People's Democratic Republic of Algeria
Ministry of Higher Education and Scientific Research
University of Echahid Hamma Lakhdar - El Oued -

Faculty of Nature and Life Sciences
Department of Biology

Field: Nature and Life Sciences
Division: Biological Sciences

Course Title :

Cell Biology and Plant Development

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Intended for Students:

1st year of Master's Level

Specialty: Biodiversity and Plant Physiology

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Summary

Introduction

This comprehensive course, titled " Cell Biology and Plant Development ", provides an in-depth exploration of the genotypic and phenotypic aspects of plant development. Through a combination of scientific, academic, theoretical, and applied information, the course delves into the molecular mechanisms and genetic regulation underlying various stages of plant growth and reproduction.

The course is designed for students in the first year of a master's degree program in the specialty of Biodiversity and Plant Physiology. It covers a wide range of topics, from the regulation of gene expression during development to the intricate processes of gametophyte formation, fertilization, and seed maturation. Additionally, the course examines the role of programmed cell death in plant morphogenesis, as well as the mechanisms governing vegetative development, flowering, and self-incompatibility.

Throughout the course, relevant figures and explanatory documents are provided to support the key information presented. At the end of each section, a list of references is included to allow students to delve deeper into the subject matter.

This course is expected to provide students with a comprehensive understanding of the fundamental principles and mechanisms underlying plant development, from the genotypic to the phenotypic level. The content and resources presented will equip students with the necessary knowledge and tools to further explore this dynamic and ever-evolving field of plant biology.

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Part I.

Genotypic Aspects of Plant Development

Course 1.

Mutants and their role in understanding development

The use of mutants has been a cornerstone in deciphering the intricate genetic mechanisms underlying plant development. By identifying and characterizing developmental mutants, researchers have gained invaluable insights into the functions of specific genes and the regulatory networks that govern various developmental processes in plants.

1.1. Identification and characterization of developmental mutants

Plant mutants exhibiting abnormal developmental phenotypes can be generated through various mutagenesis techniques:

1. **Chemical mutagenesis**: Ethyl methanesulfonate (EMS) is commonly used to induce point mutations in plant genomes. It typically causes G/C to A/T transitions, leading to a wide range of potential effects on gene function.
2. **Radiation-induced mutagenesis**: X-rays or gamma rays can cause chromosomal breaks and rearrangements, often resulting in large-scale mutations.
3. **T-DNA insertional mutagenesis**: This technique involves the insertion of a known DNA sequence (T-DNA) into the plant genome, often disrupting gene function at the insertion site. It has the advantage of facilitating easy identification of the mutated gene.
4. **CRISPR/Cas9 genome editing**: While not a traditional mutagenesis technique, CRISPR/Cas9 allows for targeted gene modifications and has become increasingly important in creating specific mutants for developmental studies.

Once mutants are generated, they undergo rigorous screening and phenotypic characterization. Advanced imaging techniques play a crucial role in this process:

- **Confocal laser scanning microscopy (CLSM)**: Allows for high-resolution, three-dimensional imaging of plant tissues and cellular structures. It's particularly useful for visualizing fluorescently tagged proteins and studying their localization during development [9].
- **Scanning electron microscopy (SEM)**: Provides detailed surface morphology of plant structures, helping to identify subtle changes in organ shape, cell arrangement, and epidermal features that might be indicative of developmental abnormalities.
- **Light sheet fluorescence microscopy (LSFM)**: Enables long-term, live imaging of developing plant tissues with minimal phototoxicity, allowing researchers to track developmental processes in real-time.

1.2. Genetic analysis of mutant phenotypes to elucidate gene function

Once developmental mutants are identified, a series of genetic and molecular analyses are conducted to determine the underlying genetic basis of the observed phenotypes:

1. **Genetic mapping**: This involves crossing the mutant with a wild-type plant of a different ecotype and analyzing the segregation of the mutant phenotype in the F2 generation. Techniques like bulk segregant analysis (BSA) and next-generation sequencing-based mapping have greatly accelerated this process.
2. **Gene cloning**: Once a mutation is mapped to a specific genomic region, the corresponding gene is isolated and cloned. This often involves complementation tests, where the wild-type gene is introduced into the mutant to rescue the phenotype.
3. **Expression analysis**: The spatial and temporal expression patterns of the identified genes are studied using techniques such as:
    - In situ hybridization
    - Promoter-reporter fusions (e.g., GUS staining)
    - Quantitative RT-PCR
4. **Protein localization and interaction studies**: These involve:
    - Generating transgenic plants expressing fluorescently tagged proteins
    - Yeast two-hybrid assays or co-immunoprecipitation to identify protein-protein interactions
    - ChIP-seq to identify DNA-binding sites of transcription factors
5. **Functional characterization**: This may include:
    - Overexpression studies
    - RNAi-mediated knockdown

  - CRISPR/Cas9-mediated knockout
  - Biochemical assays to determine protein function

Key findings from mutant analysis

The analysis of developmental mutants has led to the identification of numerous key regulatory genes and pathways:

1. **Homeotic genes**: MADS-box genes like the ABCE model genes in flower development (e.g., APETALA1, APETALA3, PISTILLATA, AGAMOUS).
2. **Transcription factors**:
   - LEAFY (LFY) in floral meristem identity
   - SHOOT MERISTEMLESS (STM) in shoot apical meristem maintenance
   - MONOPTEROS (MP) in embryonic axis formation
3. **Hormone signaling components**:
   - PINFORMED (PIN) family in auxin transport
   - DELLA proteins in gibberellin signaling
4. **Cell cycle regulators**:
   - CYCLIN-DEPENDENT KINASES (CDKs) and CYCLINS in cell division control
5. **Epigenetic regulators**:
   - CURLY LEAF (CLF) in maintaining gene repression during development

These findings have significantly advanced our understanding of the genotypic control of plant development at the molecular level, revealing complex gene regulatory networks and signaling pathways that orchestrate developmental processes.

1.3. Physiological implications of developmental mutants:

The study of developmental mutants has also provided insights into the physiological aspects of plant development:

1. **Hormone biosynthesis and signaling**: Mutants defective in hormone pathways have revealed the critical roles of plant hormones in various developmental processes. For example, auxin mutants like pin1 have demonstrated the importance of polar auxin transport in organ initiation and phyllotaxis.

2. **Cell wall modifications**: Mutants in cell wall biosynthesis genes, such as CESA (cellulose synthase) mutants, have highlighted the importance of cell wall composition and modification in plant growth and development.
3. **Photomorphogenesis**: Analysis of mutants like hy5 (long hypocotyl 5) has elucidated the molecular mechanisms underlying light-regulated development.
4. **Stress responses**: Some developmental mutants show altered responses to environmental stresses, revealing connections between developmental pathways and stress adaptation mechanisms.

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Course 2.

Genes with Varying Expression During Plant Development

A fundamental aspect of plant development is the precise temporal and spatial regulation of gene expression. As plants progress through different stages of their life cycle, various genes are selectively expressed or repressed to orchestrate the complex processes involved in growth, organogenesis, and reproduction. This dynamic regulation of gene expression allows plants to respond to both endogenous developmental signals and environmental cues.

2.1. Transcriptional Regulation of Gene Expression

The expression of genes in plants is primarily controlled at the transcriptional level. This involves a complex interplay of cis-regulatory elements and trans-acting factors.

2.1.1 Cis-regulatory elements

These are DNA sequences located in the promoter regions or enhancers of genes that serve as binding sites for transcription factors. They include:

- Core promoter elements (e.g., TATA box, Initiator element)
- Proximal promoter elements
- Distal enhancers or silencers

2.1.2 Trans-acting factors

These are proteins that bind to cis-regulatory elements to modulate gene expression. Key examples include:

2.1.2.1 MADS-box transcription factors

These play crucial roles in various aspects of plant development, particularly in floral organ specification. The ABCDE model of flower development involves several MADS-box genes:

- A-class: APETALA1 (AP1)
- B-class: APETALA3 (AP3) and PISTILLATA (PI)
- C-class: AGAMOUS (AG)

- D-class: SEEDSTICK (STK)
- E-class: SEPALLATA (SEP) genes

These factors work combinatorially to specify floral organ identity.

2.1.2.2 Homeodomain proteins

- KNOX family proteins (e.g., SHOOT MERISTEMLESS, BREVIPEDICELLUS) are involved in shoot apical meristem maintenance and leaf development.
- BELL family proteins interact with KNOX proteins to regulate various developmental processes.

2.1.2.3 bZIP transcription factors

These are involved in various processes including seed maturation, flower development, and stress responses. For example, ABI5 (ABA INSENSITIVE 5) is crucial for ABA-mediated regulation of seed maturation and germination.

2.1.2.4 MYB transcription factors

These regulate diverse processes including secondary metabolism, cell fate, and development. For instance, WEREWOLF (WER) is involved in root hair patterning.

2.1.3 Chromatin remodeling

Chromatin structure plays a significant role in transcriptional regulation. ATP-dependent chromatin remodeling complexes, such as SWI/SNF and CHD, can alter nucleosome positioning to facilitate or inhibit transcription factor binding.

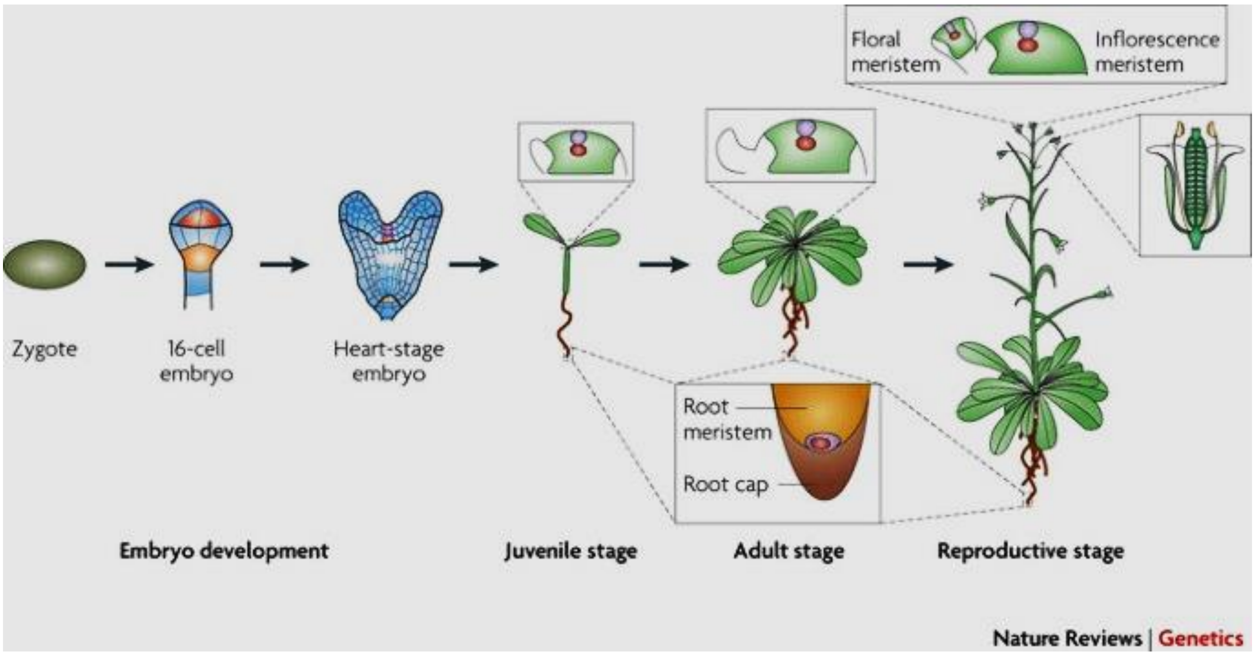

Figure 1. Transcriptional regulation of gene expression in plants (Kaufmann et al., 2010).

2.2. Post-transcriptional Regulation of Gene Expression

In addition to transcriptional control, plants employ various post-transcriptional mechanisms to modulate gene expression:

2.2.1 RNA processing

2.2.1.1 Alternative splicing

This process generates multiple mRNA isoforms from a single gene, increasing protein diversity. In Arabidopsis, over 60% of intron-containing genes undergo alternative splicing. Key regulators include:

- Serine/arginine-rich (SR) proteins
- Heterogeneous nuclear ribonucleoproteins (hnRNPs)

For example, the SR protein SR45 regulates alternative splicing of several developmental genes, including those involved in flowering time control.

2.2.1.2 Alternative polyadenylation

This affects mRNA stability, localization, and translation efficiency. For instance, FCA, a gene involved in flowering time control, undergoes alternative polyadenylation, which is crucial for its function.

