

## LITERATURE ANALYSIS ON PLANT DEVELOPMENTAL COORDINATION AND ITS REGULATION MECHANISMS

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### ABSTRACT

Plant development involves the results of complex interactions between genetic regulation, hormones, and environmental responses. This article aims to provide an analysis of plant development coordination and its regulatory mechanisms, to reveal how plants coordinate their growth and adapt to dynamic environments. The method used is a descriptive qualitative approach using a systematic literature review method to identify, classify, and analyze. Article searches were carried out through various scientific databases such as Google Scholar, ScienceDirect and pubmed. Plant development coordination involves complex growth and differentiation processes. Starting with germination triggered by water and enzyme activity, followed by primary growth through apical meristems that produce plant organs (roots, stems, leaves, flowers, fruits, and seeds) and secondary growth, which involves lateral meristems that cause thickening of stems and roots. In addition, genetic regulation functions as a mechanism that allows plants to grow, develop, and respond to the environment effectively. Hormones such as auxins, gibberellins, cytokinins, ethylene, and abscisic acid work together to regulate growth and stress responses. Plants can also remember previous stress through epigenetic modifications to increase their resilience to repeated stress. All of these systems allow plants to adapt and survive in changing environmental conditions.

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### Introduction

Plant development is a biological process that includes structural, functional, and physiological changes that occur gradually during the plant life cycle, from the embryo to the adult and reproductive stages. This development not only includes growth but also includes cell differentiation, and morphogenesis. Plant growth is the event of increasing plant size, which can be measured from the increase in size and height of plant organs (Khosro et al., 2024). Differentiation is a condition in which meristematic cells develop into two or more types of cells/tissues/plant organs that are qualitatively different from each other, while morphogenesis is a life process that involves the interaction between growth and differentiation by several cells that stimulate the formation of organs (Sulichantini et al., 2020).

Plant development involves the results of complex interactions between genetic regulation, hormonal regulation, and stress responses. Genetic regulation in plants regulates gene expression to control growth, development, and responses to the environment. Hormonal

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regulation involves phytohormones such as auxins, gibberellins, cytokinins, abscisic acid (ABA), and ethylene which play a role in regulating physiological processes such as cell division, flowering, ripening, and stress responses. In addition, plants respond to abiotic and biotic stress through activation of defense genes, production of protective compounds, and physiological adjustments to increase resistance to adverse environmental conditions (Li et al., 2023).

The interaction of these three regulatory mechanisms is synergistic and often specific to the type of plant and its environmental conditions. Therefore, this article aims to provide an analysis of plant development coordination and its regulatory mechanisms to reveal how plants coordinate their growth and adapt to dynamic environments.

## **Method**

This article uses a descriptive qualitative approach using a systematic literature review method to identify, classify, and analyze. This method allows for an in-depth understanding of plant developmental coordination and its regulatory mechanisms reported in the scientific literature. Data were obtained from relevant secondary literature sources, including scientific journals, textbooks, and previous review articles.

Literature search was conducted through various scientific databases, such as ScienceDirect, Google Scholar, PubMed, SpringerLink, and JSTOR. In this study, 58 relevant articles were reviewed on plant development coordination and its regulatory mechanisms. The analysis was conducted to extract data on plant development coordination including growth and development. In addition, the analysis also discusses plant regulatory mechanisms including genetic regulation, hormonal regulation, and plant responses to environmental stress.

