CLEAVAGE OF 9-CIS-EPOXYCAROTENOIDS (NCED), and ABSCISIC ALDEHYDE OXIDATION (AAO) (Figure. 1). Arabidopsis thaliana and *Nicotiana plumbaginifolia* were the first two plants where the ZEP/ABA locus was discovered. The oxidation of zeaxanthin into antheraxanthin and violaxanthin, which is believed to be an initial step of ABA biosynthesis, was impaired in their mutants (aba1/aba2) with deficient ABA (Figure. 1).

A defect in the oxidation of zeaxanthin during ABA synthesis was found to cause viviparous sprouting in a Tos17 viviparous mutant of rice. Numerous additional ABA auxotrophic mutants (vp2, vp5, vp7, and vp9) found in maize through genetic screening have zeaxanthin epoxidase activity flaws and prevent the initial stages of carotenoid biosynthesis as well. All of these demonstrated that the oxidation of zeaxanthin is a significant and cautious stage in the plant's ABA synthesis. The process of converting all-trans-violoxanthin and all-trans-neoxanthin to 9-cis-violoxanthin and 9-cis-neoxanthin is never entirely obvious. However, it was discovered that ABA4 was in charge of the shift from all-trans-violoxanthin to all-trans-neoxanthin , offering some guidance for the investigation of these changes. The next crucial gene in the following stages of ABA biosynthesis was first identified as NINE-CIS-EPOXYCAROTENOID DIOXYGENASE in the maize viviparous mutant vp14. (NCED9). The vp14 mutant shows reduced ABA content in the dry seed and have a defect in the oxidation of 9-cis-epoxycarotenoid during the final stages of ABA biosynthesis.

It is known that the Arabidopsis homologs of VP14, NCED2, NCED3, NCED5, NCED6, and NCED9, participate in a rate-limiting stage in ABA biosynthesis (Figure. 1). Additionally, the PvNCED1, LeNCED1, and BdNCED1 genes isolated from the tomato, *Brachypodium distachyon*, and bean, respectively, also demonstrate the significance of these genes in ABA biosynthesis and seed formation. The oxidative cleavage of xanthophyll is the primary stage in the regulation of ABA biosynthesis for dormancy and development mediation in seeds, according to all the studies mentioned above. The final stage of ABA biosynthesis, abscisic aldehyde oxidation, involves the oxidative conversion of an abscisic aldehyde into ABA (Figure. 1).

Firstly, discovered mutants defective in the oxidation of abscisic aldehyde into ABA were flacca and sitiens in tomato. Later, abscisic aldehyde oxidase3 (AAO3), which is involved in the final two steps of ABA production in seeds and is expressed in embryonic vascular tissues during the middle and late stages of development, was discovered in Arabidopsis. The ABA synthetic pathway provides an active ABA pool that is regulated by different homologous genes throughout the entire plant development. Understanding the entire network of ABA synthesis would benefit from the identification of cofactors of the enzymatic processes in the ABA synthesis pathway.

Hordeum vulagre, Pseudotsuga menziesii, Cupressus nootkatensis, and yellow-cedar seed germination can be changed from dormant condition to germination, and this has been demonstrated. Through subsequent hydroxylation and conjugation processes, the ABA is broken down. The ABA is converted to phaseic acid by the CYTOCHROME P450, FAMILY 707, SUBFAMILY A (CYP707As), which has cytochrome P450 monooxygenase and ABA 8 prime-hydroxylase activity. (PA). The degradation of ABA occurs as a consequence of the catalysis of PA reductase (PAR), ABH2, and glycosyltransferase (GT) in converting PA to dihydrophaseic acid (DPA) and DPA-4-O-b-D-glucoside (DPAG) (Figure. 2). In lettuce, Arabidopsis, and *H. vulgare* seed, a higher level of PA and DPA accumulation is caused by a decreased level of ABA at the moment of ingestion. Additionally, it was shown that the coleorhiza, a crucial tissue from which germination begins, was primarily where the ABA catabolic enzyme HvABA80OH-1 expression was found in non-dormant *H. vulgare* seeds.

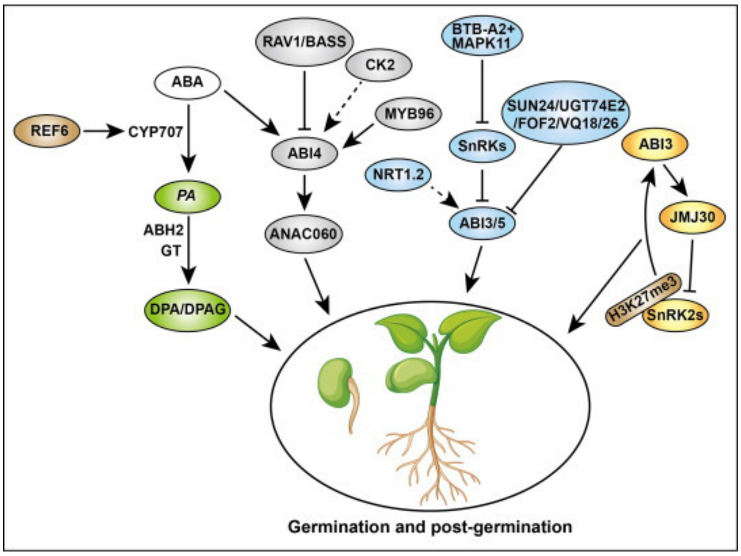

Figure 2: ABA in seed germination: Diagram showing the signaling pathway by the ABA during seed germination (Science direct).

A mechanism known as seed dormancy allows seeds to delay germination while they wait for more hospitable environmental circumstances. However, the first impacts of abscisic acid during seed development result in dormancy. These seedlings might not ever sprout. Newly harvested seeds of plants like barley (*Hordeum vulgare L.*) typically cannot germinate at temperatures greater than 20 C. The process of dormancy in barley is brought on by the glumellae's fixation of oxygen during the oxidation of phenolic products, which limits the amount of oxygen supply available to the embryo. Although the hormone does not regulate seed dormancy, gibberellins have the ability to awaken inactive seeds. ABA can prevent maize from germinating by interfering with the cell cycle. This explains why ABA-deficient seeds germinate more quickly than healthy seeds. A residual G1 kinase that is triggered by ABA's cell cycle inhibitory effects becomes inactive in the absence of ABA.

LITERATURE REVIEW

Reactive oxygen species (ROS) and phytohormones are important regulators of plant growth and stress responses. Plant growth regulator signaling networks and ROS signaling networks interact during the life cycle of these organisms to produce a suitable developmental and environmental response. Stress, which in severe instances can be fatal to cells, an entire organ, or even an organism, is frequently linked to enhanced and suboptimal ROS production in the photosynthetic (such as leaves) and non-photosynthetic (such as seeds) tissues of plants. However, it is beneficial for cellular signaling when ROS are produced under control. Regardless of the current progress that has been made in plant biology and expanding number of results that have revealed roles of ROS and hormones indicating in the germination process some inquiries still arise, e.g., what are the downstream protein targets modified by ROS enabling stimulus-specific cellular responses of the seed? Alternatively, what role do the molecular regulators that permit ROS/phytohormone relationships play in seed life? In this review, the function of a few transcription factors, kinases, and phosphatases is reviewed, particularly those that are frequently associated with the regulation of ROS and hormonal signal transduction in stressed plants. These enzymes may also be involved in the regulation of processes that take place in seeds. The summed up recent findings about particular ROS- and phytohormones-related regulatory proteins, as well as their integration, allowed to propose a novel, possible model of action of LESION SIMULATING DISEASE 1, ENHANCED DISEASE SUSCEPTIBILITY 1, and PHYTOALEXIN DEFICIENT 4 functioning during seeds life[4]–[6].

The process by which a creature emerges from a seed is known as seed germination. It needs the proper circumstances and natural elements. One of the most significant crops in the globe is maize. Both the ultimate yield and quality of maize are impacted by germination. A sophisticated gene regulatory network controls seed development. Additionally, it is affected by exogenous (temperature and water) and endogenous (phytohormones and nutrients) inputs, involving molecular networks that have only partially been discovered so far. In addition to highlighting knowledge gaps that need to be filled, this review explains current understanding of the role that temperature, water, phytohormones, and nutrients play in controlling maize seed germination.

Seed plants have developed to keep newly grown seeds dormant until the right moment for germination. The physiological processes of seed dormancy and germination are different, and the change from dormancy to germination is crucial for the growth of plants and for agricultural output. Diverse endogenous hormones and environmental cues exactly control these processes. Although ABA (abscisic acid) and GAs (gibberellins) are known to be the primary phytohormones that antagonistically regulate seed dormancy, recent findings demonstrate that another phytohormone, auxin, is also critical for inducing and maintaining seed dormancy, and therefore might act as a key protector of seed dormancy. In this study, we present an overview of our current knowledge of the complex molecular networks involving the crucial functions of phytohormones in controlling seed dormancy and germination, in which transcription factors with the AP2-domain play significant roles. We also go over the interactions (crosstalk) between various hormonal cues during seed dormancy and germination, putting the ABA/GA balance, which makes up the central node, as our main point of focus.

The phases of seed germination and early seedling establishment are crucial in the life cycle of a plant. Numerous internal factors, including phytohormones and outside cues like light, exactly control these stages. Karrikins (KARs), a family of small compounds found in wildfire smoke, are essential for a number of biological processes, such as seed emergence, germination control, and seedling establishment. KARs and strigolactone (SL) exhibit striking similarities in their chemical composition and signal transmission mechanisms. The biosynthesis and/or signaling transmission of auxin [indoleacetic acid (IAA)], gibberellin (GA), and abscisic acid (ABA) may be regulated by KARs, according to current research. It's interesting to note that various species have different KARs that control seed germination. Additionally, the promotion impact on seedling establishment suggests that KARs have a significant potential application in reducing the shade avoidance response, which is gaining increasing attention in plant molecular biology. KARs may engage intricately with phytohormones in these processes, particularly with IAA. The relationship between KARs and SL in the chemical structure, signaling pathway, and the control of plant growth and development are summarized in this updated overview. Additionally, the interactions between KARs and phytohormones that control seed germination, seedling development, and shade responses are addressed, as well as those between KARs and IAA. Finally, suggestions are made for future difficulties and study directions for the KAR research field.

Abiotic stresses that frequently affect plants, such as drought, salinity, heat, cold, and heavy metals, cause complex reactions that decrease crop yield and growth. Phytohormones are well known for controlling how plants grow and develop. They also act as vital chemical messengers, enabling plants to survive when they are subjected to a variety of stressors. Seed priming is a physiological technique that entails drying and hydrating seeds to enhance metabolic processes prior to germination. This technique increases the percentage and rate of germination as well as seedling development and crop production when subjected to both typical environmental conditions and various biotic and abiotic stresses. Plants can increase their ability to quickly and successfully fight various stresses by seed priming. As a result, phytohormone seed priming has become a crucial instrument for reducing the effects of abiotic stress. As a result, this review examines the potential value of priming with phytohormones to reduce the negative effects of abiotic stresses, potential methods for doing so, and the contributions of priming to improving crop production.

The current study explains how heavy metal stress affects the phytohormone content of chickpea (Cicer arietinum cv. Aziziye-94) seeds as they germinate. For this purpose, chickpea seeds growing at concentrations of 0.1, 1.0, and 5.0 mM Pb or 0.1, 1.0, and 10 mM Zn were monitored for 24, 48, and 72 h for endogenous abscisic acid (ABA), gibberellic acid (GA3), zeatin (Z), and zeatin riboside (ZR) contents. The outcomes demonstrated that Pb and Zn greatly slowed and prevented chickpea seed germination. Pb had a more detrimental impact on development than Zn. Additionally, Pb reduced GA3 content while increasing ABA and Z content in the germination seeds. High Zn concentrations (1.0 and 10 mM) reduced Z, ZR, and GA3 content while 0.1 mM Zn increased the same hormones' content. In all of the used amounts, Zn increased the ABA content.

To investigate the biochemical and molecular changes involved in hydrogen peroxide (H2O2) homeostasis and its signaling linked with hormone interactions for promoting vigor, tomato seeds were magnetoprimed at 100 mT for 30 min, followed by imbibition for 12 and 24 h, respectively, at 20 °C. The relative transcript profiles of genes involved in the synthesis of H2O2 like Cu-amine oxidase (AO), receptor for activated C kinase 1 (RACK1) homologue (ArcA2) and superoxide dismutase (SOD1 and SOD9) increased in magnetoprimed tomato seeds as compared to unprimed ones with a major contribution (21.7-fold) from Cu-amine oxidase. The transcript abundance of the H2O2 scavenging genes metallothionein (MT1, MT3, and MT4), catalase (CAT1), and ascorbate peroxidase (APX1 and APX2) was increased 14.4 and 15.4 times, respectively, in prepared seeds compared to the control. According to our research, metallothionein and RACK1 are essential components of the signal transmission pathway activated by reactive oxygen species that speeds up germination in tomato seeds that have been magnetized. At 12 hours after imbibition, the magneto-primed seeds showed increased catalase and ascorbate peroxidase enzymatic activity, suggesting their roles in maintaining H2O2 levels in the primed seeds. The abscisic acid/gibberellic acid (ABA/GA3) ratio in the primed seeds ultimately dropped due to the upregulation of the ABA 8′-hydroxylase and GA3 oxidase1 genes, indicating the critical role of H2O2 in improving the germination capacity of magnetoprimed tomato seeds[7]–[9].