2.2.2 RNA stability and degradation

2.2.2.1 microRNAs (miRNAs)

These small non-coding RNAs regulate gene expression by promoting mRNA degradation or translational repression. Examples include:

- miR156, which targets SPL transcription factors to regulate developmental transitions
- miR172, which regulates AP2-like transcription factors involved in flowering and floral organ identity

2.2.2.2 Small interfering RNAs (siRNAs)

These are involved in transcriptional and post-transcriptional gene silencing. For example, trans-acting siRNAs (ta-siRNAs) derived from the TAS3 locus regulate leaf patterning by targeting AUXIN RESPONSE FACTOR genes.

2.2.2.3 RNA-binding proteins

These proteins can stabilize or destabilize mRNAs. For instance, the PUMILIO (PUM) proteins bind to specific sequences in target mRNAs, often promoting their degradation. PUM proteins have been implicated in various developmental processes, including stem cell maintenance and leaf development.

2.2.3 mRNA localization

The subcellular localization of mRNAs can influence their translation and function. In plants, this is particularly important in large cells like those in the early embryo. For example, the WUSCHEL (WUS) mRNA, crucial for stem cell maintenance, is tightly localized within the shoot apical meristem.

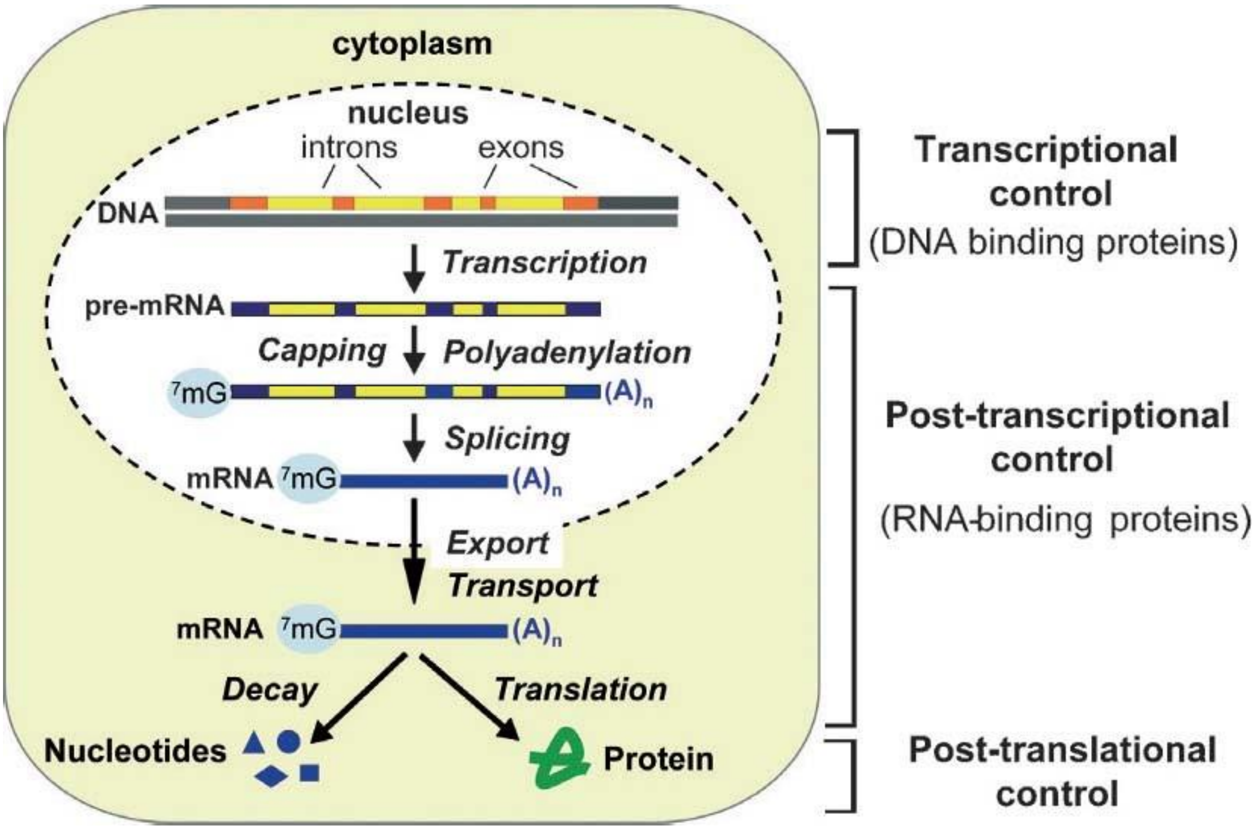

Figure 2. Post-transcriptional regulation of gene expression in plants (Halbeisen et al., 2008).

2.3. Epigenetic Regulation of Gene Expression

Epigenetic mechanisms play a crucial role in regulating gene expression during plant development:

2.3.1 DNA methylation

In plants, DNA can be methylated at cytosine residues in CG, CHG, and CHH contexts (where H is A, T, or C). DNA methylation is generally associated with gene silencing. Key players include:

- DNA METHYLTRANSFERASE 1 (MET1): maintains CG methylation
- CHROMOMETHYLASE 3 (CMT3): maintains CHG methylation
- DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2): involved in de novo methylation in all contexts

DNA methylation patterns change during development, influencing processes such as embryogenesis, flowering, and fruit ripening.

2.3.2 Histone modifications

Various post-translational modifications of histone tails can influence gene expression:

- H3K4 trimethylation is associated with active transcription
- H3K27 trimethylation, deposited by Polycomb Repressive Complex 2 (PRC2), is associated with gene silencing

For example, the FERTILIZATION INDEPENDENT ENDOSPERM (FIE) protein, a component of PRC2, is crucial for maintaining H3K27 trimethylation and repressing seed development genes in vegetative tissues.

2.3.3 Chromatin remodeling

ATP-dependent chromatin remodeling complexes can alter nucleosome positioning, affecting gene accessibility. For instance, the SWI/SNF chromatin remodeling ATPase SPLAYED (SYD) is required for proper expression of homeotic genes during flower development.

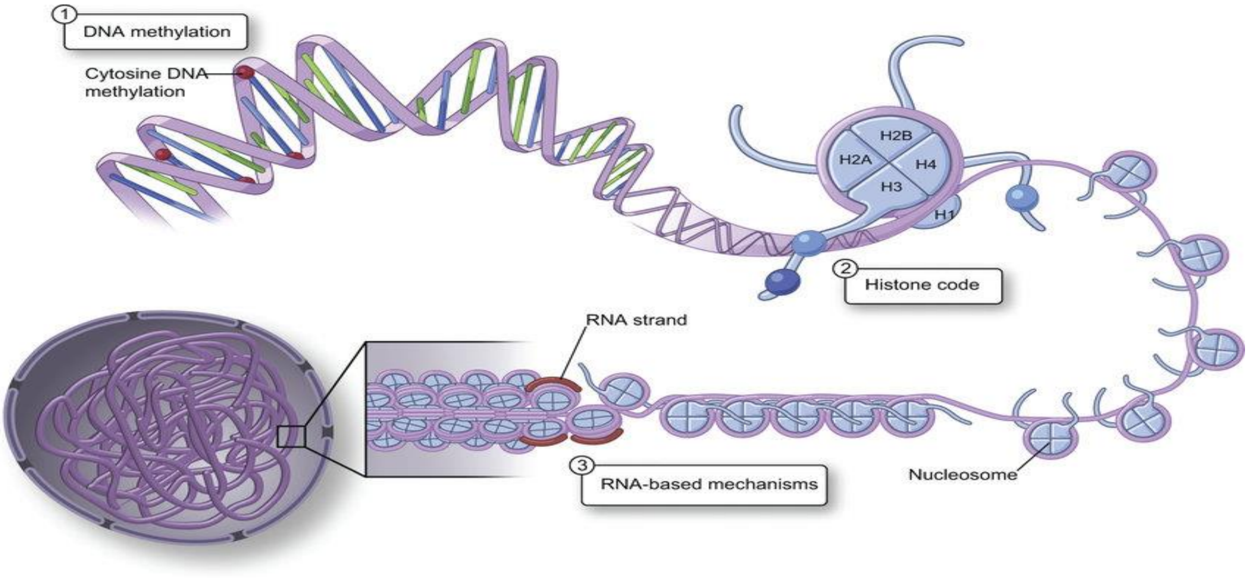

Figure 3. Three fundamental mechanisms of epigenetic regulation of gene expression in plants (Yan and Marsden, 2015). Epigenetic mechanisms of gene expression are subserved by three distinct, yet highly interrelated, mechanisms. 1) DNA methylation refers to the addition of a methyl group to the 5-position of cytosine in the context of CpG dinucleotides to define the "fifth base of DNA." 2) The fundamental repeating unit of chromatin is the nucleosome comprised of an octamer of core histone proteins. Posttranslational modifications of the amino-terminal tails of histone proteins (light and dark blue balls) and the density of these proteins per unit length of DNA, can

importantly affect chromatin structure and constitute a putative "histone code." 3) RNA-based mechanisms have also recently been shown to impact on the higher-order structure of chromatin.

2.4. Integration of Regulatory Mechanisms

These various levels of regulation do not operate in isolation but are integrated to fine-tune gene expression. For example:

- Transcription factors can recruit chromatin remodeling complexes to their target genes
- miRNAs can affect the expression of transcription factors and epigenetic regulators
- Epigenetic marks can influence alternative splicing patterns

This multi-layered regulation allows for precise control of gene expression in response to developmental and environmental cues, enabling the complex and dynamic processes of plant development.

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Course 3.

Regulatory Genes Controlling Plant Development

Plants employ a sophisticated network of regulatory genes to orchestrate the various stages of their development, from embryogenesis to flowering and senescence. This intricate genetic control system allows plants to respond to both endogenous signals and environmental cues, ensuring proper growth and development. Two crucial classes of regulatory genes involved in this process are homeotic genes and transcription factors.

3.1. Homeotic Genes and Their Role in Patterning

Homeotic genes, often referred to as "master regulators," play a pivotal role in establishing the basic body plan and patterning of plant organs. These genes are characterized by the presence of a highly conserved DNA-binding domain called the homeodomain, which enables them to regulate the expression of downstream target genes.

3.1.1 MADS-box Family

The MADS-box family is one of the best-studied examples of homeotic genes in plants. These genes are crucial for specifying the identity of floral organs and other developmental processes.

3.1.1.1 ABCE Model of Flower Development

The ABCE model explains how MADS-box genes interact to specify floral organ identity:

- A-function genes (e.g., APETALA1, AP1): Specify sepals
- A + B-function genes (e.g., APETALA3, AP3; PISTILLATA, PI): Specify petals
- B + C-function genes (e.g., AGAMOUS, AG): Specify stamens
- C-function genes (e.g., AGAMOUS, AG): Specify carpels
- E-function genes (e.g., SEPALLATA1-4, SEP1-4): Act redundantly to specify all floral organs

Mutations in these genes can lead to homeotic transformations, where one organ type develops in place of another. For example, in ap2 mutants (A-function), sepals are transformed into carpel-like structures, and petals into stamen-like structures.

3.1.1.2 MADS-box Genes in Other Developmental Processes

MADS-box genes are not limited to flower development. They also play roles in:

- Fruit development (e.g., FRUITFULL, FUL)
- Seed development (e.g., AGAMOUS-LIKE61, AGL61)
- Root development (e.g., AGL17, AGL21)

3.1.2 KNOX and BELL Families

These homeodomain-containing proteins are crucial for shoot apical meristem (SAM) maintenance and leaf development.

3.1.2.1 KNOX Genes

- SHOOT MERISTEMLESS (STM): Required for SAM formation and maintenance
- BREVIPEDICELLUS (BP): Involved in internode patterning and leaf shape determination
- KNAT1/BP: Regulates lignin biosynthesis in stems

KNOX proteins generally promote meristematic identity and repress differentiation.

3.1.2.2 BELL Genes

BELL proteins form heterodimers with KNOX proteins, enhancing their DNA-binding specificity and regulating their activity. Examples include:

- PENNYWISE (PNY): Interacts with STM to maintain the SAM
- BELLRINGER (BLR): Involved in inflorescence architecture and fruit patterning

3.1.3 Other Important Homeotic Gene Families

3.1.3.1 HD-ZIP III Family

These genes play crucial roles in establishing adaxial-abaxial polarity in lateral organs and vascular development. Key members include:

- PHABULOSA (PHB)
- PHAVOLUTA (PHV)
- REVOLUTA (REV)

Mutations in these genes can lead to radially symmetrical leaves and altered vascular patterns.