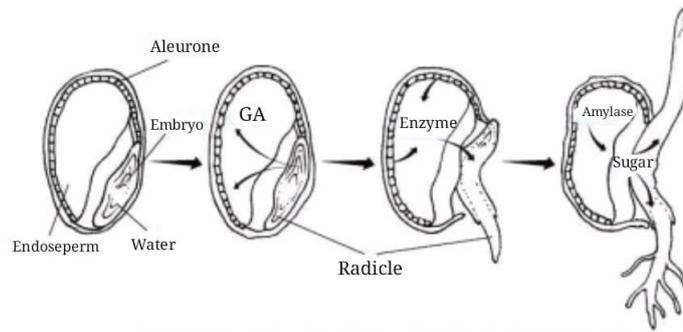
## **Results and Discussion**

### **A. Coordination of Plant Development**

Plant development coordination is a highly complex and dynamic biological process, involving interactions across levels of cellular organization to integrate multiple physiological and molecular activities. This process includes growth and development (Haffmann et al., 2021). Growth is a biological change event that occurs in all living things in the form of an increase in volume, height, and mass that is irreversible, while development is the process of differentiation and specialization of cells towards achieving the adult phase of the plant. Growth and development in plants go through 3 phases, namely: germination, growth and development (Leimena et al., 2023).

#### **1. Germination (Reproductive Phase)**

Germination is the initial phase of new individual growth. This process is greatly influenced by the availability of water in the growth medium to stimulate the activity of enzymes needed in the metabolism of germination in the tissue in the seed. The germination phase begins with imbibition which makes the seed coat soft and increases enzymatic activity. During germination, water imbibition stimulates the activity of gibberellin which is needed to activate the  $\alpha$ amylase enzyme. This enzyme then enters the food reserves and catalyzes the process of changing food reserves, starch into sugar which is then used as an energy source for cell division and growth (Fig. 1) (Junaidi & Ahmad, 2021).

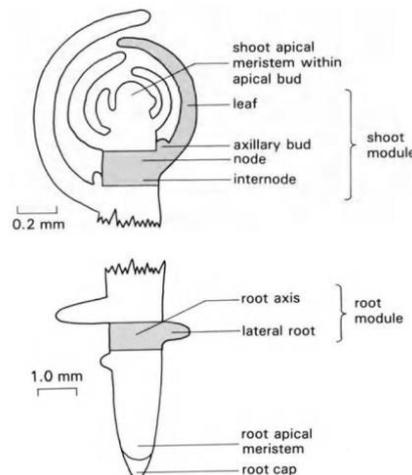


**Figure 1.** Germination Mechanism (Purnamasari, 2020).

There are two types of seed germination, namely epigeal and hypogeal germination. Epigeal germination is a type of germination in which the cotyledons are lifted above the soil surface due to the growth of the hypocotyl, such as in green beans (Wijayatno et al., 2021). Hypogeal germination occurs when the cotyledons remain underground because what extends is the epicotyl, such as in corn (Mahardika et al., 2023). Germination is influenced by internal and external factors. Internal factors are seed maturity level, seed size, and seed dormancy. External factors are water, temperature, oxygen and light (Junaidi & Ahmad, 2021).

## 2. Growth and Development

There are two types of plant growth, namely primary growth and secondary growth. Primary growth is a growth process that occurs due to the activity of the primary meristem, namely the embryonic tissue that continues to divide and is found at the tip of the root and the tip of the stem. Primary growth includes the formation of basic plant organs such as roots, stems, leaves, flowers, fruits and seeds (Irawan et al., 2023).



**Figure 2.** Modular structure of plant shoots and roots (Black & Chapman, 1990).

Plant growth (Fig. 2) consists of a modular structure of the plant shoot which includes stem segments (internodes), stem nodes (nodes), one leaf blade, and one axillary bud. Meanwhile, the root module includes root segments that support the growth of lateral roots. When the plant begins to flower, the shoot module becomes smaller and denser, with the lateral organs developing differently to form flowers. However, the basic modular pattern continues through the formation of male and female reproductive organs, followed by fertilization, which produces a zygote that develops into a new embryo. This recurrent growth originates from the apical meristem, a self-renewing tissue consisting of young, undifferentiated cells that continue

to divide. This meristem forms a new module behind the growing point. Root meristems tend to be simpler, continuing their activity without major changes, producing only one main axis from which lateral roots will emerge a few millimeters or centimeters behind. In contrast, shoots form leaves or flowers directly from the meristem, so their growth is repetitive and follows a certain cyclical pattern (Kinoshita & Alice, 2020).