In Arabidopsis thaliana, exogenous glucose slows seed germination in both wild-type (WT) and a variety of mutants in hormone signaling pathways. This research shows the critical roles of the RGA-like 2 (RGL2), SPINDLY (SPY), and ABA Insensitive 3 (ABI3) genes in the ABA signaling pathway as well as the RGL2 and SPINDLY (SPY) genes in the GA signalling pathways in the glucose-induced delay of seed germination. Glucose increases the transcription of the ABI3 and RGL2 genes. The results of this research also provide evidence for the hypothesis that various sugars, including the hexose stereoisomers, glucose, and mannose, delay or inhibit seed germination by acting on various hormone signaling pathways. Growth of WT and spy seedlings in response to varying glucose concentrations indicates that the GA or cytokinin signaling pathways are partially responsible for the stimulatory effects of glucose. Depending on the stage of development, the impacts of glucose on plant growth and development may be stimulatory or inhibitory. The activation of the ABA signaling pathway through ABI3 and inactivation of the GA signaling pathway through RGL2 and SPY appear to be how the inhibitory impact on seed germination is achieved. On the other hand, the GA and/or cytokinin signaling pathways may be involved in the stimulatory impact of glucose on seedling growth.

Flooding has recently become a major natural abiotic stress as a result of global warming, which has a significant impact on plant growth and development, particularly seed germination. However, it is still mainly unclear how flooding stress inhibits the germination of land crop seeds. Here, we report that flooding inhibits seed germination by mediating cascades related to glycometabolism, anaerobic respiration, and phytohormone biosynthesis using soybean (Glycine max), one of the most significant oil products in the world. According to phenotypic analysis, flooding stress greatly reduces seed vigor and consequently seed germination. According to biochemical analysis, flooding causes a reduction in the amount of different types of sugars present in the seed during imbibition as well as an increase in cell conductivity and ethanol levels, which notably inhibits seed germination. The expression levels of genes linked to glycometabolism, anaerobic respiration, and ABA (abscisic acid) and GA (gibberellin) biosynthesis/signaling are consistent with the phenotypic and biochemical evidences, according to later transcriptomics and qPCR assays. In addition, treatments with exogenous sucrose or GA can partly reverse the inhibition of seed germination caused by inundation or hypoxia. Together, these findings show that water stress reduces sugar and phytohormone biosynthesis and increases anaerobic respiration, both of which are detrimental to seed germination.

The aim of this study was to evaluate the effect of mucilage and its removal, as well as phytohormones [gibberellic acid (GA3) and indole-3-acetic acid (IAA)] in light and in darkness on germination of five cactus species (Coryphanta maiz-tablasensis, Echinocactus platyacanthus, Ferocactus latispinus, Ferocactus pilosus and Stenocereus queretaroensis) from the Chihuahuan Desert. C. maiz-tablasensis, E. platyacanthus, and F. pilosus are three of them that are in danger. In all species, the mucilage layer was present. Even in the micropyle, the mucilage was eliminated during the cleaning process. Mucilage resulted in higher germination percentage in E. platyacanthus (88.5 % vs. 21.1 % without mucilage), F. latispinus (88.5 % vs. 48.2 %) and S. queretaroensis (96.0 % vs. 1.0 %), as well as a lower germination time for E. platyacanthus (10.0 days vs. 19.5 days without mucilage), F. pilosus (14.1 days vs. 16.4 days) and F. latispinus (7.8 days vs. 14.0 days). In E. platyacanthus (higher at 500 and 1000 mg l-1 than at 50 and 100 mg l-1), F. latispinus (higher at 1000 mg l-1 than at control and at other concentrations), and F. pilosus (higher at 1000 mg l-1 than at control and 50 mg l-1), GA3 did influence germination percentage. For F. latispinus, the interaction between the mucilage layer and GA3 was only significant in that seeds with mucilage exhibited greater germination at 0, 50, 100, and 250 mg l1 of GA3 than seeds without mucilage, whereas at 500 and 1000 mg l1 of GA3, germination was similar for both. Auxins did not aid in cactus seed germination, and most cactus seeds did not germinate in the shade. The micropyle is covered in mucilage, and in most species, seeds without mucilage had a more colourful interior. According to our hypothesis, the mucilage layer in the micropyle can act as a barrier to control the flow of water to the interior seed[9]–[11].

CONCLUSION

Crop output is significantly impacted by the processes of plant germination and dormancy. Because they are present in both plants and microorganisms, plant hormones have a significant influence on the process of plant seed germination. There are several phytohormones involved in the growth and germination of seeds. However, the primary players who have a significant influence on the seed development and germination process are the ABA and gibberellin. Some plant genes are necessary for the operation of plant hormones and other plant genes are activated by plant hormones. By investigating the molecular pathways, specific details about the germination of seeds and the function of these plant hormones are examined. In this chapter, we summarized the recent findings regarding the impact of phytohormones on seed germination and development.

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CHAPTER 22

PHYTOHORMONES SIGNALING DURING THE PLANT SEX DETERMINATION

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ABSTRACT:

In this chapter, we briefly discussed the sex differentiation in the plant and the roles of the phytohormones involved in sex determination. The plan for determining sexual orientation is regulated by phytohormones under the impact of environmental factors. Gibberellins and cytokinins, in particular, are key players in the division and determination of sex in plants. In this chapter, we covered another phytohormones impact on the roles of the two major phytohormones, cytokinins, and gibberellins for sex differentiation.

KEYWORDS:

Floral Development, Gene Expression, Jasmonic Acid, Sex Determination, Sex Expression.

INTRODUCTION

The organism's sex is typically viewed as a collection of physical, physiological, biochemical, behavioral, and other characteristics that result in a particular reproductive strategy. The successful process of sexual reproduction involving both male and female gametes, and amphimixis (from the Greek "amphi" - from both sides and "mixis" - mixing), is ultimately made possible in angiosperms by the complete development of flower generative structures. A huge variety of types and forms of sexual polymorphism are created as a result of plant sexualization, which is the ability to produce predominately female or male reproductive organs. Hermaphroditism, monoecy, dioecy, trimonoecy, and polygamy are the five fundamental types of sexual polymorphism of flowering plants that can be categorized based on differences in the sexual type of flowers within a single plant or population.

Monoecious and dioecious plants have been the subject of the most research regarding polymorphism of sexual forms and molecular mechanisms of sex control. The classification of different sexual polymorphism types and forms sheds light on the extent of sexual phenotypic variety and the extreme plasticity of plant sex. As a result, it is understood that some dioecious plants, like hemp, can exhibit hermaphrodite or monoecious traits when under duress. Every known classification of the various types and forms of sexual polymorphism appears to some extent conventional [1]. because there are so many instances of sex plasticity that are known.

Plant growth and development processes are commonly closely related to the processes of sex differentiation in plants. However, the data is highly ambiguous. According to some authors, plants that grow quickly tend to be more female, while those that develop slowly tend to be more male. In this instance, the quick progression of plant developmental stages benefits the expression of the female sex. Other writers provide proof that plant feminization occurs as a result of general growth retardation. It was proposed that the effect of phytohormones on sex expression is mediated by their impact on the rate of plant growth because phytohormones play a crucial role in controlling plant growth, development, and sexuality. In fact, the elongation of the shoot was always associated with an increased maleness brought on by gibberellin, whereas the inhibition of growth was always associated with an enhanced femaleness brought on by cytokinin. While cytokinin primarily impacted sex expression in the late cv. Odesskaya-1 of maize, gibberellic acid had a stronger effect on sex expression in the early cv. Voronezhskaya-76. However, growth mechanisms alone cannot likely explain how phytohormones affect sex expression. As a result, in our experiments, retardants, which stunt plant development, were unable to fully reverse the GA-induced induction of hemp maleness. Furthermore, not all instances showed a strong correlation between the quantity of natural growth regulators and the speed of the development processes. The concentrations of IAA and ABA used in our studies essentially never stimulated the linear growth of plants but did enhance female sex expression[2].

It is well known that environmental (ecological) variables significantly affect how sex is expressed in plants. This theory states that environmental variables can alter the amount of endogenous phytohormones that control sex expression by influencing the activity of differentiating genes during the development of the generative organs (Figure. 1). Based on this idea and experimental data, we developed a computer model of how phytohormones affect cucumber plants' manifestation of sex in a comprehensive way. This program simulates the treatment of plants with different combinations and dosages of gibberellic acid, BA, IAA, and ABA. It allows for evaluation of changes in the proportion and overall number of male and female flowers on the entire plant as well as on its individual parts. (Figure.1).

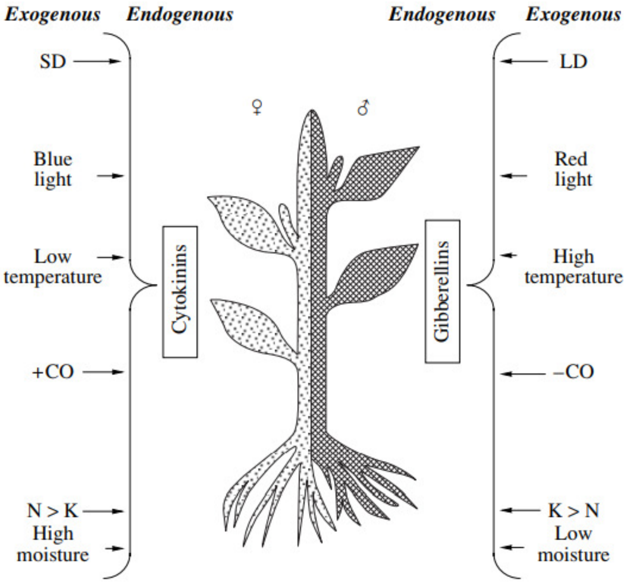

Figure 1: Sex determination by phytohormones: Diagram showing the overview of the phytohormones involved in the sex determination in the plants (link springers).

The model shows a synergism in the pairs of phytohormones IAA-BA and gibberellic acid-ABA shifting towards the female sex expression at the level of the complete plant. Gibberellic acid is an antagonist of all other phytohormones in terms of the overall number of flowers. (Figure. 1). As a whole, this pattern of hormone interplay also applies to the various cucumber stem parts, though it is much more complicated in this instance. As a result, sex expression tends to vary along the length of the shoot according to a cycle, and the size and regularity of this cycle rely on the indices of the exogenous hormonal complex. According to the location of a specific internode and the specificity of an acting factor, the degree of sex expression variability also varies. The sex change happens most quickly in the first internodes, and masculinization happens a little more quickly than feminization. The model effectively demonstrates how gibberellins and cytokinins are a key combination of phytohormones that control how sex is expressed in plants. The model will need to be further developed by including more endogenous and exogenous variables as well as paying closer attention to how they combine. One might anticipate that computer modeling would help people better grasp how phytohormones and the environment interact to control plant sex at the organismic level [2].

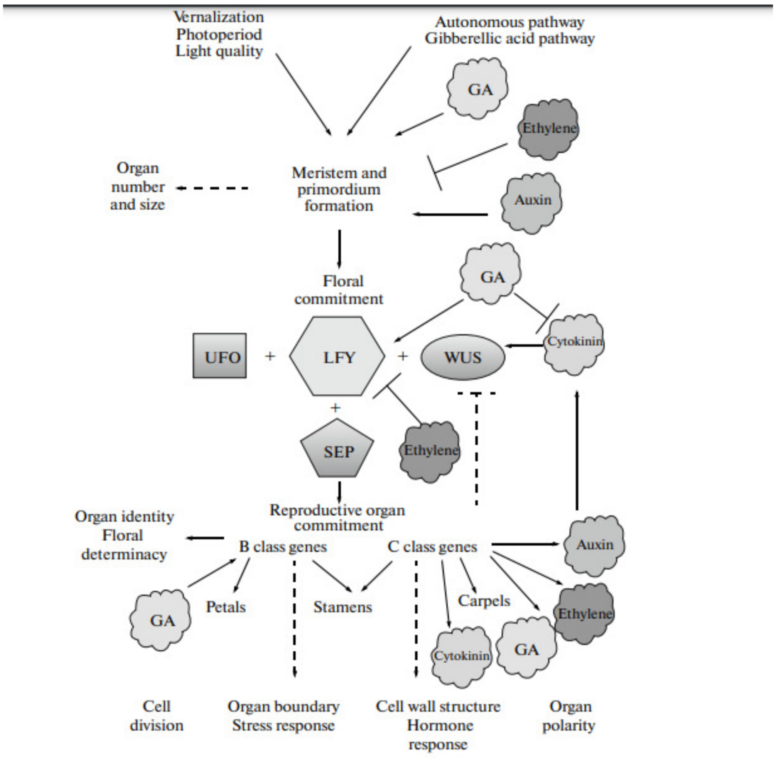

Figure 2: Signalling pathways: Diagram showing the different signalling pathways involved in floral development and differentiation (Springer link).