3.1.3.2 YABBY Family

YABBY genes promote abaxial cell fate in lateral organs. Examples include:

- FILAMENTOUS FLOWER (FIL)
- YABBY3 (YAB3)

These genes are crucial for leaf and floral organ development.

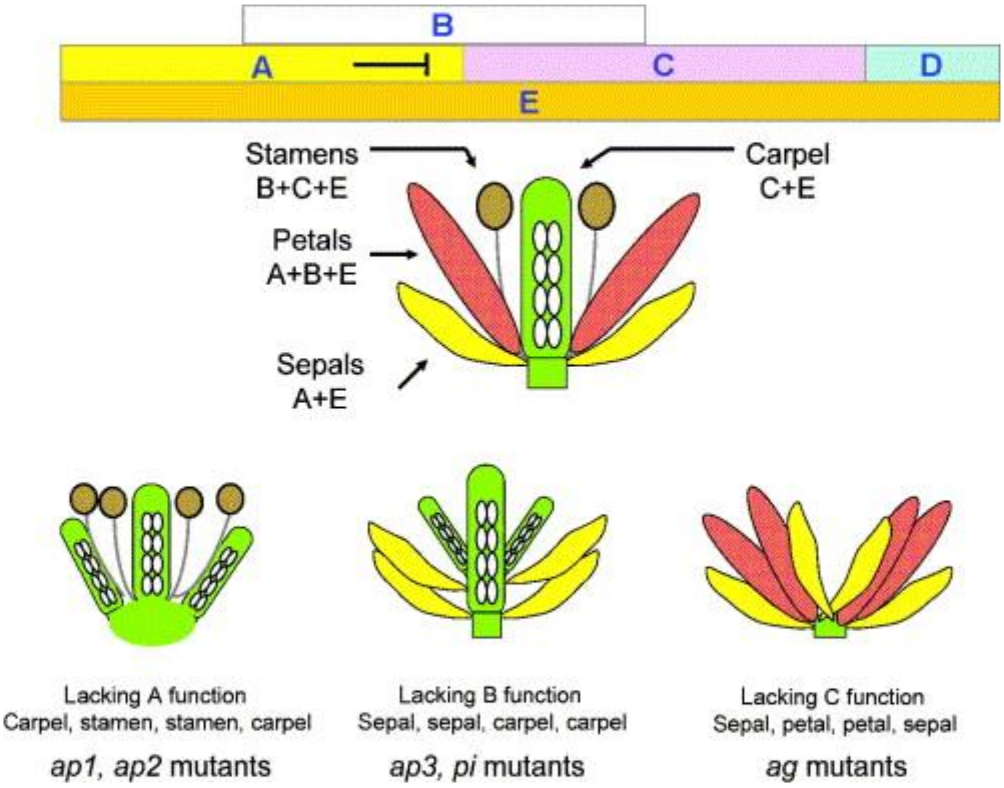

Figure 1. Homeotic genes and their role in patterning plant organs. Example: Beyond the ABC-Model: Regulation of Floral Homeotic Genes (Zahn et al., 2006).

3.2. Transcription Factors Involved in Developmental Transitions

In addition to homeotic genes, plants rely on a diverse array of transcription factors to regulate the timing and progression of developmental processes. These transcription factors respond to various endogenous and environmental cues to activate or repress the expression of genes involved in specific developmental transitions.

3.2.1 Floral Transition Regulators

3.2.1.1 LEAFY (LFY)

LFY is a key regulator of the transition from vegetative to reproductive growth in Arabidopsis:

- Directly activates floral homeotic genes like AP1 and AG
- Integrates signals from multiple flowering pathways
- Mutations in LFY result in partial conversion of flowers to shoot-like structures

3.2.1.2 APETALA1 (AP1)

While also a MADS-box gene, AP1 acts as a crucial transcription factor in floral meristem identity:

- Specifies floral meristem identity
- Activates genes involved in flower development
- Represses genes associated with inflorescence meristem identity

3.2.1.3 FLOWERING LOCUS T (FT)

FT is a key component of the photoperiod flowering pathway:

- Produced in leaves in response to long days
- Moves through the phloem to the shoot apex
- Interacts with FD to activate floral meristem identity genes like AP1

3.2.2 DOF (DNA-binding with One Finger) Family

DOF transcription factors regulate various aspects of plant growth and development:

- CYCLING DOF FACTOR 1 (CDF1): Represses CONSTANS to regulate flowering time
- DOF AFFECTING GERMINATION 1 (DAG1): Involved in seed germination
- OBP1: Regulates cell cycle progression

3.2.3 GRAS Family

GRAS proteins are involved in diverse developmental processes:

3.2.3.1 DELLA Proteins

- Act as repressors of gibberellin (GA) signaling
- Regulate processes such as seed germination, stem elongation, and flowering time
- Examples: GAI, RGA, RGL1, RGL2, RGL3 in Arabidopsis

3.2.3.2 SCARECROW (SCR) and SHORT-ROOT (SHR)

- Crucial for radial patterning in roots
- SCR and SHR interact to specify the endodermis

3.2.3.3 LATERAL SUPPRESSOR (LS)

- Involved in axillary meristem formation
- Mutations lead to reduced branching

3.2.4 Other Important Transcription Factor Families

3.2.4.1 TCP Family

TCP (TEOSINTE BRANCHED1, CYCLOIDEA, PCF) transcription factors regulate various aspects of plant development:

- BRANCHED1 (BRC1): Controls axillary bud outgrowth
- CINCINNATA (CIN)-like TCPs: Regulate leaf development and senescence

3.2.4.2 NAC Family

NAC (NAM, ATAF1/2, and CUC2) transcription factors are involved in various developmental processes:

- CUP-SHAPED COTYLEDON (CUC) genes: Essential for organ boundary formation [29]
- VASCULAR-RELATED NAC-DOMAIN (VND) proteins: Regulate xylem vessel element differentiation

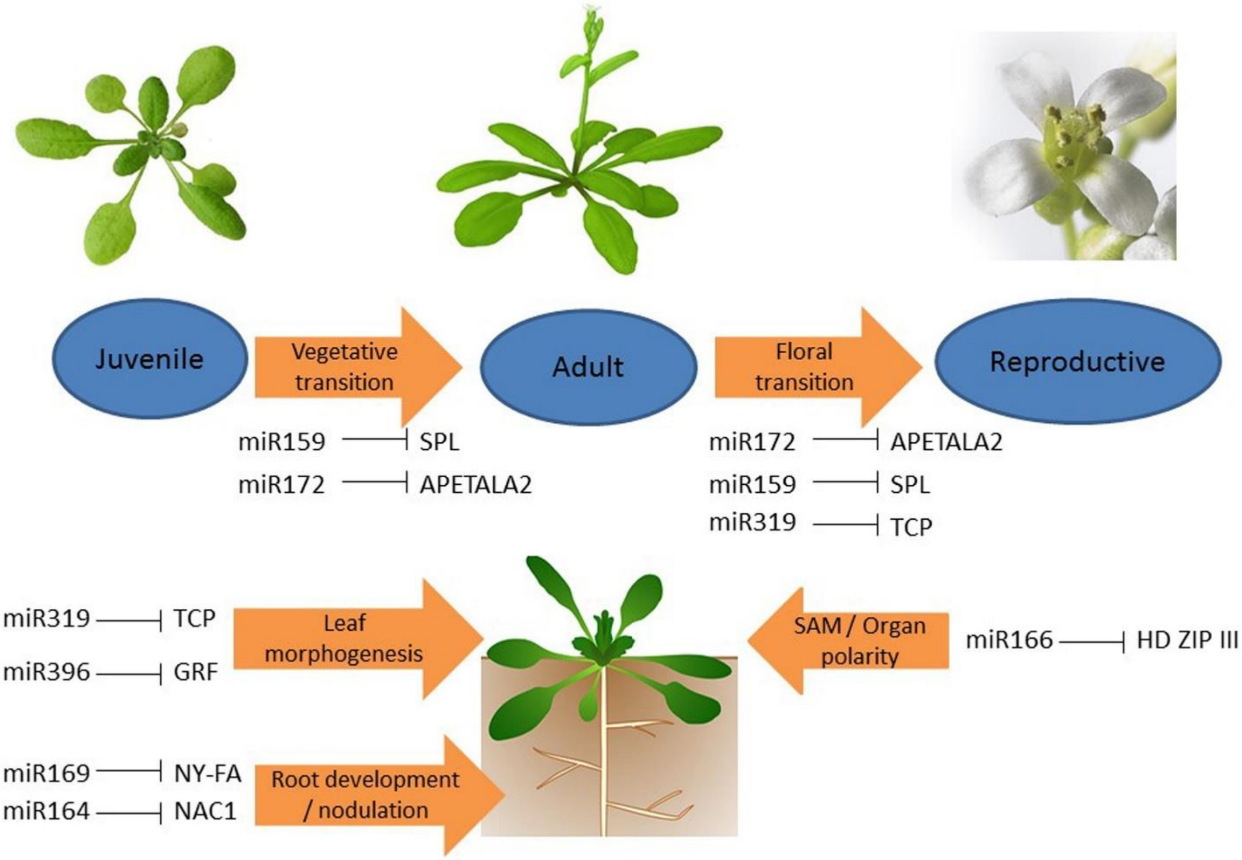

Figure 2. Transcription factors regulating developmental transitions in plants. Interaction between different microRNAs (miRNAs) and transcription factors (TFs) in plant development under normal condition (Samad et al., 2017). Interaction between miR156-SPL and miR172-AP2 leads plant transition from juvenile to adult; miR156-SPL, miR172-AP2, and miR319-TCP regulate the flowering process; miR319-TCP and miR396-GRF control leaf morphogenesis; miR169-NY-FA and miR164-NAC1 regulate root development and nodule formation, and miR166-HD ZIP III responsible for shoot apical meristem (SAM) development and organ polarity.

3.3. Integration of Regulatory Networks

The complex interplay between homeotic genes and transcription factors, along with their downstream target genes, is crucial for the precise spatial and temporal control of plant development. These regulatory genes often function in complex feedback loops and feed-forward networks:

- LEAFY activates AP1, which in turn reinforces LFY expression
- AGAMOUS represses WUSCHEL to terminate floral meristem activity

- KNOX proteins interact with BEL1-like homeodomain proteins to regulate target gene expression

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Course 4.

Mechanisms of Cell Growth in Plants

Plant growth and development are primarily driven by the expansion and division of individual cells. Understanding the mechanisms that regulate plant cell growth, in terms of both cell size and cell number, is crucial for comprehending the overall growth and morphogenesis of plants. This process involves complex interactions between cell wall biosynthesis, turgor pressure, various signaling pathways, and hormonal regulation.

4.1. Cell Wall Composition and Biosynthesis Pathways

The plant cell wall is a complex and dynamic structure that plays a crucial role in regulating cell growth. It provides mechanical strength, determines cell shape, and mediates cell-cell interactions. The primary cell wall is composed of a network of cellulose microfibrils embedded in a matrix of hemicellulose, pectin, and various structural proteins.

4.1.1 Cellulose Biosynthesis

Cellulose, the main load-bearing component of the cell wall, is synthesized by large protein complexes called cellulose synthase (CesA) complexes, which are located at the plasma membrane.

- CesA proteins form hexameric rosette complexes in the plasma membrane.
- Each CesA protein uses UDP-glucose as a substrate to polymerize β-1,4-glucan chains.
- The glucan chains are extruded through the plasma membrane and spontaneously crystallize into microfibrils.
- In Arabidopsis, 10 CesA genes have been identified, with different isoforms involved in primary and secondary cell wall formation.

The orientation of cellulose microfibrils is guided by cortical microtubules, which influence the movement of CesA complexes in the plasma membrane.

4.1.2 Hemicellulose Biosynthesis

Hemicelluloses, such as xyloglucans, xylans, and mannans, are synthesized in the Golgi apparatus and then incorporated into the cell wall matrix.

- Xyloglucan is synthesized by CSLC4 (Cellulose Synthase-Like C4) and various xylosyltransferases.
- Xylan biosynthesis involves IRX9, IRX10, and IRX14 proteins, among others.
- These hemicelluloses cross-link with cellulose microfibrils, providing additional structural support and flexibility.

4.1.3 Pectin Biosynthesis

Pectins are complex polysaccharides that contribute to cell wall porosity, charge, and adhesion properties.