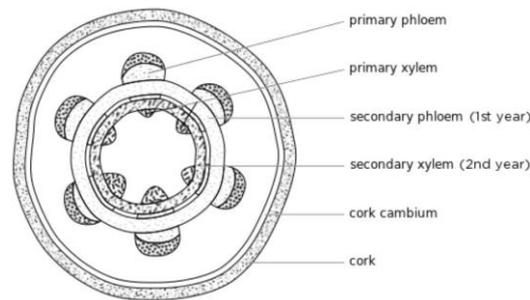
The first process in leaf growth is cell proliferation that occurs in the leaf apical meristem. The apical meristem is a meristematic tissue located at the tip of a shoot or young leaf, which contains dividing cells. At the proliferation stage, cells in this meristem begin to divide actively, producing new cells that will form leaf tissue. After cell division is complete, a number of new cells are formed around the meristem and develop into layers of leaf tissue such as epidermis, mesophyll, and vascular tissue containing xylem and phloem. At this stage, leaf cells begin to show signs of differentiation according to their function (for example, epidermal cells that will form the cuticle or stomata) (Vercruyssen et al., 2020).

After cell proliferation, the next stage is cell expansion or enlargement. At this stage, the cells that have been formed begin to grow larger and longer. This cell expansion process is very important for increasing the overall size of the leaf. Cell enlargement occurs due to the absorption of water into the cell vacuole, which causes the cell to expand (He et al., 2021). In addition, this process also involves a decrease in cell wall tension which allows the cell to grow larger. This expansion process occurs in almost all parts of the leaf, including in the mesophyll, which consists of palisade cells and spongy cells. Palisade cells function for photosynthesis because they contain many chloroplasts, while spongy cells allow gas exchange (such as CO<sub>2</sub> and O<sub>2</sub>) through the stomata found in the leaf epidermis. At this stage, although cell division no longer occurs, leaf cells continue to grow larger, causing the leaves to grow larger and develop (Kalve et al., 2020).

Flower growth marks the transition from the vegetative phase to the reproductive phase in plants. This process begins with flower induction, where the shoot apical meristem transforms into a floral meristem. Flower development involves the formation of floral organs such as petals, corollas, stamens, and pistils (Chen & Jin, 2024). After fertilization, the flower ovary develops into a fruit. This process involves cell division and expansion, as well as the accumulation of substances such as sugars and organic acids that determine fruit quality (Feng et al., 2023).

The seed growth process includes the formation and development of three main parts: the embryo, endosperm, and seed coat (testa). The embryo is formed from the zygote which undergoes cell division and differentiation to form a new plant candidate, consisting of the embryonic root (radicle), embryonic stem (hypocotyl), and cotyledon. Meanwhile, the endosperm is formed from the results of double fertilization and functions as a tissue that stores food reserves such as starch, proteins, and lipids that are important for embryo growth. Around the embryo and endosperm, a seed coat is formed from the ovule integument, which acts as a protector of the seed from physical damage and water loss (Nurdin et al., 2023).

In addition, there is growth that causes an increase in the diameter of the stem and roots of the plant, which is usually called secondary growth. This growth occurs due to the activity of lateral meristems (secondary meristems), namely vascular cambium and cork cambium (phellogen) (Fig. 3) (Strock & Jonathan, 2020).



**Figure 3.** Cross section of a dicotyledonous plant stem undergoing secondary growth (Purnamasari, 2020).

In the deepest part of the secondary tissue of woody plant stems (Fig. 3) there is primary xylem, which is a transport tissue that functions to carry water and minerals from the roots to the leaves. This primary xylem is surrounded by secondary xylem, which is formed from the activity of the vascular cambium towards the inside. Over time, the secondary xylem continues to grow and thicken, forming a strong layer of wood and producing annual rings. Towards the outside of the cambium, secondary phloem is formed, which functions to transport the results of photosynthesis from the leaves to all parts of the plant. The primary phloem, which is even further outside, will gradually be compressed, damaged, or pushed out by the growth of new secondary tissue. The outermost layer of the stem is then formed by the cork cambium (phellogen), which produces cork (phelogen) as a protective layer on the outside and phelloderm on the inside. Cork is impermeable to water and gas, so it can prevent excessive evaporation and protect the inner tissue from mechanical damage and infection. This structure reflects the secondary growth process that allows woody plant stems to thicken and survive in the long term (Cao et al., 2024).