The development of flower organs from the floral meristem and subsequent organogenesis, which is dependent on local IAA biosynthesis and its polar transport, are both crucially influenced by auxin. Therefore, a disruption in IAA transport during the initial stages of flower development can halt the formation of lateral flowers and lead to the development of terminal flowers with defects. Local peaks in IAA activity-inducing floral organ formation are caused by IAA accumulation and its polar transport. IAA has been shown to be necessary for stamen formation. Affected stamen growth is a characteristic of auxin response factor (ARF) (AUXIN RESPONSE FACTORS) gene mutations in arabidopsis (Figure.2). IAA synthesis in anthers is crucial for their growth and eventual opening, whereas IAA transport within the stamen filaments is necessary for pollen development. IAA has a particular function in the growth of flowers.

It helps to synchronize the development of flower organs and has the power to restrain the expansion of nearby organs. It has been demonstrated that the low level of IAA in petals is joined by the high concentration of IAA in young anthers and mature pollen grains. It is known that the auxin gradient in primordia regulates the growth of gynoecia. Thus, the genotype of the female flower is caused by mutations in a few genes implicated in auxin signaling. Since gibberellins play a crucial role in the growth of flowers and stamens, many mutants with disrupted GA synthesis have underdeveloped floral organs. Through the suppression of DELLA proteins, gibberellins control pollen filament length, petal development, and fertility. The LFY and API genes of the arabidopsis floral organ identity are immediately activated by gibberellins. The clearest illustration of phytohormone involvement in floral development is the development of functional anthers in GAsensitive mutants of dwarf maize (Zea mays). It has been proven that GA actively participates in the control of corn sex expression. It is well known that cytokinin has an impact on homeotic genes and meristem growth. As a result, cytokines control the actions of WUS and other meristematic homeobox genes. The growth of anthers and pollen also requires cytokinins.

It has been demonstrated that male sterility is caused by cytokinin depletion at the high expression of the CKX1 gene implicated in its metabolism in maize, a condition that is treatable with cytokinin. One of the key regulators of anther growth and pollen maturation is jasmonic acid. Male sterility occurs in mutants with disrupted jasmonic acid synthesis, but this condition can be treated with jasmonic acid. Jasmonic acid controls the reproductive behavior of maize. Brassinosteroids build up in the pollen grains and regulate how the anthers grow. Pollen development abnormalities are present in Ara bidopsis mutants with altered brassi nosteroid metabolism. Recent research has shown that brassinosteroids play a role in the sex determination of corn through the feminization of male flowers. Additionally, ethylene controls flower organ development and degeneration as well as cell and tissue differentiation. Its potential involvement in the beginning of Arabidopsis anther formation was shown. Due to the inhibition of anther growth, feminization is brought about by ethylene treatment or by the intense synthesis of ethylene within the plant. The sex of cucumber and melon (Cucumis melo) is known to be regulated by ethylene.

LITERATURE REVIEW

In plants, environmental and genetic cues work together to regulate the development of inflorescences and flowers. Jasmonate (JA), a phytohormone, has been found to serve a crucial role in plant reproduction, including male fertility, sex determination, and seed maturation. Here, we review new developments in JA synthesis, signaling, the interaction of JAs with other hormones, and the regulatory network of JA that regulates the growth of the male organ, flower, and inflorescence. The multiple regulatory networks of JAs in stamen development are emphasized, along with the conserved and diverse roles of JAs in meristem transition, specification of flower organ identity and number, and meristem transition. Additionally, this review offers viewpoints on potential directions for future studies to clarify the mechanisms underpinning JAs homeostasis and transport throughout plant reproductive development [3].

A developmental cascade that results in the formation of unisexual florets from an originally bisexual floral meristem regulates the sex of maize plants. Tasselseed-mediated cell death regulates the abortion of pistil primordia in staminate flowers. The sex-determination gene tasselseed1's function was described by positional cloning. (ts1). The plastid-targeted lipoxygenase that the TS1 protein encodes has expected 13-lipoxygenase specificity, which raises the possibility that TS1 is involved in the biosynthesis of the plant hormone jasmonic acid. Lipoxygenase activity was absent and endogenous jasmonic acid levels in developing inflorescences were decreased in the lack of a functional ts1 gene. A function for jasmonic acid in maize male flower development has been identified by the application of jasmonic acid to developing inflorescences, which restored stamen development in mutant ts1 and ts2 inflorescences [4].

The information relating to phytohormone regulation of plant sex is given. Consideration is given to the operation of signaling networks that control floral development and sex expression, including those that involve phytohormones. Analyzed is the part phytohormones play in the operation of the systems and processes that control sex. Examples of sex reversion caused by phytohormone therapy of plants are shown. It has been shown that many sex-related genes contain proteins that are involved in the metabolism of phytohormones. The importance of phytohormone research for comprehending the molecular processes regulating plant sex is discussed [1].

Jasmonate (JA), a plant hormone, plays crucial functions in plant development and defense. While Arabidopsis thaliana, a dicotyledonous model plant, accounts for the majority of our current knowledge of the JA pathway, recent research in monocotyledonous plants is adding to our grasp of this crucial hormone signaling pathway. We give a comparative overview of the signaling and JA biosynthetic pathways in monocots in this study. We highlight recent research that uncovered the (mostly conserved but also diverged) molecular mechanisms underpinning JA signaling and biosynthesis in rice and maize, two economically significant plants. Cereal crops, which supply the majority of the world's food and feed supply, should experience a substantial increase in pest and pathogen resistance as a result of an improved understanding of the JA pathway in monocots [5].

Numerous studies have used cucumber as a paradigm to determine the sex of flowers. With the help of a computer program, we were able to create a computer program that would allow us to create a computer program that would allow us to create a computer program that would allow us to create a computer program. According to the profiling study, the mutation caused numerous changes in gene expression that led to the up- or down-regulation of 143 genes and the down-regulation of 600 genes. Reverse transcription polymerase chain reaction (RT-PCR) and real-time quantitative RT-PCR were used to validate the Solexa results. (qRT-PCR). According to a gene ontology (GO) study, the differentially expressed genes were primarily involved in translation, localization, macromolecular and cellular biosynthesis, transport and organization of cellular components, and biogenesis. Additionally, the tissue and state of development of the gynoecious mutant flowers affected the expression of some of these genes. The findings of this research point to two key ideas that control how cucumbers determine their sexual orientation. The differential expression of genes such as ACS, Asr1, CsIAA2, CS-AUX1, and TLP that are involved in plant hormone signaling pathways suggests that phytohormones and their interaction may be crucial in the determination of sex. Second, this developmental process may also be influenced by the control of some transcription factors, such as EREBP-9 [6].

The energy plant Jatropha curcas's monoecious germplasm predominates. The following are the results of a survey conducted by the American Psychological Association. A comparative transcriptome study between gynoecious and monoecious inflorescences was carried out to look into the regulatory mechanism of the transition from monoecious to gynoecious plants. 3,749 distinct genes were found to express differently during the two phases of inflorescence development. 32 of them were related to floral growth, and 70 to the biosynthesis and signaling of phytohormones. Six genes homologous to KNOTTED1-LIKE HOMEOBOX GENE 6 (KNAT6), MYC2, SHI-RELATED SEQUENCE 5 (SRS5), SHORT VEGETATIVE PHASE (SVP), TERMINAL FLOWER 1 (TFL1), and TASSELSEED2 (TS2), which control floral development, were considered as candidate regulators that may be involved in sex differentiation in J. curcas. In contrast to monoecious inflorescences, gynoecious inflorescences had greater levels of cytokinin biosynthesis and lower levels of abscisic acid, auxin, gibberellin, and jasmonate biosynthesis. Gibberellic acid (GA3) was also applied exogenously to produce neutral flowers in gynoecious inflorescences by promoting perianth growth in male flowers and partially inhibiting it in female flowers. Male flowers presumably abort at an early stage due to the arrest of the stamen primordium, leading to the development of gynoecious individuals. These findings imply that a few genes involved in floral development and phytohormone signaling networks control how the sex of J. curcas is determined. Our research offers a fundamental foundation for the networks that control sex determination in J. curcas, and it will be useful for understanding how the plant reproductive system has evolved

Sex-specific floral development processes have developed in dioecious plants. The exact gene expression patterns involved in the development of dioecious plant flowers are still unknown. Here, we used the exceptional model system of andromonoecious poplar to remove the confounding impacts of dioecious plants' genetic backgrounds. We were able to describe the sex-specific development of female and male blossoms through comparative transcriptome and physiological analysis. Genes involved in floral development, phytohormone synthesis and metabolism, and DNA methylation were found to have substantially different expression levels between the sexes as a result of transcriptome analysis. A significant correlation between phytohormone signaling and gene expression was found by correlation analysis, which helped to pinpoint particular phytohormone-responsive genes and their cis-regulatory components. The expression of two DNA methylation-related genes, METHYLTRANSFERASE1 (MET1) and DECREASED DNA METHYLATION 1 (DDM1), differs between female and male flowers and is found in the sex-determination area of chromosome XIX. According to a time-course analysis, the expression of MET1 and DDM1 may result in different amounts of DNA methylation in female and male flowers. Understanding the interactions between DNA methylation, target gene expression, and phytohormone signaling should help to better comprehend the variations in floral development between sexes. This study links sex-specific floral development to physiological and epigenetic changes, identifying a collection of candidate genes for additional research on poplar sexual dimorphism [7].

Plants have developed a number of different mechanisms to support sex determination, the process by which flowers become male or female, in order to improve outcrossing. There is no singular sex determination mechanism or gene because sex determination has independently evolved several times. However, the cloning of sex determination genes from both monocots and dicots has revealed a shared set of pathways involving plant hormones. An intriguing conundrum connects hormone signaling to numerous developmental pathways, including those involving flower homeotic genes and small RNAs[8], and asks why these pathways were chosen for.

In plants, determining sex is a complex process of correlated events that includes genes that are differentially and/or specifically expressed at various stages of development. Understanding the process of sex determination in plants will be improved by examining gene expression patterns from various sex types. In order to learn more about the genes that may be involved in sex determination in this species, we sequenced the RNA of Ginkgo biloba's female and male branches (FB and MB), as well as ovulate and staminate strobilus (OS and SS). From eight cDNA libraries, roughly 60 Gb of clear reads were recovered. The clean reads' de novo assembly produced 108,307 unigenes with an average length of 796 bp. Of these unigenes, 51,953 (47.97%) had at least one gene sequence in the public datasets accessed that had at least one significant match. In MB vs. FB and SS vs. OS, a total of 4709 and 9802 differently expressed genes (DEGs) were found.

There were discovered to be differences in the expression of genes encoding DNA methyltransferase, plant hormone signal and transduction genes, and sex kinds. They were discussed in relation to their possible roles in G. biloba sex determination. In female buds, anther-specific genes were found, whereas pistil-related genes were expressed in male buds, indicating that dioecism in G. biloba was caused by the selective halt of reproductive primordia. Between the findings of the quantitative real-time PCR and RNA-Seq, there was a strong correlation in the expression level. With the help of the transcriptome resources we created, we were able to describe gene expression patterns and look at differential expression patterns, laying the groundwork for finding functional genes connected to sex determination in G. biloba.

The Chinese chinquapin (Castanea henryi) nut is an abundant source of nutrients and starch for food and feed, but the low proportion of female to male flowers reduces its output. The developmental processes underpinning the sex differentiation of flowers are poorly understood. To investigate the involvement of phytohormones during sex differentiation, we described the morphology of male and female floral organs and the cytology of flower sex differentiation, analyzed endogenous levels of indole-3-acetic acid (IAA), gibberellins (GAs), cytokinins (CKs), and abscisic acid (ABA) in the flowers, investigated the effects of exogenous hormones on flower development, and evaluated the expression profiles of genes related to biosyntheses and signaling pathways of these four hormones using RNA-Seq combined with qPCR. According to morphological findings, the flowers can be divided into four developmental phases and are made up of unisexual and bisexual catkins. According to HPLC findings, CK accumulated significantly more in female flowers than in male flowers, while GA and ABA showed the opposite results and IAA did not exhibit any trend. Exogenous hormones had similar impacts to endogenous hormones in terms of sex differentiation. Inferred from RNA-Seq and qPCR studies that a number of genes may be important for hormone biosynthesis and sex differentiation. In this research, phytohormone biosynthesis and signaling during the sex differentiation of *C. henryi* are described in detail for the first time. This report should serve as a basis for future mechanistic studies of sex differentiation in Castanea Miller species and other nonmodel plants.