- Homogalacturonan (HG) is synthesized by GAUT1 (Galacturonosyltransferase 1) and related enzymes.
- Rhamnogalacturonan I (RG-I) and Rhamnogalacturonan II (RG-II) involve multiple glycosyltransferases.
- Pectins are synthesized in the Golgi and deposited in the cell wall in a highly methyl-esterified form.
- Pectin methylesterases (PMEs) in the cell wall can modify pectins, affecting their properties and interactions.

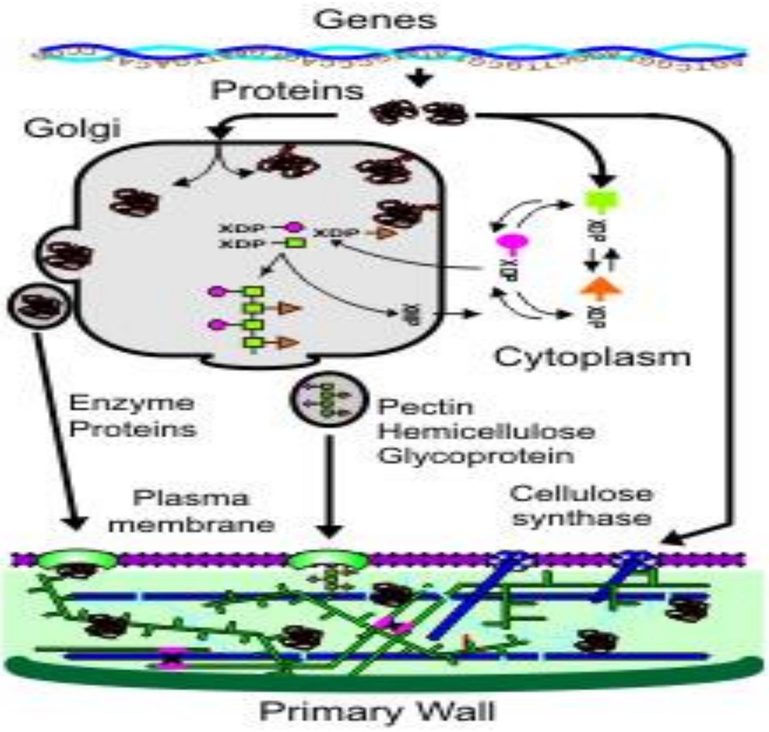

Figure 1. Schematic representation of the plant cell wall structure and biosynthesis pathways (https://glygen.ccrc.uga.edu/ccrc/mao/cellwall/main.htm).

4.1.4 Regulation of Cell Wall Biosynthesis

The coordinated biosynthesis and assembly of cell wall components are regulated by various signaling pathways and transcription factors:

- The brassinosteroid signaling pathway, involving BES1 and BZR1 transcription factors, regulates the expression of many cell wall-related genes.
- NAC and MYB transcription factors play crucial roles in regulating secondary cell wall biosynthesis.
- The ROP (Rho of Plants) GTPase signaling pathway influences both the actin cytoskeleton and the localization of CesA complexes.

4.2. Cell Expansion Mechanisms

Cell expansion in plants is primarily driven by turgor pressure acting against the cell wall. This process involves:

4.2.1 Turgor-driven Growth

- Water uptake into the vacuole generates turgor pressure.
- Turgor pressure exerts force on the cell wall, causing it to yield and expand.
- The rate of expansion is determined by the balance between turgor pressure and cell wall extensibility.

4.2.2 Cell Wall Loosening

To allow expansion, the cell wall must be loosened in a controlled manner:

- Expansins: These proteins disrupt hydrogen bonds between cellulose and hemicellulose, allowing slippage of cell wall polymers.
- Xyloglucan endotransglycosylases/hydrolases (XTHs): These enzymes cut and religate xyloglucan chains, facilitating cell wall restructuring during growth.
- Pectin modification: PMEs and pectate lyases can modify pectin structure, affecting wall properties and expansion.

4.2.3 Cytoskeleton Involvement

The cytoskeleton plays a crucial role in guiding cell expansion:

- Cortical microtubules guide the deposition of cellulose microfibrils, influencing the direction of cell expansion.

- The actin cytoskeleton is involved in trafficking of cell wall components and positioning of CesA complexes.

4.3. Hormonal Regulation of Cell Growth: Physiological and Biochemical Aspects

Plant hormones, particularly auxin, regulate cell growth through intricate physiological and biochemical mechanisms. This section focuses on the interplay between these processes in auxin-mediated growth control.

4.3.1 Auxin-Mediated Growth Control: Physiological and Biochemical Effects

4.3.1.1 The Acid Growth Theory

- Auxin stimulates plasma membrane H^+-ATPases, leading to proton extrusion into the cell wall space.
- Cell wall pH typically decreases from about 7 to 5 in the apoplast.

- Auxin activates H^+-ATPases through phosphorylation, particularly of the penultimate threonine residue.
- This activation involves the SAUR proteins, which inhibit PP2C-D phosphatases, maintaining H^+-ATPase phosphorylation.

4.3.1.2 Ion Fluxes and Water Uptake

- Proton extrusion is balanced by potassium ion (K^+) influx into the cell.
- Increased cellular K^+ concentration leads to osmotic water uptake, raising turgor pressure.

- Auxin activates inward-rectifying K^+ channels (e.g., KAT1, AKT1) through phosphorylation.
- Aquaporins are also regulated by auxin, facilitating rapid water uptake.

4.3.1.3 Cell Wall Loosening and Expansion

- Acidic cell wall environment activates wall-loosening enzymes.
- Increased turgor pressure, combined with wall loosening, drives cell expansion.

- Expansins: Acid-activated proteins that disrupt hydrogen bonds between cellulose and hemicellulose.
    - α-expansins and β-expansins have slightly different modes of action.
- Xyloglucan endotransglycosylases/hydrolases (XTHs):
    - XET activity: Cuts and religates xyloglucan chains.
    - XEH activity: Hydrolyzes xyloglucans.
- Pectin methylesterases (PMEs) and pectin lyases:
    - Modify pectin structure, affecting wall properties.

4.3.1.4 Cell Wall Synthesis and Remodeling

- Auxin promotes synthesis of new cell wall components during expansion.
- Maintains cell wall integrity under increased turgor pressure.

- Activation of cellulose synthase complexes (CesA):
    - Auxin influences CesA localization and activity.
- Upregulation of genes encoding enzymes for hemicellulose and pectin synthesis:
    - E.g., GAUT genes for pectin synthesis, CSL genes for hemicellulose synthesis.
- Regulation of cell wall remodeling enzymes:
    - E.g., polygalacturonases, pectate lyases.

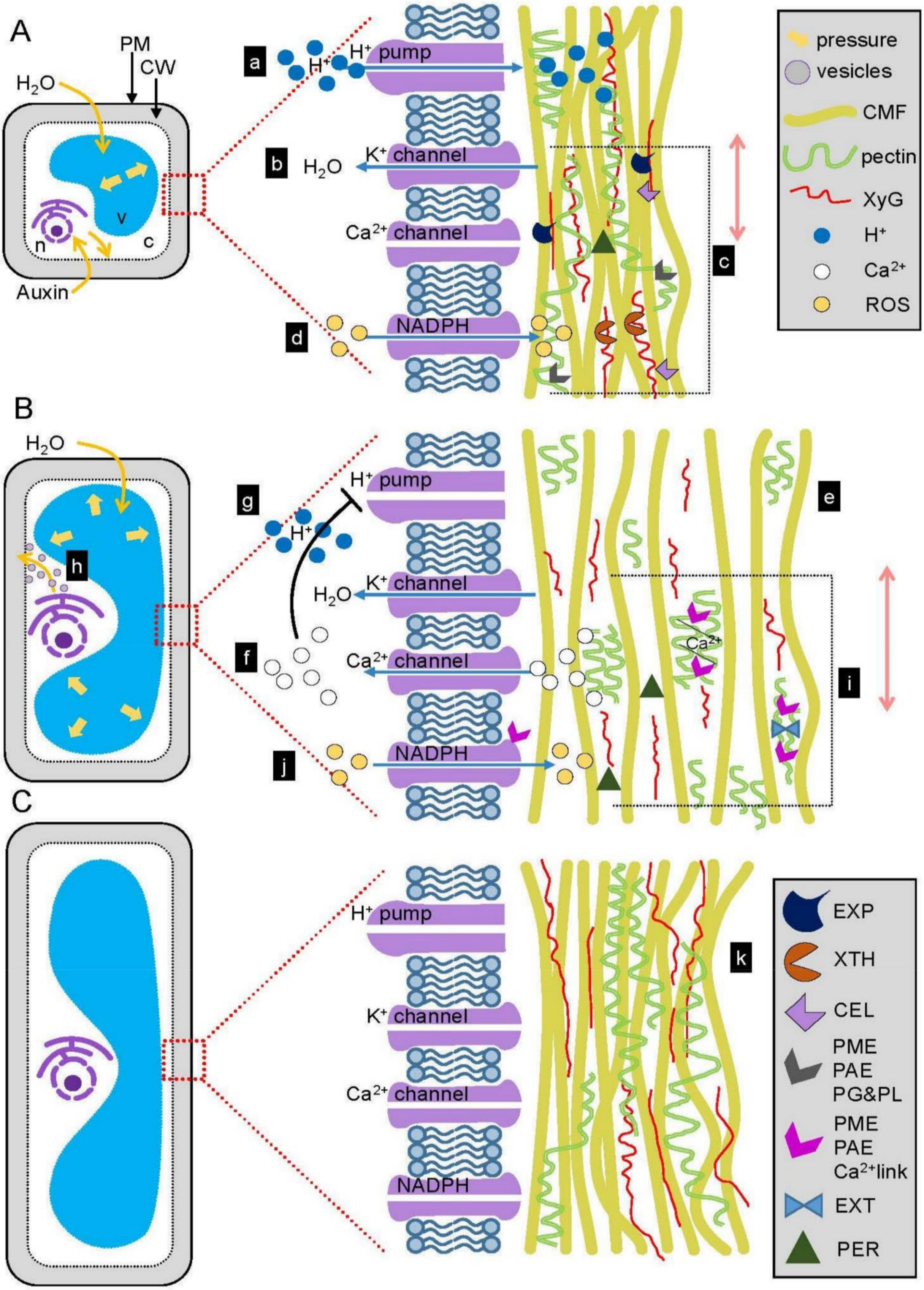

Figure 2. The role of auxin in cell wall expansion (Majda and Robert, 2018).

Isodiametric plant cell preparing for elongation (**A**), undergoing elongation (**B**) and fully elongated (**C**). nucleus (n); vacuole(s) (v); cytosol (c) ; plasma membrane (PM) ; cell wall (CW); The phospholipid bilayer (in blue); polysaccharides such as cellulose microfibrils (CMFs in yellow), pectins (green double line), XyGs (red line) and other polysaccharides (not shown). Auxin activates plasma membrane H^+-ATPase proton pumps, which pump protons (H^+) into the wall matrix, leading to wall acidification (**a**). Acidification of the apoplast activates potassium channels, which transport potassium ions (K^+) to the cytosol, stimulating water (H_2O) uptake and maintaining tensile stress (yellow arrows in **A** and **B**) (**b**). Acidic pH activates wall-loosening proteins and enzymes, which loosen the connections between different cell wall polysaccharides (**c**). PMEs activate plasma membrane nicotinamide adenine dinucleotide phosphate (NADPH), transporting superoxide anions to the cell wall where they are converted to hydrogen peroxide (**d**). Wall-loosening proteins and enzymes cause CMF sliding and moving apart, which increases wall porosity (**e**). Cell wall extension leads to the activation of calcium channels and calcium efflux into the cytosol (**f**). Accumulation of cytosolic calcium inhibits H^+-ATPase proton pumps and protoplast alkalization (**g**). Newly synthesized polysaccharides are inserted into the wall, where they arrive via vesicular trafficking (**h**). Wall alkalization activates PMEs, which in turn activate wall-degrading enzymes (**i**) and NADPH (**j**) causing crosslinking of the wall polysaccharides and growth cessation (**k**).

4.3.2 Auxin Signaling and Growth Regulation

- Rapid, non-transcriptional responses (within minutes).
- Slower, transcription-dependent responses (hours to days).

- Rapid responses:
  - ABP1 (Auxin Binding Protein 1) mediates some fast auxin responses, although its role is debated.
  - Activation of calcium channels and changes in cytoplasmic pH.
- Transcriptional regulation:
  - TIR1/AFB-Aux/IAA-ARF pathway:
    - Auxin binds to TIR1/AFB receptors.
    - This promotes ubiquitination and degradation of Aux/IAA repressors.
    - ARF transcription factors are released to regulate gene expression.