## **B. Plant Regulatory Mechanisms**

Regulatory mechanisms in plants are a series of complex and coordinated biological systems, allowing plants to regulate growth and development processes, and respond to various external and internal stimuli. This regulation includes genetic regulation, hormonal regulation and stress response (Lucibelli et al., 2022).

### **a. Genetic Regulation**

Genetic regulation in plants is a complex process that regulates gene expression through DNA elements and their interactions with various factors, without involving changes in the DNA sequence itself. This process includes various mechanisms that allow plants to grow, develop, and respond effectively to the environment. Genetic regulation includes cis-regulatory elements, transcription factors, chromatin modifications, post-transcriptional regulation, translation processes, non-coding RNAs, and regulation at the tissue and organ levels (Natri et al., 2022).

#### **1. Cis-regulatory elements**

Cis-regulatory elements are DNA segments that do not encode proteins, but function as regulators of gene expression by interacting with transcription factors and other proteins. These elements are located near or far from the regulated gene, and play an important role in controlling when, where, and how much the gene will be expressed. The most well-known cis-regulatory element is the promoter, which is located at the beginning of the gene and provides

a place for transcription factors and RNA polymerase to initiate transcription (Meyer & Shirley, 2021).

In addition, there are also enhancers, which increase transcription by binding to certain transcription factors even though they are located far from the target gene, and silencers, which suppress gene expression by blocking or inhibiting the binding of transcription factors. Insulators function to prevent unwanted interactions between enhancers and promoters of different genes, maintaining the specificity of gene expression. In addition, there is also a Locus Control Region (LCR) which regulates gene expression in a particular genetic cluster or location, often found in genes involved in developmental processes or environmental responses (Wessinger, 2020).

## **2. Transcription Factors**

Transcription factors are proteins that play a central role in plant genetic regulation, with the main function of controlling gene expression through binding to specific DNA sequences called cis-regulatory elements, such as promoters and enhancers. These proteins can function as activators that promote gene transcription or as repressors that inhibit it. In plants, transcription factors not only determine gene expression patterns during growth and development, but also mediate responses to environmental changes, such as abiotic (drought, extreme temperatures) and biotic (pathogen infection) stresses (Zdrzałek et al., 2023).

Each transcription factor has the ability to recognize certain DNA motifs, so it will only regulate genes that have the appropriate binding motif. Once bound to DNA, transcription factors can affect chromatin structure and recruit other enzymes or protein complexes such as RNA polymerase II to initiate or stop transcription. For example, the FLC (FLOWERING LOCUS C) transcription factor in *Arabidopsis* acts as a repressor that inhibits the expression of flowering genes, while the DREB/CBF family activates cold stress response genes (Shaheen et al., 2024).

## **3. Chromatin Modification**

Chromatin modification is a chemical process that changes the complex chromatin structure of DNA and proteins (especially histones), thereby affecting the accessibility of DNA to the transcription machinery and, consequently, gene expression. This modification is an important part of epigenetic regulation, as it can activate or deactivate gene expression without changing the DNA sequence itself (Lin et al., 2024). Some of the histone modifications are as follows:

- Acetylase, namely the addition of an acetyl group (CH<sub>3</sub>CO) to the lysine residue on the histone tail by the enzyme histone acetyltransferase (HAT). This modification reduces the interaction between histones and DNA, making the chromatin structure more open (euchromatin) so that genes are more easily transcribed (Zrimec et al., 2022).
- Deacetylase, namely the removal of acetyl groups by the enzyme histone deacetylase (HDAC), causing the chromatin to become denser (heterochromatin) and suppressing gene expression (Lin et al., 2024).
- Methylation, which is the addition of methyl groups to lysine or arginine, can cause gene activation or repression, depending on the location and number of methyl groups. For example, trimethylation of H3K4 is often associated with gene activation, while H3K9 or H3K27 is associated with repression (Hirakawa & Shiniciro, 2019).
- Phosphorylation occurs in response to stress or DNA repair, which plays a role in chromatin opening and transcription regulation (Zrimec et al., 2022).