CONCLUSION

Phytohormones and external factors both have an impact on how plants differentiate their sexes. Phytohormones regulated the different gene pathways for the differentiation of the plant sex. In reality, genes that initiate programs for the development of flower-generative components using phytohormones as modulators regulate the procedures of flowering and determining sex. Numerous genes that determine sex were discovered to regulate by the biosynthetic pathways of phytohormones. Genomic regulation complicating sex regulation, which only emphasizes a variety of pathways allowing for a flexibility of varieties and forms of sexual polymorphism, does not rule out phytohormones' participation in sex determination.

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CHAPTER 23

PHYTOHORMONE SIGNALING CASCADES DURING THE CHLOROPLAST DEVELOPMENT

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ABSTRACT:

The photosynthesis mechanism occurs in the chloroplast of plants. During the development of the chloroplast in the plant, phytohormones regulate the function of the chloroplasts. It was originally believed that the only hormone that affects how plants grow their chloroplasts is cytokinin. However, some research has also covered the different phytohormones that are involved in the growth of chloroplasts. This chapter summarized the molecular roles of the phytohormones involved in the formation of chloroplasts. Currently, attempts are being made to elucidate the mechanism using methods from genomics and molecular genetics.

KEYWORDS:

Abscisic Acid, Chloroplast Development, Cytokinin Signal, Phytohormones Signaling, Transcription Factors.

INTRODUCTION

Chloroplasts, which contain chlorophyll, are the locations of photosynthesis where light energy is absorbed and transformed. They play a crucial role in the biosynthesis of numerous crucial primary and secondary metabolites in addition to being necessary for this energy conversion process. Chloroplasts, like all plastids, arise from proplastids, which are found in the developing cells of plant meristems. Proplastids transform into etioplasts, which have a semi-crystalline structure called the prolamellar body made up of lipids and the NADPH-dependent protochlorophyllide oxidoreductase if a leaf is produced in darkness. The formation of thylakoid membranes, dispersion of the prolamellar body, conversion of the protochlorophyllide accumulated in the dark to chlorophyll, and formation of a completely functional chloroplast all occur in response to illumination.

The process of de-etiolation includes the shift from etioplast to the chloroplast, which takes place at the same time as chlorophyll's biosynthesis. A side branch of the tetrapyrrole biosynthesis pathway, chlorophyll biosynthesis begins with the creation of 5-aminolevulinic acid (Figure 1). (ALA). Glu-tRNA synthetase, Glu-tRNA reductase (GluTR), and Glu-1-semialdehyde aminotransferase (GSA-AT) work together to create ALA from glutamate (Glu), which is then converted into protoporphyrinogen IX (Proto IX), a ubiquitous precursor of haem and chlorophyll. On a different branch, which is not covered in more depth here, haem biosynthesis continues. The chlorophyll cycle, which is the interconversion of chlorophyll a and b, is carried out after the chlorophyll branch introduces Mg2+ into Proto IX for chlorophyll production.

Within the chlorophyll branch, the NADPH: protochlorophyllide oxidoreductase encoded by the POR genes transforms protochlorophyllide into chlorophyllide. This is significant because it is the first stage of chlorophyll production that needs light. As a result, during development in the dark, chlorophyll intermediates, particularly protochlorophyllide, accumulate. Protochlorophyllide is instantly converted to chlorophyllin when dark-grown (etiolated) seedlings are exposed to light. Thereafter, there is a lag period during which no more chlorophyll can be synthesized. Chloroplasts are completely functional and capable of photosynthesizing once chlorophyll a and b are formed and appropriately incorporated into the thylakoid membranes and related photosystems [1].

We recently discovered that Nicotiana tabacum cv. Samsun NN cultured green tobacco cells are ideal for investigating cytokinin signal transduction because cytokinin-supplemented medium promoted cell growth and chloroplast development. Three cytokinin-inducible genes (cig) were found to be expressed during the earliest stages of chloroplast development based on the fluorescent differential display created using cultured green tobacco cells.12) Functional studies of the relationship between the development of the chloroplast and these cigarettes are being conducted. In the not-too-distant future, another novel method, i.e., the use of microarrays, will enable the identification of additional cytokinin-inducible genes [2].

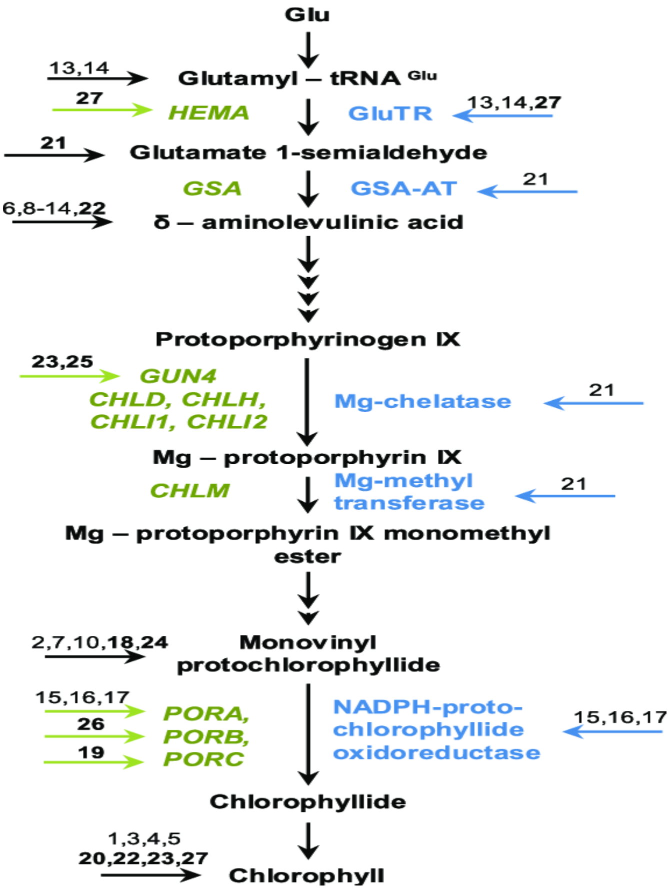

Figure 1: Cytokinin role in chlorophyll biosynthesis: Diagram showing the role of Cytokinin in the chlorophyll biosynthesis pathway (Research gate).

The following are the results of a survey conducted by the National Institute of Standards and Technology (NIST) on the use of standardized test in the United States. Because auxins have a repressive impact on chlorophyll production in the root, the research explains that roots activate chlorophyll biosynthesis production through reduced auxin signaling. Mutant analysis suggests that auxins transported from aerial tissue repress chlorophyll biosynthesis at the root via the function of IAA14/SLR, which is responsible for repressing the expression of the transcription factor LONG-HYPOCOTYL5 (HY5), a positive regulator of chloroplast differentiation and GLK2 (Figure. 2).

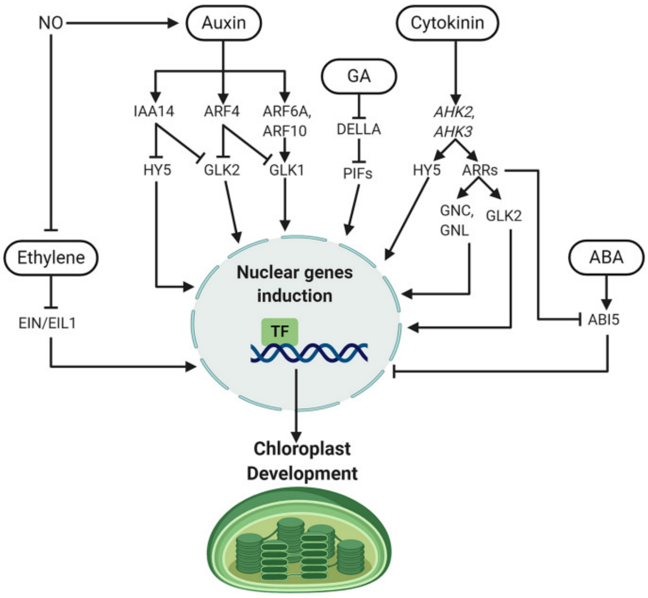

Figure 2: Phytohormones signaling for chloroplast development: Diagram showing the different phytohormones signaling during the chloroplast developments (Springer link).

Nevertheless, despite having a wealth of knowledge about networks and their constituent parts, more research is required to fully comprehend how phytohormones interact with one another to maximize effectiveness. Cytokinins positively control chlorophyll biosynthesis in the root by inducing the expression of the HY5 and GLKs genes, demonstrating a genetic network involved in chloroplast development that includes various phytohormones. (Figure. 2). By encouraging ALA synthesis and increasing POR activity, cytokinin promotes chlorophyll biosynthesis. It may also cause partial chloroplast differentiation. The cytokinin signal is sensed by the AHK2 and AHK3 receptors, which then transmit the signal to the B-type ARR transcription factors.

It is significant to note that ARRs, including GNL, GNC, HY5, and GLK2, directly control the production of genes involved in chlorophyll biosynthesis and chloroplast biogenesis. Numerous genes associated with the chloroplast, including GENOMES UNCUPLED4 (GUN4) and HEMA1, are controlled by the GATA transcription factors GNC and GNL. Additionally, HY5 controls a number of nuclear-encoding genes involved in the production of chlorophyll and photosynthesis processes, including MAGNESIUM CHELASE (CHLH), GUN4, PORC, CHLIDE A OXYGENASE (CAO), and MAGNESIUM CHELATASE27[3]. The connections between the various hormones are intriguing to observe. For instance, whereas cytokinin is crucial for regulating greening and the growth of chloroplasts, abscisic acid (ABA) has the reverse effect. The bZIP transcription factor ABSCISIC ACID INSENSITIVE5 (ABI5) mediates the inhibiting effect of ABA on greening. Contrarily, cytokinin blocks ABI5's transcription activity through ARR12.

Gibberellin (GA), a different hormone involved in this modulation, prevents photomorphogenesis in the dark by adversely regulating gibberellin signaling and suppressing GA-mediated responses. It is understood that DELLA proteins can prevent PIF3 and PIF4 from transcribing by preventing their DNA-recognition domains from binding to the DNA. (Feng et al. 2008). The expression of genes involved in photosynthesis and chlorophyll biosynthesis, such as CHLH, PORC, and CAO, is induced by DELLA proteins, which also control the biosynthetic routes for both carotenoid and chlorophyll. Ethylene is a different phytohormone that affects the production of chlorophyll. EIN3/EIL1, the master transcription factor in the ethylene signaling cascade, mediates the effects of this hormone.

A sterol-derived plant growth regulator called brassinosteroid has significant biological effects, such as promoting cell elongation and inhibiting chloroplast formation. Brassinosteroid deficiency has been linked to dwarf plants with extremely green leaves in Arabidopsis deetiolated 2 (DET2) and other newly discovered mutants involved with brassinosteroid biosynthesis as well as the potential brassinosteroid receptor brassinosteoid-insensitive dwarf 1 (BRI1). We looked for mutants that displayed resistance to these brz effects in order to examine the process of brassinosteroid signal transduction in chloroplasts and plant development. When grown in the dark with brz, some mutant Arabidopsis seeds that had undergone EMS and fast neutron mutagenesis were noticeably taller than the normal type. Three mutants at least had hypocotyl lengths equal to those of wild kinds grown in the dark without brz treatment. They had the moniker Bil. (brz-insensitive-long hypocotyl). When cultivated in the dark with brz, three additional mutants with short hypocotyls but no cotyledon opening were identified as bih. (brz-insensitive-hooked hypocotyl). Pale green leaves that could be related to chloroplast formation were found in some of the mutants. Continued studies of these bil s and bihs' roles and chloroplast development are necessary [2].

LITERATURE REVIEW

The plant hormones known as auxins have been discovered to play a crucial role in the majority of plant development processes over decades of plant study. Since photosynthesis, the process by which plants obtain the majority of their energy, takes place in the chloroplast, it forms an organelle of significant importance to plants. Over the course of at least 50 years of research on auxins' function in photosynthesis, it has become clear that auxins have an impact on several crucial elements and the shape of the chloroplast. Numerous genes have been found to be expressed in the chloroplast in recent years, and some of their mutants have been found to affect various auxin-mediated processes. The most tightly controlled genes in mutants with changes to the chloroplast include genes related to signaling pathways like IAA/AUX, ARF, GH.3, SAUR, and TIR, as well as genes related to biosynthesis and transport like YUCCA. This review seeks to provide a thorough and current summary of the interactions between auxins and various chloroplast-related processes, including pigment synthesis, redox regulation, plant albinism, and chloroplast development [3].