4.3.3 Differential Growth Responses

- In stems: Auxin typically promotes cell elongation.
- In roots: Low concentrations promote elongation, high concentrations inhibit it.

- Tissue-specific expression of auxin receptors and signaling components.
- Different auxin concentration thresholds for various responses.

- Interaction with other hormones:
    - Ethylene synthesis is induced by high auxin levels in roots, inhibiting growth.
    - Gibberellins work synergistically with auxin in stems, enhancing growth.

4.3.4 Auxin-Related Mutants Affecting Growth

Several mutants have helped elucidate auxin's role in growth regulation:

- pin1: Defective in PIN1 auxin efflux carrier, showing altered phyllotaxis and organ initiation.
- tir1: Auxin receptor mutant with reduced auxin sensitivity and growth defects.
- axr1: Auxin-resistant mutant with reduced auxin response and pleiotropic growth defects.
- yuc1D: Overexpression of YUCCA flavin monooxygenase, leading to auxin overproduction and enhanced growth.

4.3.5 Integration with Environmental Responses

- Auxin redistribution mediates tropisms (e.g., phototropism, gravitropism).
- Auxin influences stress responses and adaptive growth.

- Light regulation of auxin transport proteins (e.g., PIN proteins).
- Gravity-induced changes in auxin efflux carrier localization.
- Stress-induced changes in auxin biosynthesis and conjugation.

4.4. Analysis of Growth-Related Mutants

Genetic approaches have been instrumental in elucidating the molecular mechanisms underlying plant cell growth. By analyzing the phenotypes of mutants with altered cell size or cell number, researchers have identified numerous genes and regulatory pathways involved in this process.

4.4.1 Cell Wall Biosynthesis Mutants

4.4.1.1 Cellulose Biosynthesis Mutants

- *rsw1* (radial swelling 1): A temperature-sensitive mutation in CesA1, causing reduced cellulose content and radial swelling of roots at restrictive temperatures.

- *irx3* (irregular xylem 3): A mutation in CesA7, leading to collapsed xylem vessels and reduced secondary cell wall thickness.

4.4.1.2 Hemicellulose Biosynthesis Mutants

- *mur1* (murus 1): Defective in fucose biosynthesis, affecting xyloglucan and rhamnogalacturonan II structure, resulting in dwarfism.
- *xxt1/xxt2* double mutant: Lacks detectable xyloglucan, showing altered cell wall mechanics and root hair phenotypes.

4.4.1.3 Pectin Biosynthesis Mutants

- *quasimodo1* (qua1): A mutation in a putative galacturonosyltransferase, causing reduced cell adhesion and dwarfism.
- *gaut8/qua1* mutant: Shows reduced homogalacturonan content and defects in cell elongation.

4.4.2 Cell Expansion Mutants

- *axr2* (auxin resistant 2): A gain-of-function mutation in IAA7, an Aux/IAA protein, resulting in reduced cell expansion and auxin resistance.
- *saur19-D*: Overexpression of SAUR19 (Small Auxin Up RNA) promotes cell expansion and overall plant growth.

4.4.3 Cell Division Mutants

- *fackel* (fk): Exhibits abnormal cell division planes and embryo patterning due to defects in sterol biosynthesis.
- *cdka;1*: Mutation in CYCLIN-DEPENDENT KINASE A;1 shows reduced cell proliferation and overall plant size.
- *cycd3* triple mutant: Lack of D-type cyclins results in reduced cell number and premature differentiation in leaves.

4.4.4 Signaling Mutants Affecting Growth

- *bri1* (brassinosteroid insensitive 1): Mutation in the brassinosteroid receptor, resulting in dwarfism and reduced cell expansion.
- *pom-pom1* (pom1): A mutation affecting the cellulose synthase-interactive protein 1 (CSI1), leading to disrupted alignment between cortical microtubules and cellulose microfibrils.

These findings have implications for various areas of plant biology and agriculture, including:

1. Crop improvement: Understanding cell growth mechanisms can lead to strategies for increasing biomass and yield.
2. Stress tolerance: Cell wall modifications can enhance plant resistance to biotic and abiotic stresses.
3. Biofuel production: Manipulating cell wall composition can improve the efficiency of biomass conversion to biofuels.
4. Developmental biology: Insights into cell growth mechanisms contribute to our understanding of plant morphogenesis and evolution.

Plant cell growth is a carefully orchestrated process that involves the biosynthesis and assembly of cell wall components, regulation of turgor pressure, and coordination of cell division patterns. The interplay between these processes, mediated by complex signaling networks and transcriptional regulation, determines the final size and shape of plant cells and organs.

The regulation of plant cell growth by auxin involves a complex interplay of physiological and biochemical processes. From the activation of proton pumps and ion channels to the modulation of cell wall properties and gene expression, auxin orchestrates a multifaceted response that allows plants to fine-tune their growth in response to developmental and environmental cues.

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Course 5.

Differentiation of Specialized Plant Cells

During the course of plant development, undifferentiated cells give rise to a diverse array of specialized cell types, each with unique structures and functions. This process of cell differentiation is tightly regulated by complex genetic and epigenetic mechanisms. Two important examples of specialized plant cells are stomata and trichomes, whose development we will explore in detail.

5.1. Stomata Development

Stomata are pore-like structures found on the epidermis of leaves and other aerial plant organs. They play a crucial role in gas exchange, allowing the plant to uptake carbon dioxide for photosynthesis and release oxygen and water vapor. The development of stomata involves a series of coordinated cell divisions and cell fate decisions.

5.1.1 Genetic Regulation of Stomatal Development

The process of stomatal development is regulated by a complex network of genes, with key roles played by a family of basic helix-loop-helix (bHLH) transcription factors:

1. **SPEECHLESS (SPCH)**: Initiates stomatal lineage and promotes asymmetric divisions.
2. **MUTE**: Terminates asymmetric divisions and promotes guard mother cell formation.
3. **FAMA**: Promotes guard cell differentiation and terminates the stomatal lineage.

These bHLH proteins act in heterodimeric complexes with other bHLH proteins, SCREAM/ICE1 and SCREAM2, to regulate gene expression.

5.1.2 Key Steps in Stomatal Development

1. **Meristemoid Mother Cell (MMC) Formation**:
    - SPCH activates the expression of genes that promote entry into the stomatal lineage.
    - MMCs undergo asymmetric division to produce a meristemoid and a larger sister cell.
2. **Asymmetric Divisions**:

  - Meristemoids undergo additional asymmetric divisions, regulated by SPCH.
  - Each division produces another meristemoid and a larger sister cell (stomatal lineage ground cell, SLGC).

3. **Guard Mother Cell (GMC) Formation**:
   - MUTE expression terminates the asymmetric division phase.
   - The meristemoid differentiates into a GMC.
4. **Symmetric Division**:
   - The GMC undergoes a symmetric division to form two guard cells.
   - This process is regulated by FAMA and the FOUR LIPS (FLP) and MYB88 transcription factors.
5. **Guard Cell Differentiation**:
   - The two daughter cells differentiate into mature guard cells.
   - This involves the development of specialized cell walls and chloroplasts.

5.1.3 Stomatal Patterning

The distribution of stomata on the leaf surface is tightly controlled to optimize gas exchange while maintaining structural integrity. Key regulators include:

- **EPIDERMAL PATTERNING FACTOR (EPF) family**: Secreted peptides that inhibit stomatal development [41].
- **ERECTA** family receptor kinases: Perceive EPF signals and inhibit stomatal development.
- **TOO MANY MOUTHS (TMM)**: A receptor-like protein that modulates ERECTA signaling.
- **YODA**: A MAPKK kinase that negatively regulates stomatal development.

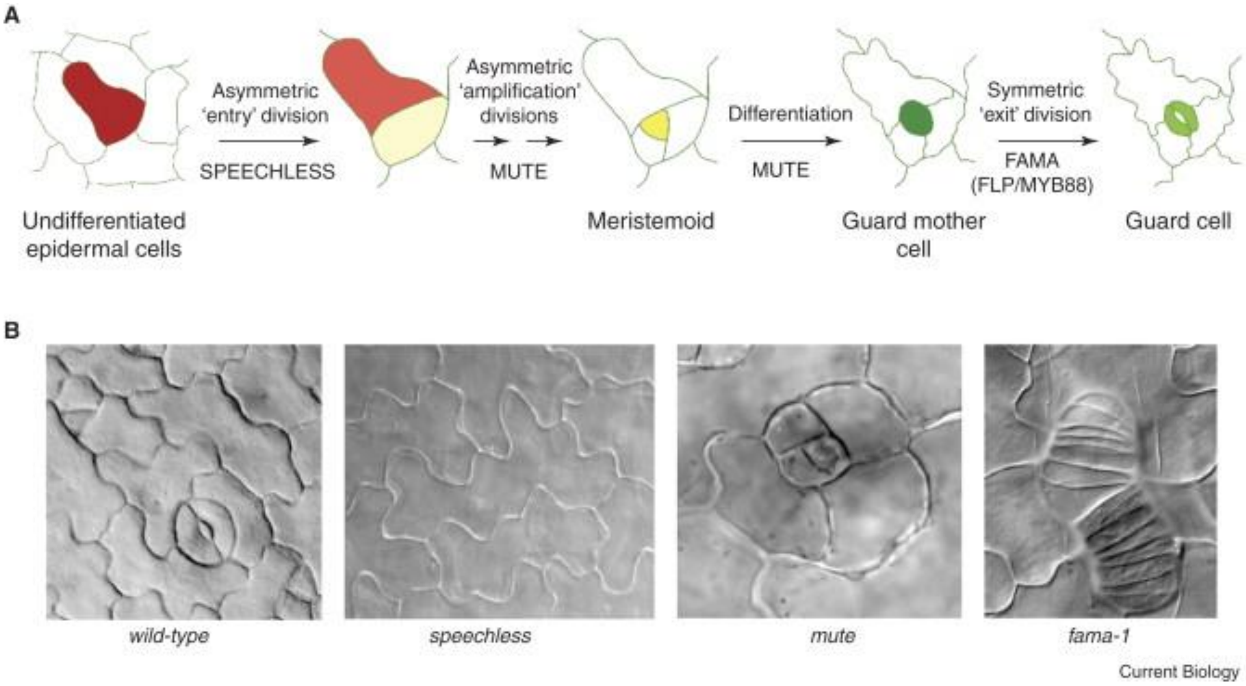

Figure 1. The stepwise development of stomata in plants (Gray, 2007).

5.1.4 Environmental Regulation

Stomatal development is also influenced by environmental factors:

- Light promotes stomatal development through the CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) and PHYTOCHROME-INTERACTING FACTOR 4 (PIF4) pathways.
- CO_2 levels affect stomatal density through the HIGH CARBON DIOXIDE (HIC) gene.

5.2. Trichome Development

Trichomes are hair-like structures found on the aerial surfaces of plants, such as leaves, stems, and flowers. They serve various functions, including defense against herbivores, reduction of water loss, and light reflectance. The development of trichomes is also under tight genetic control.

5.2.1 Genetic Regulation of Trichome Initiation

Trichome initiation is regulated by a complex of MYB and bHLH transcription factors, along with a WD-repeat protein:

- **GLABROUS1 (GL1)**: A R2R3 MYB transcription factor.
- **GLABRA3 (GL3)** and **ENHANCER OF GLABRA3 (EGL3)**: bHLH transcription factors [48].

- **TRANSPARENT TESTA GLABRA1 (TTG1)**: A WD-repeat protein.

These proteins form a trimeric complex (MYB-bHLH-WD40 or MBW complex) that activates genes involved in trichome initiation and development.

5.2.2 Key Steps in Trichome Development

1. **Trichome Cell Fate Determination**:
    - The MBW complex activates GLABRA2 (GL2), a homeodomain transcription factor that promotes trichome cell fate.
2. **Endoreduplication**:
    - Trichome cells undergo multiple rounds of DNA replication without cell division (endoreduplication).
    - This process is regulated by genes such as SIAMESE (SIM) and KAKTUS (KAK).
3. **Branch Formation**:
    - Trichome branching is regulated by genes like STICHEL (STI) and ZWICHEL (ZWI).
    - The number of branches is often correlated with the level of endoreduplication.
4. **Cell Wall Modification**:
    - Trichomes develop thickened cell walls, often with papillae.
    - This involves genes related to cell wall biosynthesis and modification.