- Ubiquitination and sumoylation modifications affect histone stability and structure, and can signal for transcriptional activity or degradation (Hirakawa & Shiniciro, 2019).

#### **4. Post-transcriptional regulation**

Post-transcriptional regulation is the process of controlling gene expression that occurs after RNA is synthesized from DNA, but before it is translated into protein. This stage is important to ensure that only the right RNA will be translated according to the cell's needs. One form of post-transcriptional regulation is alternative splicing, which is the process of rearranging exons and introns in mRNA, so that one gene can produce several types of proteins (Li et al., 2023).

In addition, modification of the ends of mRNA also plays an important role, such as the addition of a 5' cap and a poly-A tail which helps increase mRNA stability and translation efficiency. The process of mRNA transport from the nucleus to the cytoplasm is also controlled to determine the time and location of translation. The stability of mRNA is also an important aspect, because the age of mRNA in the cytoplasm affects the amount of protein produced. Finally, non-coding RNAs such as microRNA (miRNA) and small interfering RNA (siRNA) can inhibit translation or cause mRNA degradation, thereby increasing the level of control in genetic regulation. Thus, post-transcriptional regulation provides flexibility and speed in adjusting gene expression to internal and external plant conditions (Gupta, 2025).

#### **5. Translation Process**

This translation process occurs after mRNA is produced through transcription, and its purpose is to convert the genetic information contained in the mRNA base sequence into an amino acid sequence that forms a protein. Basically, translation is carried out by ribosomes, which scan mRNA and assemble amino acids into polypeptide chains according to the codon sequence on the mRNA (Yadav et al., 2024).

The translation process consists of three main stages, namely initiation, elongation, and termination. At the initiation stage of translation in plants, ribosomes first recognize mRNA and begin translating genetic information into protein. The process begins with the binding of ribosomes to the 5' end of mRNA. Initiation factors, such as eIFs (eukaryotic initiation factors), are involved in facilitating ribosome binding and searching for the initiation codon (AUG), which indicates the start of protein synthesis. tRNA carrying the amino acid methionine pairs with this initiation codon at the P site of the ribosome. After tRNA binds to the initiation codon, the large subunit of the ribosome joins the small subunit, allowing translation to begin (Mansur et al., 2022).

In the elongation stage, the ribosome moves along the mRNA and adds amino acids to the polypeptide chain according to the mRNA codon sequence. Each tRNA carrying an amino acid will enter the A site of the ribosome and match the mRNA codon with the tRNA anticodon. After a peptide bond is formed between the amino acid carried by the tRNA and the polypeptide chain, the ribosome moves one step along the mRNA (translocation). This process repeats continuously until the polypeptide grows and forms according to the codon sequence on the mRNA (Muhammad et al., 2024).

Termination occurs when the ribosome reaches a stop codon on the mRNA (UAA, UAG, or UGA). This stop codon does not carry an amino acid, but activates a termination factor (such as eRF in plants) which helps release the polypeptide that has been formed from the tRNA and ribosome. After the polypeptide chain is released, the ribosome detaches from the mRNA, and the mRNA can be reused or destroyed, while the ribosome is ready to begin translation on another mRNA (Ali et al., 2023).

## **6. Non-coding RNA**

Non-coding RNA in plants plays an important role in regulating gene expression involved in various biological processes such as growth, development, and stress response. The types of non-coding RNA involved include microRNA (miRNA), small interfering RNA (siRNA), and long non-coding RNA (lncRNA). MiRNA, which is a short RNA molecule, regulates gene expression by binding to target mRNA, inhibiting translation, or inducing mRNA degradation. In plants, miRNA plays a role in processes such as developmental phase transitions, flowering, and responses to stress conditions such as drought or salinity (Manghwar et al., 2024).