Shortly after being identified as a regulator of plant growth more than 50 years ago, the plant hormone cytokinin was also found to play a function in controlling the growth and activity of chloroplasts. Numerous studies have noted its supporting effects on chloroplast ultrastructure and chlorophyll synthesis, particularly during the etioplast-to-chloroplast transformation. Recently, it was demonstrated that the hormone has a protective function for the photosynthetic system under high light stress. Genetic and transcriptomic research are revealing more and more information about the molecular mechanisms by which cytokinins operate on plastids. The B-type response regulators, specifically ARR1, ARR10, and ARR12, which are transcription factors of the two-component system governing cytokinin functions, are primarily regulated by the cytokinin receptors AHK2 and AHK3. CGA1, GNC, HY5, GLK2, and CRF2 are additional transcription factors that connect cytokinin and chloroplast formation. In this review, we discuss the crosstalk between cytokinin, light, and other hormones during chloroplast development as well as earlier and more recent discoveries of the long-known relationship between the hormone and the organelle [1].

During ontogenesis, abscisic acid and phenolic inhibitors concentrate in the foliage of plants. According to our review (Kefeli et al., 1989) and direct tests, leaves accumulate ABA in free and bound forms 4–7 times more than roots do. Our study assistant used sterile culture of grape seedlings to collect these data. Thus, the chloroplast of verdant leaves may serve as a hub for the biosynthesis of ABA in leaves[4].As the fruit grew and ripened, researchers looked at how lycopene and phytohormone levels varied between diploid, triploid, and tetraploid plants of two watermelon varieties. Five genes were specifically examined for their patterns of expression: phytoene synthase (PSY1), phytoene desaturase (PDS), -carotene desaturase (ZDS), carotenoid isomerase (CRTISO), and lycopene -cyclase (LCYB). Lycopene content in the red-fleshed cultivar Mimei rose quickly between days 25 and 35 after pollination (DAP), before declining at day 40. Fruit that was triploid or tetraploid contained more lycopene than fruit that was diploid.

Furthermore, during the fruit's growth and ripening phases, triploids tended to have higher lycopene contents than tetraploids. However, the yellow-fleshed cultivar Huangmei contained very little lycopene (0–2 mg kg–1 FW) throughout all fruit development phases. LCYB gene expression was the lowest out of the five tested genes in Mimei, and PSY1 transcript level was usually higher than the other four genes. The mRNA levels of the PSY1, CRTISO, and LCYB genes were higher in polyploid fruit than in diploid fruit. In comparison, LCYB's transcript level in Huangmei was only slightly lower than PSY1's. The transcript levels of the PSY1, CRTISO, and LCYB genes were higher in diploid fruit than polyploid fruit. In Mimei, gibberellane (GA) content and lycopene accumulation were found to be negatively correlated, while abscisic acid (ABA) content and lycopene accumulation were found to positively correlate, but only in diploid melons. These findings suggested that the differential transcription expression of the genes involved in lycopene metabolism and phytohormones controls the different levels of lycopene present in distinct ploidy watermelons [5].

IAA and kinetin are phytohormones that prevent chlorophyll loss in aged wheat chloroplasts both in vivo and in vitro. In contrast, GA has a senescence-inhibiting effect on detached leaves and solitary chloroplasts while stimulating the pigment degradation in aged attached leaves. A change in the hormone's optimal concentration for inhibiting chlorophyll degradation points to a distinct size of endogenous hormone pool that controls chloroplast aging both in vivo and in vitro. The fact that kinetin, IAA, and GA prevented chlorophyll loss during the aging of chloroplasts in vitro suggests that hormones' ability to stop the yellowing of senescing leaves may be facilitated by their direct action on chloroplasts [6].

To improve subsequent freezing tolerance, winter cereals and other winter-hardy species must first become acclimated to the cold. C-repeat/dehydration-responsive element binding transcription factors (CBF/DREB1) are upregulated by low temps, and they in turn promote the expression of COLD-REGULATED (COR) genes. We review the evidence that the dwarf phenotype and improved photosynthetic efficiency seen in cold-acclimated and CBF-overexpressing plants are the result of the combination of these interactions. The dwarf, compact, and cold-tolerant phenotypes, as well as the improved photosynthetic performance and biomass accumulation usually associated with cold-acclimated plants, are mimicked in plants that overexpress CBFs but are grown at warm temperatures.

In this review, we suggest a model in which plants integrate low temperature, variations in light intensity, and variations in light quality to sense the cold acclimation signal. Such integration causes the CBF-regulon to be activated, which then upregulates the expression of the COR gene and GA 2-oxidase (GA2ox), resulting in a dwarf phenotype as well as improved freezing resistance and photosynthetic efficiency. We come to the conclusion that because plants are photoautotrophs, they do not only use changes in low temperature to create the cold-acclimated state but also take into account changes in light intensity, light quality, and membrane viscosity. These interconnected sensing and signaling networks appear to be controlled by CBFs as master regulators [7].

The ubiquitously present small multifunctional molecule phytomelatonin is essential for plant growth, development, and biotic and abiotic stress reactions. We now have a more complete knowledge of phytomelatonin synthesis thanks to the discovery of alternative pathways in addition to the traditional biosynthetic and metabolic pathways of phytomelatonin. Phytomelatonin primarily works through two mechanisms. Through its potent antioxidant properties, phytomelatonin controls the stress-induced burst of reactive oxygen species. Phytomelatonin functions as a signal in the indirect pathway to trigger signaling cascades and crosstalk with other plant hormones. In 2018, the PMTR1/CAND2 phytomelatonin receptor was identified, which improved our knowledge of phytomelatonin activity. The traditional and potential pathways involved in the synthesis and metabolism of phytomelatonin are outlined in this study. We concentrate on the interactions between phytomelatonin and other phytohormones to clarify the roles of phytomelatonin. To clarify how PMTR1 sends the phytomelatonin signal via the G protein and MAPK cascade, we offer two models. Our knowledge of phytomelatonin signal transmission will be enhanced by this review's facilitation of the discovery of additional signaling molecules that operate downstream of the phytomelatonin signaling pathway.

Although chloroplasts are best known for their function in photosynthesis, they also enable the absorption of nitrogen and sulfur as well as the synthesis of amino acids, fatty acids, nucleotides, and hormones. Therefore, understanding the development of chloroplasts is important for understanding these various and fundamental biological processes as well as efforts to rationally redesign them. All angiosperms must have light in order to form chloroplasts, and light directly controls the expression of hundreds of genes linked to chloroplasts. Additionally, light affects the levels of several hormones, such as gibberellins, auxins, cytokinins, brassinosteriods, and cytokinins, which in turn regulate the development of chloroplasts, especially in the early phases of plant development. To control chloroplast growth, transcription factors like GOLDENLIKE1&2 (GLK1&2), GATA NITRATE-INDUCIBLE CARBON METABOLISM-INVOLVED (GNC), and CYTOKININ-RESPONSIVE GATA FACTOR 1 (CGA1) work downstream of light and phytohormone signaling. Thus, a complex network formed by transcription factors, light signaling, and hormone signaling controls the transcription of genes linked to chloroplasts and photosynthesis in green tissues, thereby regulating the growth and number of chloroplasts per cell. With the help of this conceptual framework, we can pinpoint regulatory mechanisms that could be used to control chloroplast abundance, boost crop photosynthetic efficiency, and find new research directions to fill in knowledge gaps.

To explore the contributions of ω-3 fatty acid desaturases (FADs) to cold stress response in a special cryophyte, Chorispora bungeana, two plastidial ω-3 desaturase genes (CbFAD7, CbFAD8) were cloned and verified in an Arabidopsis fad7fad8 mutant, before being compared with the microsomal ω-3 desaturase gene (CbFAD3). CbFAD7 and CbFAD8 have the greatest expression in leaves while CbFAD3 was primarily expressed in suspension-cultured cells, despite the fact that these genes were expressed in all C. bungeana tissues examined. Trienoic fatty acids (TAs), which are produced when CbFAD3 and CbFAD8 work together in growing cells and when CbFAD7 and CbFAD8 cooperate in leaves, significantly increased at low temps. A series of studies showed that abscisic acid and gibberellin were involved in the complicated control of phytohormones in leaves, while jasmonie acid and brassinosteroids contributed to the cold-responsive translation of the -3 CbFAD genes in both C. bungeana cells and leaves. These findings indicate the non-redundant, hormone-regulated role of -3 CbFADs in maintaining a healthy amount of TAs in frigid settings, which aids C. bungeana in surviving there.

CONCLUSION

We have outlined the topic of phytohormones and chloroplast in this chapter. The bulk of studies has demonstrated that the Cytokinin signaling system controls the growth of chloroplasts in plants. Apart from cytokinins, some study has determined the impacts of other phytohormones. Cytokinin regulates two important processes in chlorophyll formation, ALA synthesis, and protochlorophyllide photoreduction. Different genes and the function of various cytokinin transcription factors are discovered in the formation of the chloroplast. Auxin is the secret driver for the production of chloroplast, according to a recent study. While plastid production is negatively regulated by brassinosteroids. To fully comprehend the process used by the other phytohormones for the formation of the chloroplast, more thorough research is required.

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CHAPTER 24

PHYTOHORMONES AND CHROMATIN REGULATORY INTERACTION

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ABSTRACT:

The major contributor to the different types of activities carried out by plants is phytohormones. Studies have looked into the connection between epigenetic change and phytohormones activity. Histone methylation/demethylation, acetylation, and other epigenetic modifications in plants can be regulated. This chapter covered the various genes involved in influencing epigenetic modifications in plants that are used to control the actions of phytohormones. These discoveries are illuminating phytohormones' mode of action and opening up a brand-new line of inquiry into both phytohormones and the processes governing epigenetic alterations.

KEYWORDS:

DNA Methylation, Epigenetics Modification, Gene Expression, Histone Methylation, Phytohormones Epigenetics.

INTRODUCTION

Throughout their post-embryonic lives, plants continue to expand and develop new structures and tissues that are generated from meristems. Plants are sessile creatures, which means that as they grow and develop, they continuously incorporate and reflect ambient variations. This can result in a high degree of embryonic flexibility in reaction to environmental changes. As an alternative, changeable settings can favor resilience, in which animals can survive in a variety of circumstances with little phenotypic variation. Thus, phytohormone communication, chromatin structure modification, and gene translation changes interact intricately to control plant development. Although it is still unclear how these regulation levels interact, there is growing molecular proof that phytohormones signaling and chromatin structure interact.Without affecting any alterations in the chromosomal DNA patterns, epigenetic modifications control heritably active genes during mitosis or meiosis, enabling fluid and reversible regulation of gene expression.

Histone alteration, chromatin rearrangement, non-coding RNAs, and DNA methylation are all examples of epigenetic changes. Gene expression patterns are governed by each of these changes individually, collectively, and in interaction with other epigenetic modifications. Numerous studies have demonstrated that the ability of epigenetic changes to modify DNA code in reaction to external factors contributes to the adaptability of sessile plants' survival strategies. The molecular cues that change the epigenome and the transmission of these signals to regulate the downstream epigenetic pathways are intriguing understudied parts of this area of study. Growing evidence points to a close connection between plant hormone communication and epigenetic control.

Auxin response factors (ARFs), the regulatory elements that initiate auxin-induced gene expression, are activated when the nucleus auxin receptors TRANSPORT INHIBITOR RESPONSE1 (TIR)/AUXIN SIGNALING F BOX PROTEINS (AFBs) recognize the plant hormone auxin. Emerging data suggest that chromatin-modifying factor PICKLE (PKL) and numerous epigenetic factors, including histone changes and microRNAs (miRNAs), regulate the ARF-dependent activation of auxin-sensitive genes.At the limiting temperature (29C), the hda19 mutation exhibits a number of tpl-1-like traits, indicating that TPL and HD19 operate on the same target. Collectively, these studies support the model that the co-repressor TPL recruits HDA19 to the AUX/IAA repressor in an EAR motif-dependent manner, and that GCN5/HAG1 histone acetylase has a role opposing the IAA12/BDL-TPL-HDA19 repressor complex in the ARF-dependent expression of auxin-responsive genes (Figure 1). Plant-specific and seemingly frequently used to control plant hormone communication is the EAR repressome.

For example, the EAR motif was identified in several proteins, including NOVEL INTERACTOR OF JAZ (NINJA), ABI-FIVE BINDING PROTEINS (AFPs), BRASSINAZOLE RESISTANT 1 (BZR1), and BRI1-EMSSUPPRESSOR 1 (BES1), and are involved in ethylene, JA, ABA, gibberellic acid (GA), and brassinosteroid (BR) signaling. Particularly, auxin and JA signaling mirror each other in terms of the EAR repressome and the signaling pathways that destroy the EAR repressors. TPL and the proteins in its family, TOPLESS-RELATED, are involved in the signaling of auxin, JA, GA, and BR. Other plant hormone regulation mechanisms might use the same HDACs via TPL processes. The lack of a direct association between TPL and HDA19, however, indicates that another bridge protein is necessary for HDAC induction.