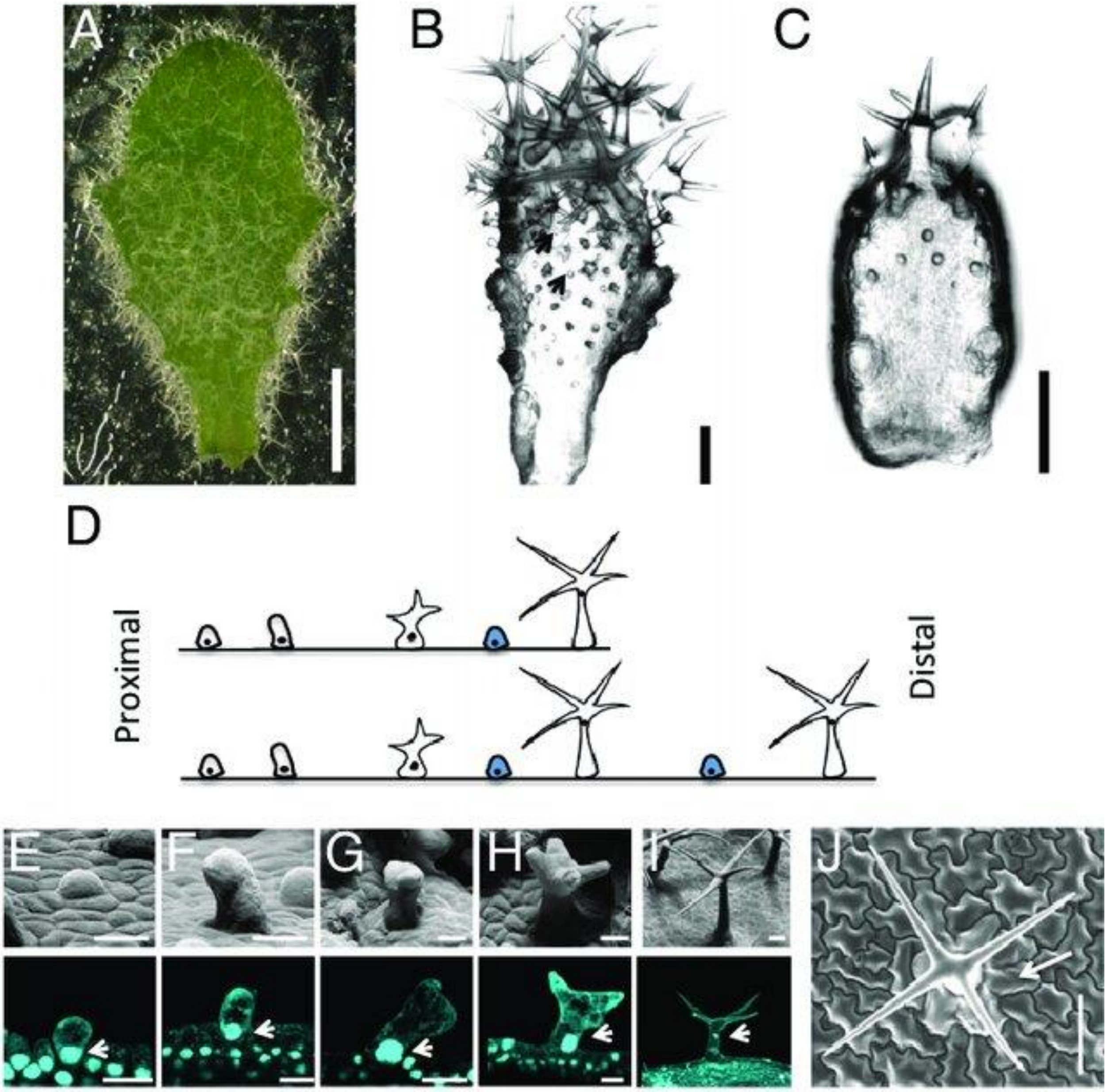

Figure 2. Trichome development on A. alpina rosette leaves. (A) Mature leaf; trichomes densely cover the whole surface. (B) In slightly older stages, incipient trichomes are found between older trichomes (arrowheads). (C) On very young leaves, incipient trichomes are found at the leaf base and advanced developmental stages in more distal regions. (D) Schematic representation of the trichome distribution along the proximal-distal axis on a very young leaf as shown in C, and an older leaf as shown in B. Blue-colored trichomes are intercalating between already existing ones. (E-J) Scanning electron micrographs and optical section of DAPI-stained trichomes at different developmental stages. (E) Incipient trichomes beginning to expand. (F) Unbranched trichomes. (G) Two-branched trichomes. (H) Four-branched trichomes. (I) Mature trichomes. (J) Top view of a mature trichome (Chopra et al., 2019). Note that the immediately adjacent cells are shaped like pavement cells. n = 20. (Scale bars: A, B, and E-I: 10 µm; C and D: 20 µm; and J: 100 µm.).

5.2.3 Trichome Patterning

The distribution of trichomes is regulated by a lateral inhibition mechanism:

- **TRIPTYCHON (TRY)**, **CAPRICE (CPC)**, and related proteins act as mobile inhibitors.
- These proteins compete with GL1 for binding to GL3/EGL3, inhibiting trichome formation in neighboring cells.

5.2.4 Diversity in Trichome Morphology

Different plant species exhibit a wide variety of trichome types:

- **Glandular trichomes**: Produce and store specialized metabolites. Their development involves additional genetic pathways related to secondary metabolism.
- **Multi-cellular trichomes**: Common in many species, involve different developmental mechanisms compared to the unicellular trichomes of Arabidopsis.

5.3. Genetic Control of Cell Fate Determination

The differentiation of specialized cell types in plants, such as stomata and trichomes, is controlled by complex genetic regulatory networks. These networks involve the coordinated expression of transcription factors, signaling molecules, and other regulatory components that guide the cells through the various stages of their development.

5.3.1 Common Themes in Cell Fate Determination

1. **Master Regulators**: Transcription factors that act as key switches in cell fate decisions (e.g., SPCH for stomata, GL1 for trichomes).
2. **Transcriptional Cascades**: Sequential activation of transcription factors guiding progression through developmental stages.
3. **Lateral Inhibition**: Preventing neighboring cells from adopting the same fate, ensuring proper spacing of specialized cells.
4. **Feedback Loops**: Maintaining or reinforcing cell fate decisions once they are made.
5. **Integration of Multiple Signals**: Environmental and developmental cues influencing cell fate decisions.

5.3.2 Epigenetic Regulation

Epigenetic mechanisms also play crucial roles in cell fate determination:

- **Histone Modifications**: For example, the CURLY LEAF (CLF) Polycomb group protein regulates trichome development through H3K27 trimethylation.
- **Chromatin Remodeling**: The BRAHMA chromatin-remodeling ATPase influences both stomatal and trichome development.

5.3.3 Hormonal Regulation

Plant hormones integrate various signals to influence cell fate:

- **Gibberellins** promote both stomatal and trichome development.
- **Cytokinins** influence stomatal development and patterning.

5.4. Implications and Applications

Understanding the genetic control of cell fate determination in plants has important implications:

1. **Crop Improvement**: Manipulating stomatal density or trichome production could enhance drought tolerance or pest resistance in crops.
2. **Biomimetics**: Understanding trichome development could inspire new materials with specialized surface properties.
3. **Evolutionary Biology**: Comparative studies of cell fate determination mechanisms provide insights into plant evolution and adaptation.
4. **Synthetic Biology**: Engineering novel cell types or modifying existing ones for biotechnological applications.

The differentiation of specialized plant cells, exemplified by the development of stomata and trichomes, is a tightly regulated process that involves the orchestrated expression of key transcription factors and signaling pathways. The complex genetic networks controlling these processes ensure the proper development and function of these crucial cell types.

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Course 6.

Gametophyte Differentiation, Fertilization, and Seed Formation in Plants

6.1. Meiosis and Gametogenesis

6.1.1 Male Gametophyte Development

The development of the male gametophyte (pollen grain) begins in the anther's microsporangia. The process involves several key stages:

1. **Microsporogenesis**: Diploid microspore mother cells undergo meiosis to produce haploid microspores.
2. **Microspore Maturation**: Each microspore develops into a pollen grain through the following steps:
    - Microspore enlargement and vacuolation
    - Asymmetric mitotic division (Pollen Mitosis I) producing a large vegetative cell and a small generative cell
    - The generative cell undergoes a second mitosis (Pollen Mitosis II) to form two sperm cells

Molecular Regulation:

- The MIKC* MADS-box transcription factors play crucial roles in pollen development.
- The DUO1 (DUO POLLEN 1) gene is essential for male germline development and sperm cell formation.
- Genes like MS1 (MALE STERILITY 1) and AMS (ABORTED MICROSPORES) are involved in tapetum development and pollen wall formation.

6.1.2 Female Gametophyte Development

The female gametophyte (embryo sac) develops within the ovule through a process called megagametogenesis:

1. **Megasporogenesis**: A diploid megaspore mother cell undergoes meiosis to produce four haploid megaspores.

2. **Megagametogenesis**: Usually, only one megaspore survives and undergoes three rounds of mitosis without cytokinesis, resulting in an eight-nucleate embryo sac.
3. **Cellularization**: The nuclei are partitioned into seven cells - one egg cell, two synergids, three antipodal cells, and one central cell with two polar nuclei.

Molecular Regulation:

- The AGO9 (ARGONAUTE 9) gene is crucial for restricting the number of functional megaspores.
- FMS1 (FEMALE GAMETOPHYTE DEVELOPMENT1) and GEX1 (GAMETE EXPRESSED 1) are essential for female gametophyte development.
- The LACHESIS (LIS) gene is involved in cell fate specification within the embryo sac.

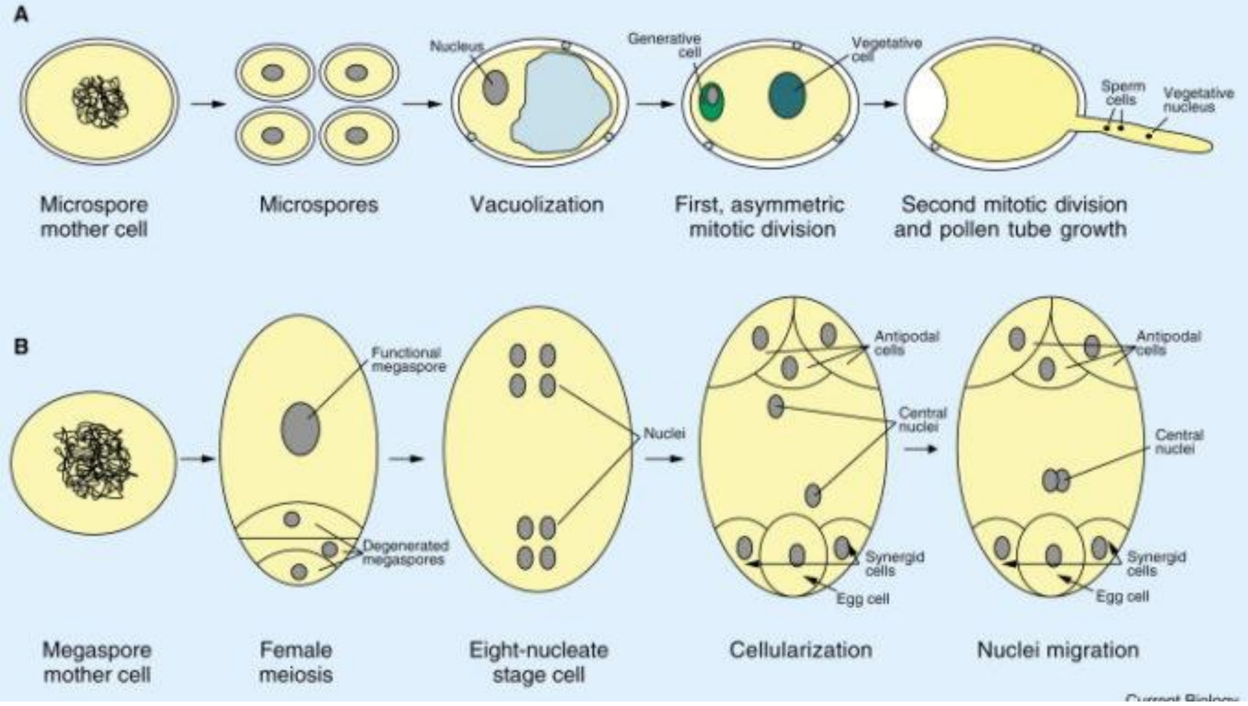

Figure 1. Gametophyte development in plants (Li and Ma, 2002).