In addition, siRNA involved in RNA interference (RNAi), functions to regulate gene expression by inducing the degradation of specific mRNAs, plays a role in defense against viruses and genetic regulation related to plant development. SiRNA also regulates gene expression through epigenetic mechanisms, maintaining the stability of the plant genome. Then, LncRNA in plants helps regulate gene expression patterns during development and response to environmental stress, by modifying chromatin structure or interacting with transcription factors (Radoeva et al., 2019).

## **7. Regulation at the Tissue and Organ Level**

Regulation at the tissue and organ level in genetic regulation refers to how gene expression is specifically controlled in different types of cells and tissues in an organism's body, including plants. Although every cell in an organism's body contains the same genetic information, gene expression can vary between tissues and organs to support their specific functions. This allows organisms to adjust their responses to different physiological and environmental needs, as well as to regulate growth and development (Ndudzo et al., 2024).

At the tissue level, genetic regulation is essential to ensure that cells in the same tissue express the genes required for specific plant functions. For example, leaf cells in plants express genes involved in photosynthesis, while root cells express genes related to water and nutrient uptake. This regulation often involves transcription factors that are specific to a particular tissue type. These factors can influence gene transcription and regulate gene expression patterns that are required for the characteristics and functions of these tissues (Ali et al., 2023).

At the organ level, genetic regulation regulates the development of plant organs, such as roots, stems, leaves, and flowers. For example, plant hormones such as auxins play a critical role in regulating root and stem development, by regulating the expression of genes that control cell division and differentiation. In addition, homeotic genes also play a role in determining organ development patterns, such as leaf placement or flower formation. For example, in flowers, the expression of genes that control the formation of petals, stamens, and pistils will be regulated very specifically to ensure that the flower organs are formed according to their reproductive function (Emeliya et al., 2024).

### **b. Hormonal**

The mechanism of hormone regulation in plants is a complex system involving the interaction of various hormones to regulate growth, development, and stress responses. Plant hormones function as chemical signals that coordinate various physiological processes in plants, from cell elongation, root formation, fruit ripening, to responses to environmental changes. There are five main hormones that play a role in this regulatory mechanism, namely auxin, gibberellin, cytokinin, ethylene, and abscisic acid (ABA) (Rankerberg et al., 2021).

## **1. Auxin**

Auxin is synthesized mainly in the apical growing point (meristem) of plants, especially at the tips of roots and stems that are developing rapidly. In addition, auxin is also produced in young leaves, flowers, and developing fruits. The auxin synthesis process begins with the compound tryptophan, an amino acid used as a precursor to form IAA (Liu et al., 2022).

The main function of auxin is to stimulate cell elongation, which leads to the growth of stem and root elongation. Auxin also plays an important role in the formation of lateral roots, especially when its concentration is high in the root area. In addition, auxin functions in regulating gravitropism and phototropism, namely plant responses to gravity and light. This hormone regulates the process of cell elongation on the side of the stem that is further from the light source (in phototropism) and on the lower side of the root (in gravitropism). Auxin also plays a role in controlling the formation of lateral shoots, where high concentrations of auxin can inhibit the formation of lateral shoots, while lower concentrations can stimulate these shoots (Saez et al., 2021).

In addition, auxin does not work alone, but interacts with other hormones in regulating various physiological processes in plants. One of the main interactions is with cytokinins, where auxin and cytokinin work together to control root and shoot formation. Auxin tends to stimulate root formation, while cytokinins stimulate shoot formation. This interaction is very important in the formation of healthy lateral roots and shoots (Chen et al., 2023). Auxin also interacts with gibberellins in regulating cell growth, where gibberellins support cell elongation that has been triggered by auxin. In addition, auxin also interacts with abscisic acid (ABA) in regulating dormancy and plant responses to stress, where auxin can reduce the effects of ABA-induced dormancy (Rutten & Kirsten, 2021).