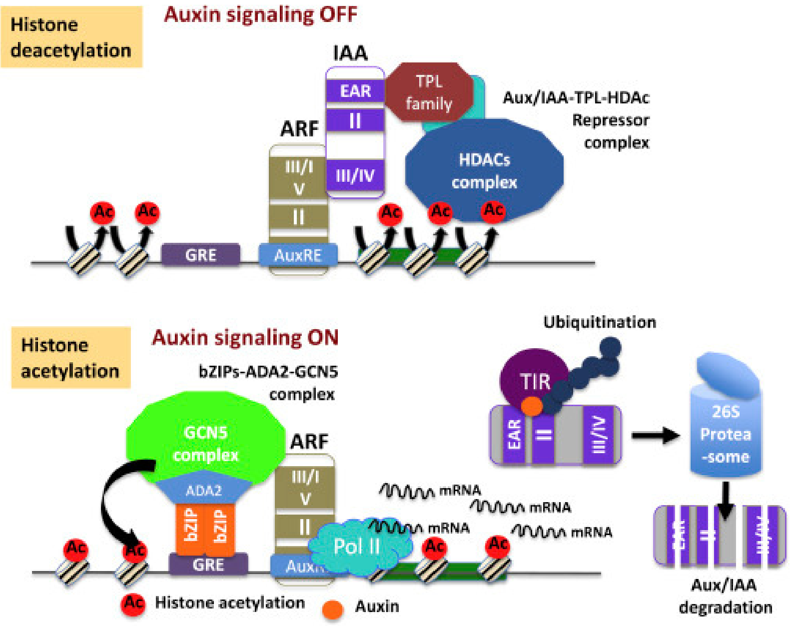

Figure 1: Acetylation and deacetylation: Diagram showing the different mechanisms of Acetylation and deacetylation in the plant (Science direct).

Plants must have developed particular companion proteins of TPL for each hormonal signaling pathway in order to regulate specialization. To determine the process underlying the functional specialization of TPL family proteins for EAR repression-mediated plant hormone signaling, more research will be required. To initiate or inactivate the production of auxin-responsive genes, ARF TFs engage AuxRE elements in the promoter. When AUX/IAA binds to ARF, the TPL-HDAC complex can approach the chromatin's AuxRE element and cause it to be in a repressed state. But it is still unclear how the GCN5/HAG1 histone acetylase complex is brought to the auxin-responsive locus to initiate gene translation. An auxin-inducible bZIP11 TF that binds ADA2b and directs the bZIP11-ADA2b complex to the G-box-related elements (GREs) motif, the binding site for bZIP TFs, is one potential method. The GCN5/HAG1 acetylase is able to be drawn to the GH3.3 promoter by the action of the bZIP11-ADA2b complex, resulting in the stimulation of GH3.3 translation. (Figure 1) [1]. Recent advances, especially in Arabidopsis, have uncovered that chromatin remodeling through histone methylation changes is not only restricted to developmental needs but also an integral part of the very complex cascade of events that lead to abiotic/biotic stress tolerance, resistance, and short-/long-term memory.

The following types of histone methylation modifications, which provide distinct chromatin structures when engaged in stress reactions, are currently being proposed as an early theory (Figure.2): (i) histone methylation changes that are basally present on stress-related genes to establish a ‘permissive’ chromatin state that may either limit the spreading of repressive chromatin marks and/or potentiate a rapid transcriptional induction upon need; (ii) histone methylation changes that are transiently induced from an inactive or a permissive chromatin state by stress, to either facilitate the transcriptional initiation and/or reinforce transcription of stress-responding genes, and finally, histone methylation changes that are established in response to stress; (iii) maintained for a certain time during the lifespan of an individual (i.e. somatic memory) or (iv) transmitted to one or more subsequent generations (i.e. transgenerational memory). However, there are still a lot of voids, errors, and divergences in this developing perspective, mostly because there are so many challenges involved in studying a process that is so intense and dynamic. In this way, various types of stressors typically present a joint task to plants in nature. Different signaling pathways can combine non-additively in response to these stress combos, controlling responses in ways that the research of either stress alone could not have anticipated. When biotic and abiotic stressors occur concurrently, an additional level of intricacy is introduced that necessitates applying pressures simultaneously and treating each particular set of natural circumstances as a separate stress. We must therefore step up our research in order to better understand the process by which histone methylation alterations control stress reactions. For example, the relationship between histone methylation/demethylation and stress reactions is still unclear, and explanations will necessitate detailed dynamic methods based on comparative studies of both the epigenomes and transcriptomes during stress responses.

The related histone-modifying enzymes are also poorly understood at the moment. This information gap will require extensive genetic studies and large-scale screens to determine which histone methyltransferases/demethylases mutations are most sensitive to various stressors, whether they are present simultaneously or not. Nearly nothing is known about the individual reader/effector that will identify particular histone methylation sites in order to decide their functional and morphological result, among other variables regulating stress-induced chromatin alterations. An endeavor in this area will probably help us gain a thorough knowledge of the basic processes linking changes in histone methylation with the regulation of the production of genes that respond to stress, which will then help plants endure stress. It is unquestionably necessary to conduct higher-resolution chromatin research in order to identify the targeted stress-responsive genes and the precise locations of histone methylation and demethylation.

However, it is challenging to investigate the immediate impacts of histone methylation/demethylation in plants. One reason is that plant genomes harbor a high-copy number of histone genes (e.g. the Arabidopsis genome comprises 47 genes that encode 33 different core histone proteins; www.chromdb.org) and the incorporation/modification of such variants can result in the formation of chromatins with particular properties and functions.

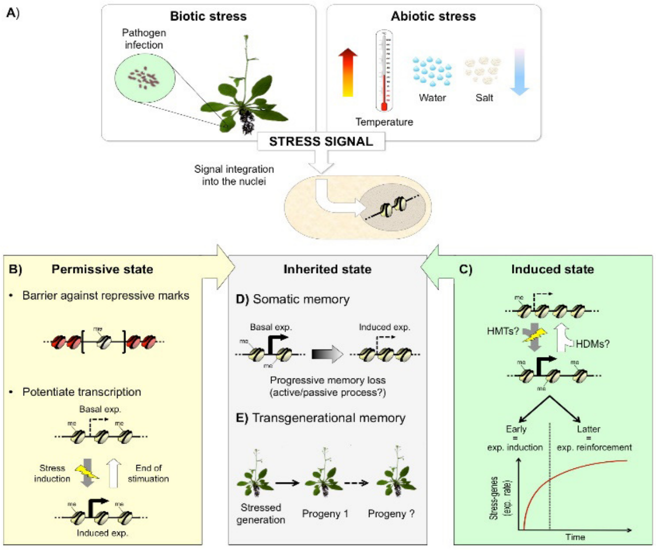

Figure 2: Methylation and demethylation of the histone: Diagram showing the various histone methylation and the demethylation mechanism during the biotics and the abiotic stress in the plants (Interchopen .com)

Even though ChIP tests have been useful in identifying changes in histone methylation, many antibodies used to detect these changes have so far been unable to differentiate between various variations. New technologies (e.g. generation of mutants with point alterations targeting amino acid in the N-terminal tail of histone using the clustered regularly interspaced short palindromic recurs (CRISPR)/CRISPER-associated (Cas) system) will need to be explored to unravel histone methylation changes of specific histone variants and their functions. The fact that plants are made up of numerous functionally distinct tissue and cell kinds, each with its distinct epigenome, transcriptome, and proteome, presents another difficulty. Since histone methylation alterations brought on by stressors have only previously been studied in whole plants or tissues, the acquired profiles most likely represent the average of several potentially disparate tissue- or cell-specific profiles. Finally, as plants have finite resources that must be balanced between growth and defense against stresses, often resulting in a growth or yield penalty, histone methylation changes in response to stress should be integrated into a more global developmental view, taking into account the involvement of several histone methyltransferases/demethylases in various processes such as root growth, flowering time, floral organogenesis, gametophyte or embryo formation. To provide both innovative models and possible instruments for further utilization towards sustainable agriculture [2], knowing such regulation networks is a crucial first step.

LITERATURE REVIEW

It has long been understood that phytohormones communication and epigenetic processes are both essential for plant growth and flexibility in reaction to environmental cues. In fact, numerous upstream cues are integrated into different signaling cascades that are controlled by phytohormones and epigenetic mechanisms to govern various plant characteristics. There is growing proof that various degrees of interaction exist between phytohormones and epigenetic mechanisms. From the viewpoint of phytohormone biology, we present a summary of the current understanding of the interaction between phytohormones and epigenetic mechanisms. As part of our overview of pharmacological regulators used in epigenetic research, we also make suggestions for interdisciplinary development methods for new regulators [3].

The spatial control of phytohormone buildup and reactions at different levels is necessary for phytohormone activity in plants. Epigenetic changes and the function of phytohormones are now being linked, according to recent research. Evidence in particular points to the role of microRNAs and epigenetic elements like DNA methylation, chromatin rearrangement, and histone alteration in the regulation of auxin production, transport, and signal transmission. Additionally, it has been demonstrated that some phytohormones influence epigenetic changes. These discoveries are illuminating phytohormones' mode of action and opening up a brand-new line of inquiry into both phytohormones and the processes governing epigenetic modifications [4]. During the wilting process, the plant hormone abscisic acid (ABA) builds up in tea leaves due to environmental stress.

The control of ABA biosynthesis's process, however, is still mainly unknown. In the current research, we discovered higher transcript of ABA biosynthetic genes during the postharvest preparation of tea under dehydration stress. Dehydration stress also increased histone acetylation of ABA anabolism genes while reducing histone H3 lysine 9 dimethylation and DNA methylation of ABA biosynthesis genes, promoting ABA buildup. We examined potential controllers of DNA methylation and histone deacetylation in dehydration stress. When viewed collectively, our findings suggest that epigenetic changes play a part in the post-harvest handling of tea[5]. Many plant species use so-called inducible defenses, which are mechanical or molecular mechanisms, to defend themselves against predators (ID).

These are controlled via an endocrine process which may be under epigenetic regulation and in which jasmonic acid (JA) plays a significant part. The creation of ID and the manufacture of hormones implicated in the ID signaling pathway were the two processes that were tangentially evaluated in this research. We sought to create Trifolium repens plants with various degrees of DNA methylation modification by applying varying doses of 5-azacytidine. We then elicited the plants together with controls, i.e. plants with natural DNA methylation status, with JA and then indirectly recorded ID production in herbivore-choice trials in which the leaves of plants with different DNA methylation statuses were provided to caterpillars of a generalist herbivore, Spodoptera littoralis. We also examined the equilibrium of several important defense chemicals in the plants, including salicylic acid, jasmonates, ABA, IAA, and indole-3-acetic acid (IAA). Demethylated plants were favored by S. littoralis over non-demethylated samples, our research showed. Demethylation also affected the amount of JA, ABA, and IAA produced. We come to the conclusion that DNA methylation modifies ID expression most likely by controlling signaling chemicals important for the development of defense [4].

Numerous methods that control the translation of regions without changing the DNA structure are used in epigenetic regulation. The main effects of these various processes are changes to the molecular structure of DNA or the architecture of chromatin, which may be heritable or transitory as a dynamic reaction to external stimuli. Through gradient creation, the phytohormone auxin contributes significantly to almost every element of plant existence. A delicate balancing act between metabolism, movement, and communication causes auxin peaks and minima. The precise processes underlying the spatial fluctuations of auxin levels in plants are only now being understood, despite the fact that epigenetic control of gene expression during growth has been known for decades. In this overview, we compile the most recent data on the epigenetic processes controlling the expression of the genes involved in indole-3-acetic acid (IAA) biosynthesis and transport in Arabidopsis, and we also address the potential directions for this young field [5].

Plants must quickly adjust to the harsh climatic circumstances they are exposed to. Abiotic stress results in the accumulation of the phytohormone abscisic acid (ABA), which signals genetic changes that result in bodily reactions. Epigenetic changes frequently make transcription easier, especially at genes with periodic, tissue-specific, and external expression patterns. MOP1 is necessary for the development of an RNA-dependent epigenetic mechanism in maize (Zea mays) that controls the transcriptional suppression of sites throughout the genome. MOP1 function has been previously correlated with genomic regions adjoining particular types of transposable elements and genic regions, suggesting that this regulatory pathway functions to maintain distinct transcriptional activities within genomic spaces, and that loss of MOP1 may modify the responsiveness of some loci to other regulatory pathways.

MOP1 and ABA networks each control particular genes and are important moderators of gene expression. Mop1-1 and Mop1 homozygous plants were exposed to external ABA and RNA-sequencing to ascertain whether MOP1 deletion affects ABA-responsive gene expression in maize. In four paired analyses, 3,242 differently expressed genes (DEGs) were discovered. Overall, mop1-1 homozygous plants showed an increased response to ABA-induced alterations in gene expression. The highest number of DEGs were identified in ABA-induced mop1-1 mutants, including many transcription factors; this suggests combinatorial regulatory scenarios including direct and indirect transcriptional responses to genetic disruption (mop1-1) and/or stimulus-induction of a hierarchical, cascading network of responsive genes. Additionally, some cultivars showed a slight rise in CHH methylation at potential MOP1-RdDM sites in reaction to ABA, indicating that epigenetic diversity may affect the transcriptional responses elicited by the environment in maize [6].