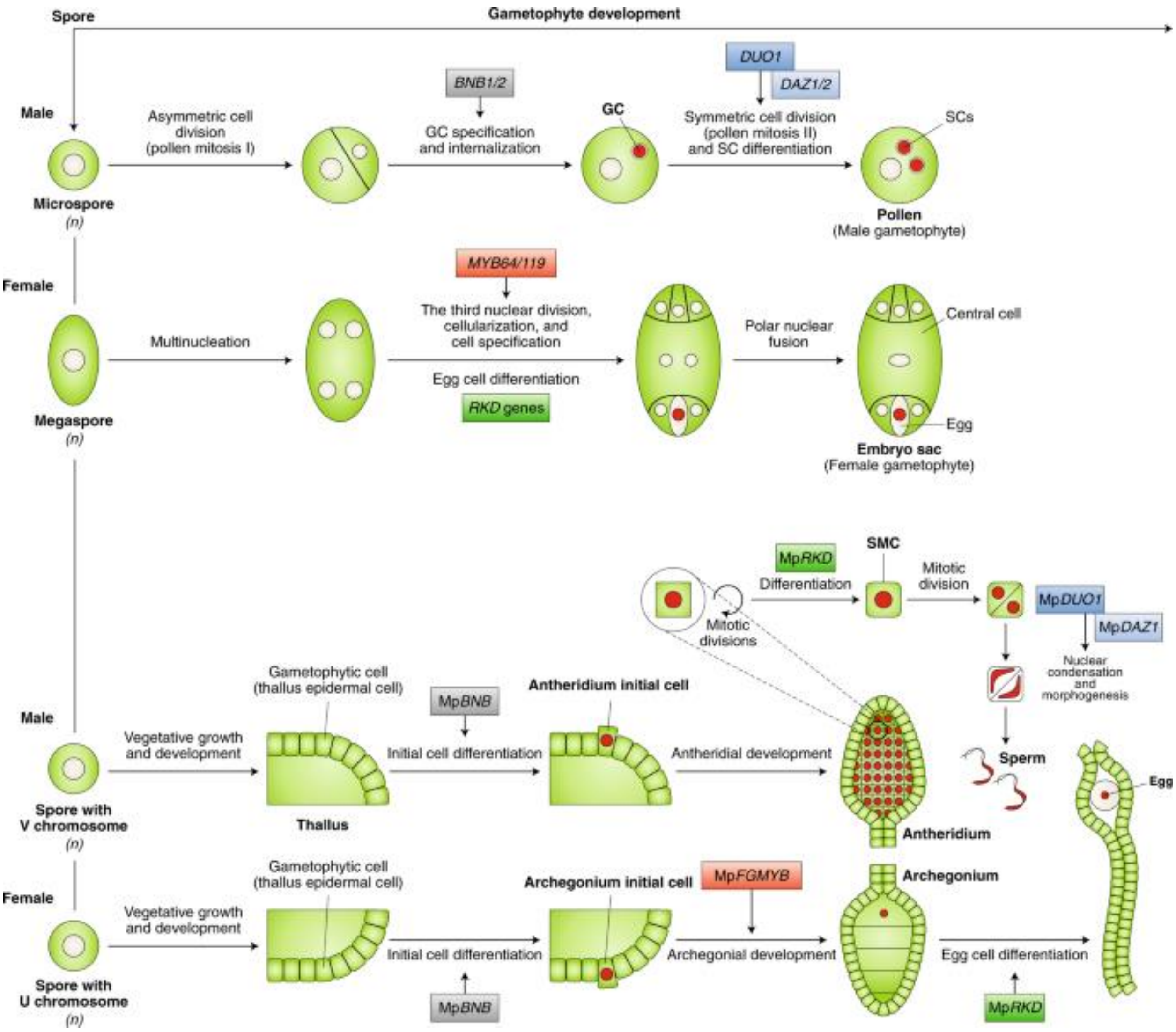

Figure 2. Comparison between the gene controls of gametogenesis in A. thaliana and M. polymorpha (Hisanaga et al., 2019). Developmental processes of female and male gametophytes from spores in A. thaliana (top) and M. polymorpha (bottom) are schematically depicted. Red- and white-coloured circles indicate nuclei of germline and gametophytic cells, respectively (not shown in M. polymorpha gametophytic cells). Developmental steps regulated by the key factors mentioned in the text are indicated. The same colour codes are used for homologous or orthologous genes between the two species.

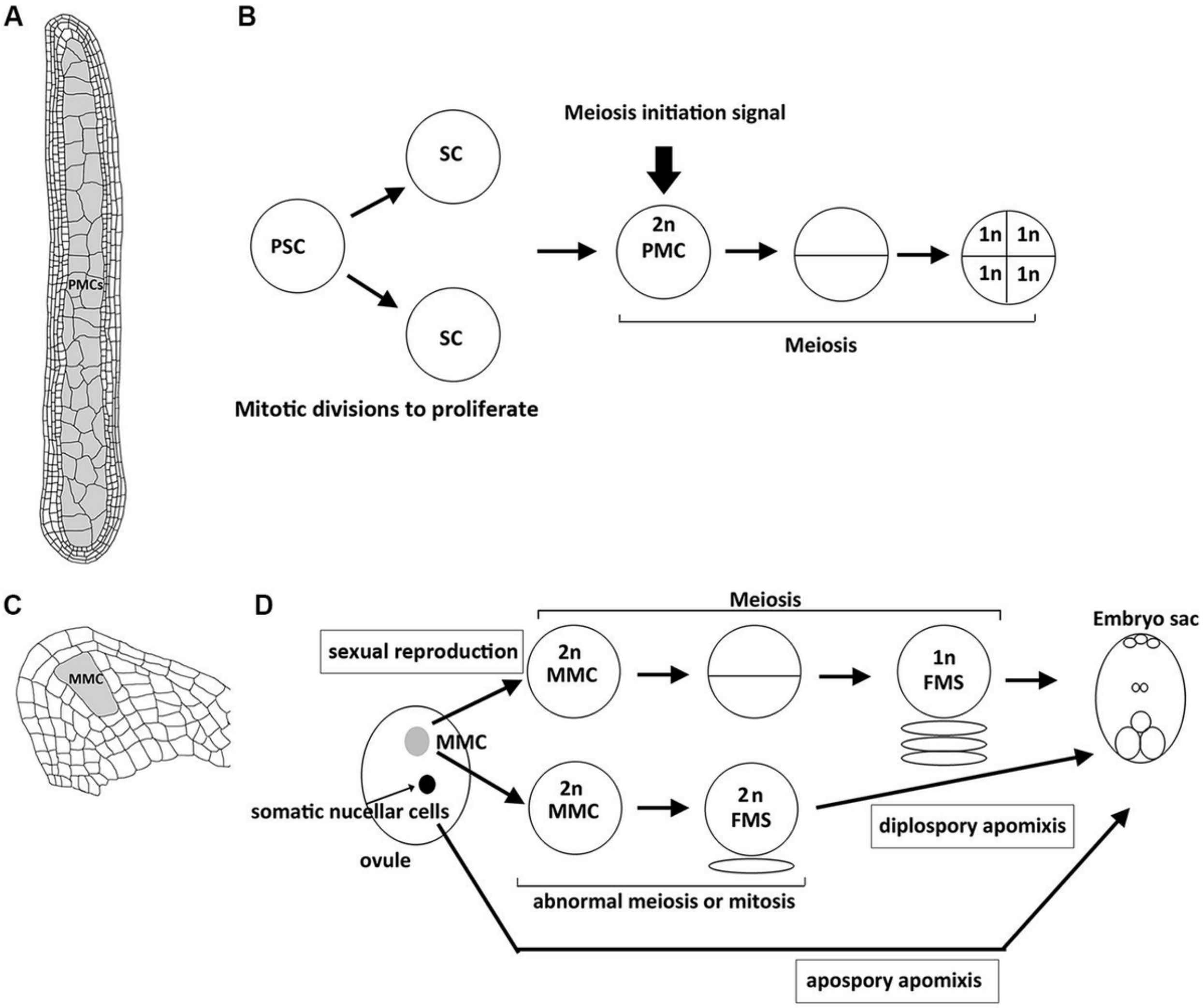

Figure 3. Meiosis and gametophyte formation in plants: Structure of plant reproductive organs in maize and sequence of events leading to spore or gametophyte formation in anthers and ovules (Wang and Tseng, 2014).

(A) Longitudinal section of an anther with numerous pollen mother cells (PMCs, shown in gray) that are proliferated from primary sporogenous cells by mitosis, which accompanies the development of surrounding 4 layers of somatic cells. **(B)** After primary sporogenous cells (PSCs) are differentiated, they first undergo mitotic divisions to produce sporogenous cells (SCs) and further develop into PMCs. By the time when the development of surrounding somatic cells (shown in **A**) is complete, unknown meiosis initiation siganl is generated to start meisois synchronously in all PMCs of an anther. Each PMC enters meiosis to produce four haploid spore cells. **(C)** Longitudinal section of an ovule with a single megaspore mother cell (MMC, shown in gray). **(D)** Schematic illustration showing the sequential development of embryo sac through sexual reproduction or apomictic pathways. In sexual reproduction, the single MMC (shown in gray) is differentiated and then enters meiosis to produce a haploid functional megaspore (FMS), and then develops into an embryo sac. In diplospory apomixis, the specified MMC unergoes an abnormal meiosis or mitosis to produce a diploid FMS. In apospory apomixis, somatic nucellar cells develop into embryo sac without meiosis.

6.2. Fertilization and Embryo Development

6.2.1 Pollen-Pistil Interaction and Pollen Tube Growth

1. **Pollen Hydration and Germination**: Upon landing on the stigma, the pollen grain hydrates and germinates, forming a pollen tube.
2. **Pollen Tube Growth**: The pollen tube grows through the style towards the ovule, guided by various chemical cues.

Molecular Mechanisms:

- Receptor-like kinases (RLKs) such as PRK1 (POLLEN RECEPTOR KINASE 1) are involved in pollen tube growth and guidance.
- LURE peptides secreted by synergids act as attractants for pollen tubes.
- The interaction between pollen tube-specific ANXUR receptors and pistil-expressed RALF peptides regulates pollen tube integrity.

6.2.2 Double Fertilization

1. **Pollen Tube Entry**: The pollen tube enters the ovule through the micropyle and releases two sperm cells into one of the synergids.
2. **Gamete Fusion**: One sperm cell fuses with the egg cell to form the zygote, while the other fuses with the central cell to form the endosperm.

Molecular Mechanisms:

- GCS1/HAP2 (GENERATIVE CELL SPECIFIC 1) is essential for gamete fusion.
- The EC1 (EGG CELL 1) peptide activates sperm cells for fusion.
- CDK inhibitors like RBR1 (RETINOBLASTOMA-RELATED 1) prevent multiple fertilization events.

6.2.3 Embryo Development

After fertilization, the zygote undergoes a series of precisely coordinated cell divisions and differentiation events:

1. **Zygote Elongation and Asymmetric Division**: Establishes the apical-basal axis of the embryo.
2. **Globular Stage**: Formation of the protoderm, ground tissue, and vascular tissue precursors.

3. **Heart Stage**: Establishment of cotyledon primordia and shoot apical meristem.
4. **Torpedo Stage**: Elongation of the embryonic axis and further organ development.

Molecular Regulation:

- The WUSCHEL-RELATED HOMEOBOX (WOX) gene family is crucial for early embryo patterning.
- Auxin gradients, established by PIN-FORMED (PIN) proteins, guide embryo axis formation.
- The GNOM gene is essential for correct cell division orientation during early embryogenesis.