## **2. Gibberellin**

Gibberellin is synthesized in various parts of the plant, especially in germinating seeds, roots, and young leaves. The process of gibberellin synthesis involves a complex metabolic pathway, starting with the basic compound mevalonic acid and converted into the compound geranylgeranyl pyrophosphate (GGPP), which is a precursor for gibberellin. Furthermore, GGPP is metabolized through a series of enzymes into the active form of gibberellin (Gao et al., 2023).

One of the main functions of gibberellin is to overcome seed dormancy and stimulate germination by activating enzymes that break down food reserves in the endosperm, so that the embryo can grow. Gibberellin also promotes internodal elongation, so that plants grow taller, and stimulates flower and fruit development, especially in plants that require hormonal treatment to flower or bear fruit without fertilization (parthenocarpy) (Hongfeng et al., 2020).

In addition to its broad functions, gibberellin also interacts closely with other hormones in regulating plant growth synergistically and antagonistically. With auxin, gibberellin works together to increase cell elongation and support the growth of vegetative and generative organs. Interaction with cytokinins occurs in cell division, where gibberellins help enlarge the size of cells that have been divided by the influence of cytokinins. On the other hand, gibberellins have an antagonistic relationship with abscisic acid (ABA), especially in the process of germination and dormancy, gibberellins eliminate dormancy maintained by ABA (Deng et al., 2024).

## **3. Cytokinins**

Cytokinins are synthesized in the roots, especially in the part called the calyptra (the part of the root that stimulates root growth). In addition, cytokinins are also synthesized in

young leaves, seeds, and developing fruits. The main function of cytokinins is to stimulate cell division or cytokinesis, which is important for plant vegetative growth (Ran et al., 2023).

This hormone also plays a role in the formation of new shoots and branches, regulates the formation of lateral roots, and influences morphogenesis in the formation of new organs such as leaves and flowers. In addition, cytokinins have the ability to delay the aging of leaves and other organs, by increasing chlorophyll synthesis and extending the period of leaf photosynthetic activity. Cytokinins also interact with other hormones, such as auxins and gibberellins, to regulate root and shoot formation and optimize overall plant growth (Feng et al., 2023).

#### **4. Ethylene**

Ethylene is synthesized in almost all plant tissues, but its production is most active in organs undergoing intensive physiological changes, such as ripening, aging, or stress. The main location of ethylene synthesis is the root meristematic tissue. Especially in the elongation and calyptra areas that often experience environmental stress (Olaetxea et al., 2021).

The hormone ethylene plays an important role in various physiological processes of plants, especially in fruit ripening, organ aging, leaf fall (abscission), and responses to environmental stress. Ethylene acts as the main trigger in the ripening process of climacteric fruits such as bananas, tomatoes, and apples, by activating enzymes that break down cell walls, convert starch into sugar, and cause changes in color and aroma (Suzuki et al., 2023).

Ethylene also works in a complex with other hormones. For example, auxin can stimulate ethylene production, and the interaction of the two is important in the process of leaf abscission and the formation of lateral and adventitious roots. In contrast, gibberellins and cytokinins are often antagonistic to ethylene in regulating vegetative growth, such as stem elongation and cell division. Ethylene also shows cooperation with abscisic acid (ABA) in regulating responses to environmental stress (Qian et al., 2023).

#### **5. Abscisic acid (ABA)**

Abscisic acid (ABA) is synthesized in various plant tissues, with the main site of synthesis depending on physiological and environmental conditions. In general, ABA is produced in large quantities in leaf tissues that experience stress, especially drought stress, where leaf mesophyll cells become the main production center. In addition, ABA is also actively synthesized in the roots, especially at the root tips that experience water stress, and then transported through the xylem to the leaves to induce stomatal closure. Under normal conditions, ABA is also produced in developing fruits, dormant seeds, and embryonic tissues (Fatima et al., 2023).

Abscisic acid interacts in a complex manner with other hormones, such as ethylene, which often work together in response to environmental stress. For example, under water stress, ABA can increase ethylene production which then plays a role in regulating plant organ senescence and abscission. In addition, ABA functions as an antagonist to gibberellin, which stimulates growth and germination. Under conditions of seed dormancy, ABA inhibits gibberellin activity and slows down the germination process until environmental conditions are more supportive (Sadura & Anna, 2024).