In-depth molecular regulation mechanisms in plants subjected to different external limitations have been the main emphasis of recent study in plant stress biology. It would be easier for agricultural biotechnologists to create genetically enhanced plants with stress-tolerant traits and slightly reduced output if these molecular switches were clarified. A quickly expanding area of study is epigenetic control, which changes the chromatin layout to promote gene translation at particular genomic locations. Epigenetics has also identified a stress memory in plants that enables the stress-exposed plants to more effectively handle comparable stress in the future. We have emphasized in this analysis the findings that are currently accessible on plant epigenetic research in relation to abiotic stressors like salt and drought, which are the two major environmental stresses that occur worldwide and significantly reduce yearly agricultural yields [7].

Numerous adaptive traits in plants have been linked to epigenetic variance, but there aren't many straightforward ways to take advantage of this variation. Multiple plant species experience a variety of embryonic changes as a result of the RNAi silencing of the plant-specific gene MutS HOMOLOG1 (MSH1), along with modifications to the defense, phytohormone, and abiotic stress response pathways and methylome reorganization. Transgene-null'memory' effects result from this msh1-conditioned embryonic rewiring, which is maintained regardless of transgene division. A offspring family with greater diversity in resilient characteristics that react to selection is produced when an isogenic memory line is transferred to the wild type. In this research, the MSH1 system's suitability for causing agronomically advantageous epigenetic diversity in soybean is examined. By combining MSH1 epi-populations with soybean memory lines that had obtained the mutation. In both glasshouse and outdoor experiments, derived soybean epi-lines demonstrated a rise in variation for several yield-related characteristics, including pods per plant, seed weight, and ripening time. Over wild type, a few epi-F2:4 and epi-F2:5 genotypes produced more seeds. We noticed a recovery of MSH1-derived increased growth to wild-type values by epi-F2:6. Additionally, epi-populations demonstrated less epitype-by-environment (e E) interaction, which suggests greater yield consistency. The potential markers of increased growth behavior across generations were discovered through the transcript analysis of epi-lines. Genes associated with the cell cycle, the production of abscisic acid, and the auxin response, especially SMALL AUXIN UP RNAs (SAURs), were expressed differently in epi-F2:4 lines compared to epi-F2:6 lines. The promise of MSH1-derived epigenetic diversity in plant genetics for improved production and crop consistency is supported by these data [8].

Growing evidence points to epigenetic markers, particularly DNA methylation, as important fruit maturation factors. We performed tests at the transcriptional, regulatory, and metabolic stages to see if this holds true for sweet pepper (Capsicum annuum). McrBC PCR, bisulfite sequencing, and real-time PCR demonstrated that DNA hypomethylation occurred in the upstream region of the transcription start site of some genes related to pepper ripening at the turning stage, which may be attributed to up-regulation of CaDML2-like and down-regulation of CaMET1-like1, CaMET1-like2, CaCMT2-like, and CaCMT4-like. Silencing of CaMET1-like1 by virus-induced gene silencing led to DNA hypomethylation, increased content of soluble solids, and accumulation of carotenoids in the fruit, which was accompanied by changes in expression of genes involved in capsanthin/capsorubin biosynthesis, cell wall degradation, and phytohormone metabolism and signaling.

While endogenous IAA exhibited a tendency in the reverse direction, endogenous ABA rose as the fruit ripened. During maturation, there was no ethylene indication found. Auxin and gibberellin biosynthesis genes, as well as cytokinin breakdown genes, were expressed less when DNA hypomethylation was present, whereas ABA biosynthesis genes were expressed more when it occurred. Exogenous ABA increased the transcript of CaDML2-like but decreased CaCMT4-like in the mature-green pericarp. IAA therapy induced CaMET1-like1 and CaCMT3-like transcription. The transcript of CaDML2-like was substantially upregulated by ethephon. At the transcriptome level, treatment with GA3 and 6-BA had ambiguous impacts on DNA methylation. Based on the findings, a model is suggested that raises the possibility that DNA methylation plays a significant part in the control of maturation in the non-climacteric pepper plant [9].

CONCLUSION

In this chapter, we discussed in the part on DNA methylation/demethylation, these regulatory mechanisms do not reside solitarily in the regulatory network but are intertwined. Here, we also discussed the role of various chromatin changes in hormones' actions. The fact that epigenetic alterations are reversible processes means that they are also likely to occur concurrently at the same location, where they may interact positively or negatively in response to a variety of internal or exterior cues. Interaction between the plant hormones mechanism and signaling pathways is also controlled by the different epigenetic modifications. Here we also discussed the role of the different phytohormones in the modification of the epigenomes. Exploring the information of these plant hormones and the regulation of these epigenetic changes provide a new approach to the response of the plant against abiotic and biotic stress.

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CHAPTER 25

PHYTOHORMONES STUDY IN VITRO CONDITION, MODEL PLANT, AND FUTURE DIRECTION

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ABSTRACT:

Plant phytohormones that control a plant's growth and development are also used to grow a plant in a culture dish. Several ratios of phytohormones are employed for the explant plant's growth during micropropagation. In addition to phytohormones, other microorganisms that promote plant development also play a significant role during the growth of the plant. Where these organismal groupings are present, the availability of nutrients and phytohormones for plant development is increased. Understanding the molecular mechanisms underlying phytohormones can help develop new tools for horticulture and contemporary agriculture. The relevance of phytohormones for plant development under *in vitro* conditions and their advantages for the agricultural industry are briefly discussed in this chapter.

KEYWORDS:

Fruit Crops, Genome Editing, Growth Promoting, Plant Tissue, Tissue Culture.

INTRODUCTION

Plant tissue culture is the process of growing a whole plant from an explant or even just one plant cell under aseptic conditions. This aspect of plant biotechnology depends on the phenomenon known as cell totipotency, which describes any single cell's capacity to create all the differentiated cells that are characteristic of organs and to regenerate into a whole plant. The fast mass replication of elite genotypes on huge scales in a relatively short amount of time is made possible by micropropagation, which makes use of this essential characteristic of plant cells. Because it produces healthy seedlings all year long and shortens the vegetative cycle, micropropagation is now widely used in horticulture, agriculture, and industry . It is also a key technique for environmental preservation.

It is also a key method for genetic engineering, agricultural enhancement, and the propagation of novel kinds resulting from somaclonal variation. Yet practically at every stage of the growth and development process, the approach calls for the application of chemical disinfectants, varying quantities of the right phytohormones, and occasionally antibiotics, antifungals, and antivirals. Several of these plant growth regulators (PGRs) are quite expensive, which restricts or limits the development of this technology and its viability in agriculture.

In order to achieve the bulk propagation of crop plants, micropropagation using in vitro procedures has been extensively employed in horticulture and other agricultural industries. It is a good strategy for multiplication of prospective elite genotypes of sugarcane in short time frame. Hence, a lot of farmers may benefit from this procedure by receiving a new cane genotype. Also, it has evolved into a desirable and potent tool for genetic modification, plant genetic resources preservation, and the preservation of priceless germplasm. Moreover, micropropagation aids in the development of high-quality, disease-free plant material for sale[1]–[3].

There are two general types of organ regeneration in plants: direct and indirect. In the former, shoots or roots are directly generated from tissue explants, whereas callus development occurs as an intermediary step before shoot or root induction in indirect organogenesis. Indirect organ regeneration in culture in Arabidopsis is a two-step procedure. Auxin-rich callus-inducing media (CIM) is initially applied to small pieces of plant tissue (explants) in order to create callus; endogenous cytokinin levels are normally sufficient for this procedure. Many traits of the lateral root meristem have been linked to the differentiation status of callus-forming cells.The induction of shoot or root tissues is favoured, respectively, by subsequent culture of the callus on shoot- or root-inducing medium (SIM or RIM), which contains varying ratios of auxin to cytokinin. A higher ratio of cytokinin to auxin favours the production of shoots (Figure.1)

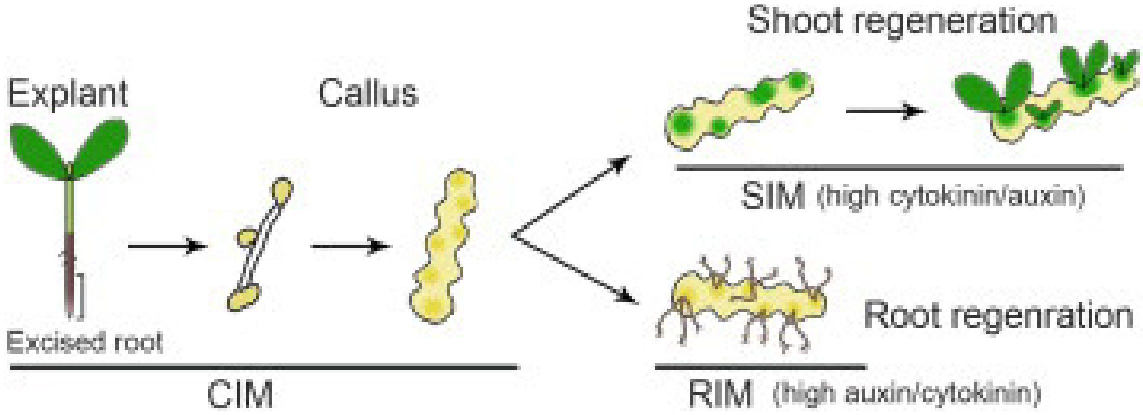

Figure 1: Micropropagation: Diagram showing the overview of the micropropagation *in vitro* condition (Science direct.com).

The ability of plants to regenerate *in vitro* differs greatly between species. Some several families and genera have a strong ability for regeneration, including the Solanaceae (*Nicotiana, Petunia,* and *Datura*), Cruciferae (*Brassica* and *Arabidopsis*), Gesneriaceae (*Achimenes* and *Streptocarpus*), Asteraceae (*Chichorium* and *Chrysanthemum*), and Liliaceae (*Lilium* and *Allium*). Regeneration is difficult in families like the Malvaceae (*Gossypium*) and Chenopodiaceae (*Beta*), indicating that the necessary mechanisms for *in vitro* regeneration are either lacking or inadequate. Even across several *Arabidopsis* ecotypes and rice cultivars, there is a significant variation in their capacity for regeneration. This offers a substantial difficulty for micropropagation and transformation of agricultural plants. The ability for *in vitro* regeneration varies naturally depending on one's capacity to produce and react to cytokinins. More bioactive cytokinin accumulation in plants makes them more susceptible to de novo shoot organogenesis induction techniques.

For instance, the Arabidopsis hoc mutant, which accumulates larger quantities of endogenous cytokinin, may easily go through de novo shoot organogenesis, even though it also shows diminished apical dominance, slower shoot development, delayed leaf expansion, and delayed blooming. Yet, if tissues are not receptive to the phytohormone, raising cytokinin levels is pointless. In fact, attempts to stimulate organogenesis using endogenous phytohormone applications have failed in a number of species. Many soil microorganisms from a variety of taxa have been shown to be effective PGPMs. Rhizospheric PGPMs are soil-borne organisms that live on plant roots or invade plant tissues internally (referred to as PGP endophytes). They perform a variety of tasks including mineral solubilization (Zn, P, and K), iron chelation, nitrogen fixation, phytohormone production, and biocontrol of plant pathogens. They are divided into three major groups according to their activities, which correspond to three growth promotion methods (Figure 2).

Plants establish a variety of interactions with soil fungi. Diverse taxa, belonging to arbuscular mycorrhizal fungi (e.g., Gigaspora, Funneliformis, and Rhizophagus), orchid mycorrhizal fungi (Russula, Rhizoctonia, and Tulasnella species), ericoid mycorrhizal fungi (Harpophora oryzae and Colletotrichum tofieldiae), ectomycorrhial fungi (e.g., Laccaria, Pisolithus, and Scleroderma), Trichoderma spp., Piriformospora, and other root endophytes fungi such as Fusarium spp., Penicillium spp., Aspergillus spp., etc., have been recognized as PGPF.

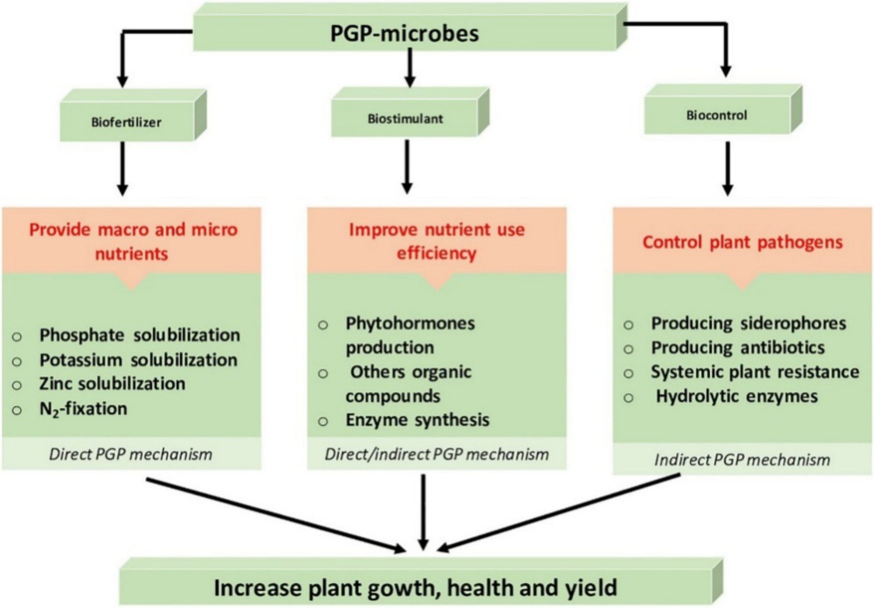

Figure 2: Plant growth promoting microbes: Diagram showing the different roles of the plant-growing microbes in micropropagation (Frontier).

Plants from micropropagation are negatively impacted by water stress, because of the inadequate absorption capacity of their roots. AMF influences the post-transplant performance of in vitro-grown plants by enhancing nutrient availability and generating disease resistance through the manufacture of phytohormones or PGRs. Auxins, cytokinins (CKs), abscisic acid (ABA), gibberellic acids (GAs), ethylene (ET), salicylic acid (SA), and jasmonic acid are only a few of the phytohormones that fungus create (JA). Under biotic and/or abiotic stressors, these hormones regulate plant growth and turn on signaling pathways.Moreover, fungi, particularly AMF, have a significant role in the absorption and availability of water, which boosts photosynthesis and osmotic adjustment in response to environmental challenges. The absorption of micronutrients like P, Zn, Cu, Fe, etc. is also increased by AMF.

Because in vitroplants' adventitious and feeble root systems which are hairless do not permit adequate absorption of nutrients from the soil during the initial stages of the weaning step, AMF input is particularly crucial during the acclimatization phase. By their hyphae and arbuscules, which move nutrients, particularly phosphate, from the soil to the plant, AMF can assist in resolving this issue. Beneficial endophytic fungi increase the absorption of phosphate, potassium, and zinc and/or produce phytohormones such as cytokinins and indole acetic acid to stimulate plant development.By increasing phosphorus, potassium, and zinc intake and/or producing plant hormones such as cytokinins, indole acetic acids, and gibberellic acids, favorable endophytic fungi help plants flourish. The transplanted in Vitro plants may not have found their original microsymbiont partner, which may account for their decreased survival rate and poor establishment in outdoor circumstances[4]–[6].

In the future, a significant study is needed to identify efficient, multifunctional, stress-tolerant PGRs-producing microorganisms and exhibit ecological flexibility for their usage in plant tissue culture. The numerous applications for helpful microbes in plant tissue culture open up new opportunities for selecting suitable PGPMs to use at the various stages of micropropagation, with a focus on mixed-strain consortiums rather than mono-strain inoculums to benefit from functional complementarity. On the other hand, significant effort has to be put into bioformulating these microorganisms for use in plant tissue culture. PGPM delivery is currently limited, particularly during explant culture, elongation and multiplication, and rooting. Researchers should devise plans to enhance microbial inoculants and inoculation techniques in order to apply PGPMs in plant tissue culture. In this regard, the use of bionanotechnologies may open up new possibilities for the creation of microbial carriers for inoculants.

By using nanoformulations, biofertilizers may be more resistant to UV inactivation, desiccation, and heat.*In vitro* tissue cultivation using bionanotechnology is currently the subject of very few investigations. In order to create custom bioformulations employing PGPMs, specifically for the biotization purpose in plant tissue culture, research would be based on what is being done in the pharmaceutical business. The other difficulty is raising the standard of microbial inoculants for vitro plants and creating appropriate inoculation procedures.In this regard, the use of genetically modified inoculants may provide chances to accomplish a particular goal in the agricultural and/or food sectors. Current developments in biotechnological technologies, such as functional genomics, rhizosphere signaling, etc., may help design microorganisms to provide increased advantages to plants, particularly in the field of plant tissue culture.

LITERATURE REVIEW

Due to outstanding developments in integrative research models during the past ten years, the functional analysis of phytohormone synthesis, interaction, and regulation in higher plants has come to light once again. Nevertheless, in natural circumstances, plants are not axenic and are frequently colonized or directly impacted by various microbes, such as rhizobacteria, many of which can produce phytohormones. The model plant-growth-promoting rhizobacteria (PGPR) from the genus Azospirillum, which is thought to be one of the most representative PGPR, is the source of phytohormones. This review summarises information related to biosynthesis, metabolism, regulation, physiological role, and agronomical impact of phytohormones produced by PGPR. We offer detailed information regarding the phytohormones auxins, gibberellins, cytokinins, ethylene, and abscisic acid, as well as the plant growth regulators polyamines and nitric oxide. We take care of their metabolism. We discuss the metabolism of these substances by Azospirillum species in chemically defined media, in plant-microbe interactions, or the context of Azospirillum species' employment in agronomy.

Abscisic acid (ABA), a phytohormone related to isoprenoid stress, is now known to have a variety of biological roles in mammals and to have substantial therapeutic effects on a number of clinically significant human disorders. It has been conclusively demonstrated through studies using human specimens that ABA maintains the stress-related functional characteristics that were previously observed in plants and which support improved inflammatory defense systems in mammals. Moreover, research using animal models showed that ABA had strong anti-inflammatory capabilities, which were demonstrated by a significant decrease in immune cell infiltrates at the sites of inflammation. As a result, ABA therapy finally results in a significant improvement of both communicable and non-communicable illnesses, which are linked to a generalized reduction in inflammation. ABA was also demonstrated to have effects on the mammalian immune system.It has been demonstrated that ABA has a variety of physiological effects on non-immune components in addition to its influence on the mammalian immune system. One of ABA's most noteworthy qualities is its ability to increase mesenchymal stem cells, which may provide a novel use for the drug in the field of regenerative medicine. Additionally, it has been suggested that ABA is crucial for maintaining glycemic control. ABA's importance in the mammalian system, its preventative and therapeutic benefits in different disease situations, and the future possibilities for the development of ABA as a potential pharmacological candidate for the better treatment of inflammatory and infectious human illnesses are all summarised in this study.

One of the most popular methods for in vitro plant regeneration is in vitro organogenesis, which is extensively employed in biotechnology and the basic research of plant biology. No similar study has been published in RAMIE, even though earlier studies have built a comprehensive regulatory network model for Arabidopsis in vitro organogenesis. We created a reference transcriptome library and 10 digital gene expression (DGE) libraries for Illumina sequencing to produce more thorough observations of the transcriptome content and dynamics during ramie in vitro organogenesis. A total of 111.34 million clean reads were collected for the transcriptome, and between 13.5 and 18.8 million clean reads were produced by the DGE libraries. After the filtering of 5,760 differentially expressed genes (DEGs), 43,222 unigenes from the de novo assembly were obtained 26 auxin-related and 11 cytokinin-related DEGs were chosen for qRT-PCR validation of two ramie cultivars with high (Huazhu No. 5) or severely poor (Dazhuhuangbaima) shoot regeneration capacity by searching against the Kyoto Encyclopedia of Genes and Genomes Pathway database. The findings showed that various genotypes had varied auxin and cytokinin regulatory patterns. Here, we provide the results of the first genome-wide gene expression profile of ramie in vitro organogenesis and give an overview of transcription and phytohormone regulation throughout the procedure. Additionally, two ramie cultivars with great or severely poor shoot regeneration abilities have unique expression patterns in auxin and cytokinin-related genes, which has improved our knowledge of the in vitro organogenesis process.This finding will serve as a starting point for future study on phytohormones and improve the ramie regeneration mechanism.

The non-climacteric octoploid strawberry (Fragaria × ananassa Duchesne ex Rozier) was utilized as a model to examine its control during fruit ripening. High-performance liquid chromatography-electrospray tandem mass spectrometry (HPLC-ESI-MS/MS) was applied to profile 28 distinct endogenous phytohormones in strawberries. Autins, cytokinins (CKs), abscisic acid (ABA), 1-aminocyclopropane-1-carboxylic acid (ACC), jasmonates, and the phenolic compounds salicylic acid (SA), benzoic acid (BzA), and phenylacetic acid (PAA), along with their various metabolic forms that have so far largely gone unstudied, fall under this category. In contrast, ABA catabolites 9-hydroxy-ABA and phaseic acid matched the pattern of climacteric decrease at the turning phase of strawberry ripening. ABA, ACC, and CK N6-(2-isopentenyl)adenine (iP) were shown to be related to ripening. Except for iP, the content of other CK types declined as the fruit matured.

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The primary sources of nutrients and fiber for the human diet are fruit crops, which include climacteric and non-climacteric fruits. Since 2013, the genome editing system CRISPR/Cas (Clustered Regularly Interspersed Short Palindromic Repeats and CRISPR-Associated Protein) has been widely used in various plants, resulting in unprecedented progress in the genetic improvement of many fruit crops that are significant from an agronomic standpoint. Here, we review recent developments in CRISPR/Cas genome editing of fruit crops, including work to understand how plants evolve and defend themselves. We also discuss prospective difficulties and advancements in the use of genome editing techniques on fruit crops, such as enhancing CRISPR/Cas cassette expression, enhancing reagent delivery effectiveness, enhancing genome editing specificity, and enhancing the transformation and regeneration system.The primary sources of nutrients and fiber for the human diet are fruit crops, which include climacteric and non-climacteric fruits. Since 2013, we have also highlighted possible difficulties and offered ideas on the use of genome editing in crop breeding, particularly in fruit crops. It is important to note that the breeding and demonstration of fruit crops urgently require attempts to modify fruit crops using genome editing techniques[7]–[9].

Protein flow between endomembrane organelles is efficiently and extremely selectively mediated by transport vesicles. For understanding the mechanics of vesicle formation, polar trafficking, and cargo selectivity in mammals and yeast, in vitro reconstitution systems have been employed extensively. Nevertheless, due to the large lytic vacuoles and stiff cell walls of plants, this method has not yet been used on them. Here, we outline a technique for creating in vitro vesicles from Arabidopsis that may be used to recreate, purify, and analyze vesicles made of the coat protein complex II (COPII) of plants. In this protocol, we outline a step-by-step procedure for isolating microsomes and cytosol from suspension-cultured Arabidopsis thaliana cells (7-8 h), purifying and reconstituting COPII vesicles in vitro (4-5 h), and performing biochemical and microscopic analysis using particular antibodies against COPII cargo molecules for reconstitution.We also offer thorough sample-preparation procedures for vesicle payloads by quantitative proteomics and cryogenic electron microscopy (1 h) analysis (4 h). The entire process typically takes 18 to 20 hours to complete and enables plant researchers to achieve organelle purification or vesicle reconstitution for subsequent characterization without specialised knowledge.

The primary source of abiotic and biotic pressures that have detrimental impacts on agricultural productivity to an irreversible degree and threaten to stifle output increases and endanger sustainable agriculture is global climate change. Saline, drought, severe heat, and other abiotic stressors brought on by climate change have an adverse effect on plant morphological, physiological, biochemical, and metabolic features. This eventually inhibits plant growth, development, and production. Yet, excessive usage and other improper applications of agrochemicals are detrimental to the preservation of the environment and natural resources, impeding the development of sustainable agriculture. Due to their capacity to enhance soil qualities and impart stress tolerance in plants, plant growth-promoting bacteria (PGPB) may be used to provide sustainable agriculture more effectively with the rapid expansion of contemporary agriculture.The fundamental mechanisms of PGPB that improve plant stress tolerance and performance under diverse abiotic and biotic conditions were uncovered in this research. Also, there was a thorough discussion of the most recent developments in PGPB inoculation methods, the commercialization of PGPB-based technologies, and the present applications of PGPB in sustainable agriculture. The prospect of microbe-assisted agriculture's future was highlighted last. Insights into the interactions between plants and PGPB under biotic and abiotic pressures, as well as proof and tactics for PGPB's improved commercialization and use, might spur the creation of creative solutions that utilize PGPB under climatological settings.Hence, enhancing the plant's ability to react to cytokinin offers prospective advantages versus choosing plants that produce larger quantities of endogenous cytokinin[10], [11].

CONCLUSION

The use of micropropagation is an important tool in plant tissue culture, horticulture, andcontemporary farming. The high risk of death during the acclimation period and the need for chemicals make the process costly, nevertheless. PGPMs can be thought of as prospective biofactories since they naturally possess the ability to create PGRs. However, due to the ability of some human pathogenic strains to be persistently maintained in cultured tissues and ex vivo plants, the use of microbes warrants careful monitoring of endophytic communities, particularly for plants used as raw food. In keeping with this idea, research on how crops and other important plants react to PGPM inoculation with symbiotic and non-symbiotic organisms will aid in determining which plants are good candidates for micropropagation. In the chapter's summation, we concluded that using model plants and the microorganisms that live on them opens up a new period for the creation of tools for studying plant biology and boosting agricultural yields.

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