#### **c. Stress Response**

Stress response in plants is a complex biological regulatory process involving multilevel interactions between cellular components, tissues, and signaling molecules to maintain homeostasis and enhance survival under environmental stress. As sessile organisms, plants rely

heavily on efficient internal perception and response systems to various types of stress, both abiotic such as drought, salinity, extreme temperatures, and biotic such as pathogen infection and herbivore attacks (Wani, 2023).

This process begins with the perception of stress through specific receptors, both located on the plasma membrane such as pattern recognition receptors (PRRs) and those located inside the cell, such as osmosensors or temperature receptors. In biotic stress, foreign molecules such as bacterial flagellin are recognized by PRRs such as FLS2, triggering an initial immune response in the form of PAMP-triggered immunity (PTI). Meanwhile, in abiotic stress, changes in osmotic pressure can be responded to by calcium channels such as OSCA, which trigger a surge of  $\text{Ca}^{2+}$  ions inside the cell (Fang et al., 2021).

Signal transduction is the next stage after stress is recognized. The main signals involved include  $\text{Ca}^{2+}$  ions as secondary signals, reactive oxygen species (ROS) as redox signals, and plant hormones such as abscisic acid (ABA) and ethylene (ET). ABA, as a key hormone in the response to drought and salinity, will activate a signaling pathway involving the interaction between PYR/PYL/RCAR receptors and SnRK2 protein kinases, by inactivating PP2C protein phosphatase as the main inhibitor of the pathway. These signals then integrate through kinase cascades and activation of transcription factors such as DREB, WRKY, MYB, and bZIP that regulate the expression of stress-specific target genes. These genes include protective proteins such as LEA and HSP that maintain the stability of proteins and cell membranes, and antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and peroxidase (POD) that protect cells from the accumulation of damaging ROS (Jahan et al., 2023).

At the physiological level, the stress response causes significant changes in plant structure and function. One example is the closure of stomata by the influence of ABA, which aims to reduce water loss during dry conditions. In addition, plants will accumulate osmoprotectant compounds such as proline, glycine betaine, and trehalose to maintain the osmotic balance of cells. At the same time, there are adjustments in secondary metabolism, such as increased production of phenolic compounds, flavonoids, and terpenoids, which function as additional protective agents against oxidative and biotic stress. This response is flexible and depends on the plant species, the duration of stress, and the type of stress experienced (Kaleh et al., 2024).

Some plants show the ability to remember previous stress experiences through a mechanism known as stress memory. This mechanism is mediated by epigenetic modifications such as DNA methylation, histone modifications (eg H3K4me3 for activation and H3K27me3 for repression), and regulation by non-coding RNAs such as miRNA and siRNA. These epigenetic changes can be mitotic and even transgenerative, allowing for a faster and more efficient response to future exposure to the same stress. This phenomenon is known as priming, where plants that have experienced previous stress become more responsive and tolerant to repeated stress. The concept of stress memory opens up great opportunities in plant breeding and the development of epigenetic-based adaptive agricultural technologies (Sharma et al., 2023).

## **Conclusion**

Coordination of plant development involves complex processes of growth and differentiation. It begins with germination, which is triggered by water and enzyme activity, followed by primary growth through apical meristems that produce plant organs (roots, stems, leaves, flowers, fruits, and seeds) and secondary growth, which involves lateral meristems that cause thickening of stems and roots. In addition, plants regulate their growth through integrated genetic, hormonal, and stress-response regulation. Genetic regulation serves as a mechanism

that allows plants to grow, develop, and respond effectively to the environment. Hormones such as auxins, gibberellins, cytokinins, ethylene, and abscisic acid work together to regulate growth and stress responses. Plants can also remember previous stress through epigenetic modifications to increase their resistance to repeated stress. All of these systems allow plants to adapt and survive in changing environmental conditions.

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