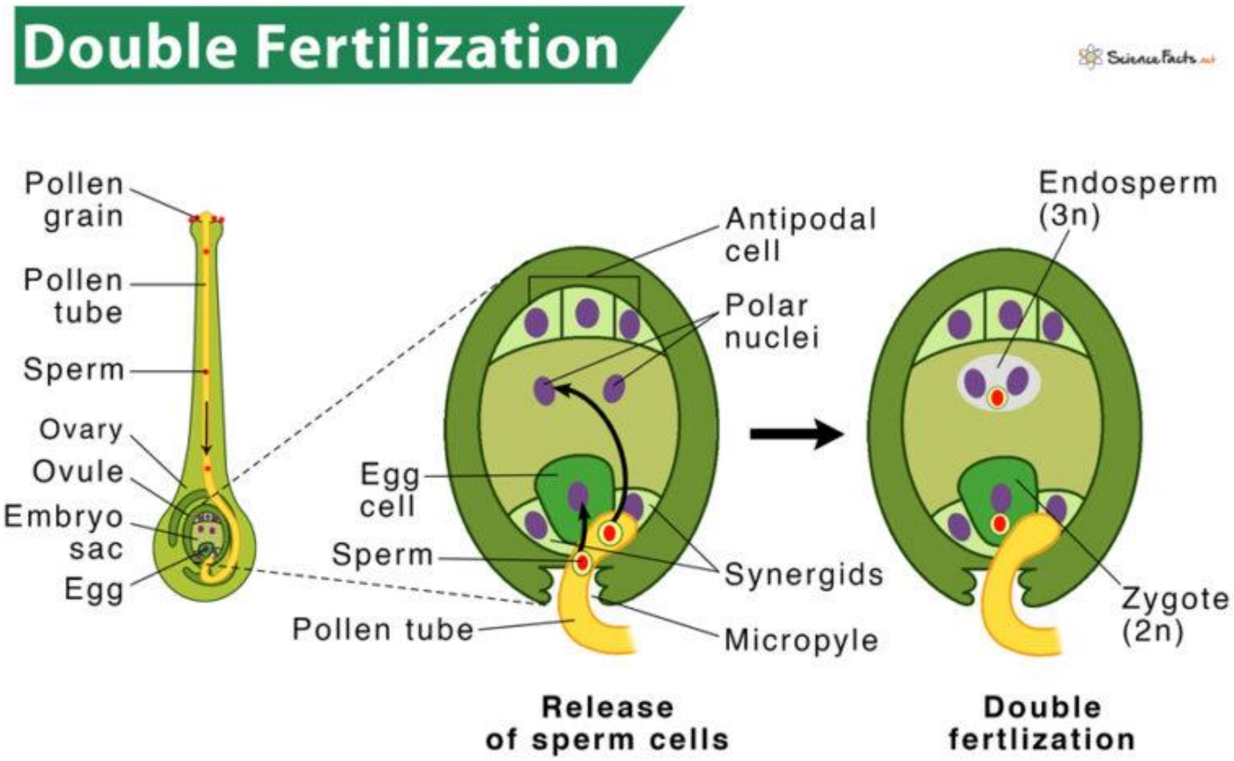

Figure 4. Double Fertilization process and embryo development in plants (https://www.sciencefacts.net/double-fertilization.html).

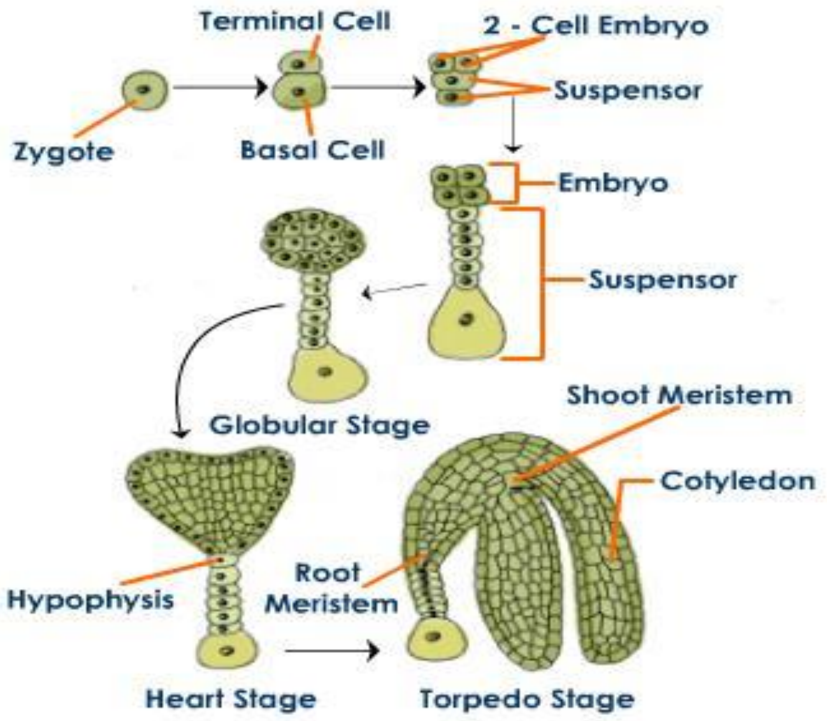

Figure 5. Fertilization and embryo development in plants (https://www.toppr.com/ask/question/write-down-the-names-of-post-fertilization-events-in-flowering/).

6.3. Seed Maturation and Dormancy

6.3.1 Seed Maturation

Seed maturation involves the accumulation of storage compounds and the acquisition of desiccation tolerance:

1. **Storage Compound Accumulation**: Synthesis and deposition of proteins, lipids, and carbohydrates.
2. **Desiccation Tolerance**: Accumulation of protective molecules like LEA (Late Embryogenesis Abundant) proteins and sugars.

Molecular Regulation:

- The B3 domain transcription factors ABI3, FUS3, and LEC2 are master regulators of seed maturation.
- The bZIP transcription factor ABI5 mediates ABA responses during seed maturation.

6.3.2 Seed Dormancy

Seed dormancy prevents premature germination and is regulated by a complex interplay of hormones and environmental factors:

1. **Establishment of Dormancy**: Occurs during seed maturation, primarily regulated by ABA.
2. **Maintenance of Dormancy**: Influenced by the balance between ABA and GA, as well as environmental factors.
3. **Breaking of Dormancy**: Triggered by environmental cues such as cold stratification or light exposure.

Molecular Mechanisms:

- The DOG1 (DELAY OF GERMINATION 1) gene is a key regulator of seed dormancy.
- Chromatin remodeling factors like HUB1 (HISTONE MONOUBIQUITINATION 1) modulate seed dormancy through histone modifications.
- The GA2ox6 gene regulates GA levels, influencing the ABA/GA balance during dormancy and germination.

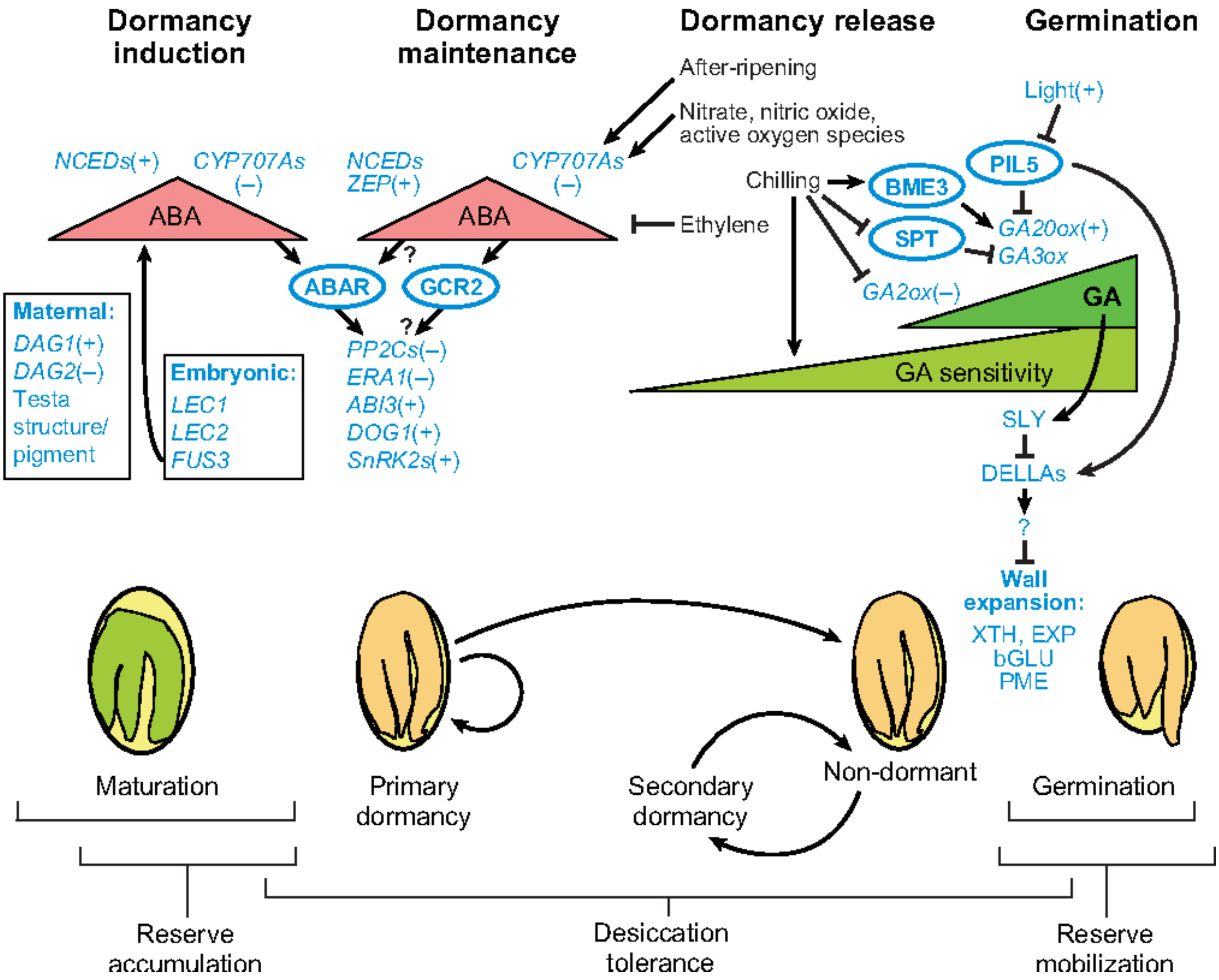

Figure 6. Seed maturation and dormancy (Finkelstein et al., 2008).

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Course 7.

Apoptosis Mechanisms During Plant Development

Programmed cell death (PCD), or apoptosis, is a fundamental process in plant development and stress responses. While initially studied extensively in animal systems, the importance of PCD in plants has gained significant recognition in recent years. This controlled cellular suicide mechanism plays crucial roles in various stages of plant growth, morphogenesis, and responses to environmental stimuli.

7.1. Roles of Programmed Cell Death in Plant Development

7.1.1 Embryogenesis

During plant embryogenesis, PCD contributes to several key developmental processes:

- **Formation of Root and Shoot Apical Meristems**: PCD helps shape these crucial growth centers by eliminating unnecessary cells.
- **Vascular System Differentiation**: The formation of xylem vessels involves PCD of specific cell types.
- **Suspensor Elimination**: The suspensor, which supports early embryo development, undergoes PCD after fulfilling its role.

Molecular Regulation:

- The GNOM gene, essential for embryo axis formation, also regulates PCD in the suspensor.
- The APL (ALTERED PHLOEM DEVELOPMENT) transcription factor is involved in xylem PCD during vascular differentiation.

7.1.2 Organ Development

PCD plays a crucial role in shaping various plant organs:

- **Leaf Morphogenesis**: PCD contributes to the formation of leaf serrations and compound leaf structures.
- **Flower Development**: The sculpting of floral organs, such as petals and stamens, involves localized PCD.

- **Root Cap Formation**: The outermost layers of the root cap undergo continuous PCD and regeneration.

Molecular Mechanisms:

- The BLADE-ON-PETIOLE (BOP) genes regulate PCD during leaf and flower development.
- ROOT CAP POLYGALACTURONASE (RCPG) is involved in the PCD of root cap cells.

7.1.3 Senescence

PCD is a key component of the senescence process in various plant tissues:

- **Leaf Senescence**: Involves the systematic breakdown of cellular components and nutrient remobilization.
- **Flower Wilting**: PCD contributes to petal wilting and abscission.
- **Fruit Ripening**: Some aspects of fruit softening and texture changes involve PCD.

Molecular Regulation:

- The NAC transcription factor ORE1 (ORESARA1) is a master regulator of leaf senescence.
- Ethylene-responsive transcription factors (ERFs) modulate PCD during petal senescence.

7.1.4 Defense Responses

PCD is an important component of plant immune responses:

- **Hypersensitive Response (HR)**: Rapid, localized cell death at the site of pathogen infection.
- **Systemic Acquired Resistance (SAR)**: PCD signals contribute to the establishment of systemic immunity.

Molecular Mechanisms:

- The RPM1 and RPS2 resistance genes trigger HR-associated PCD in response to specific pathogens.
- The EDS1 (ENHANCED DISEASE SUSCEPTIBILITY 1) gene is crucial for both local and systemic PCD responses.

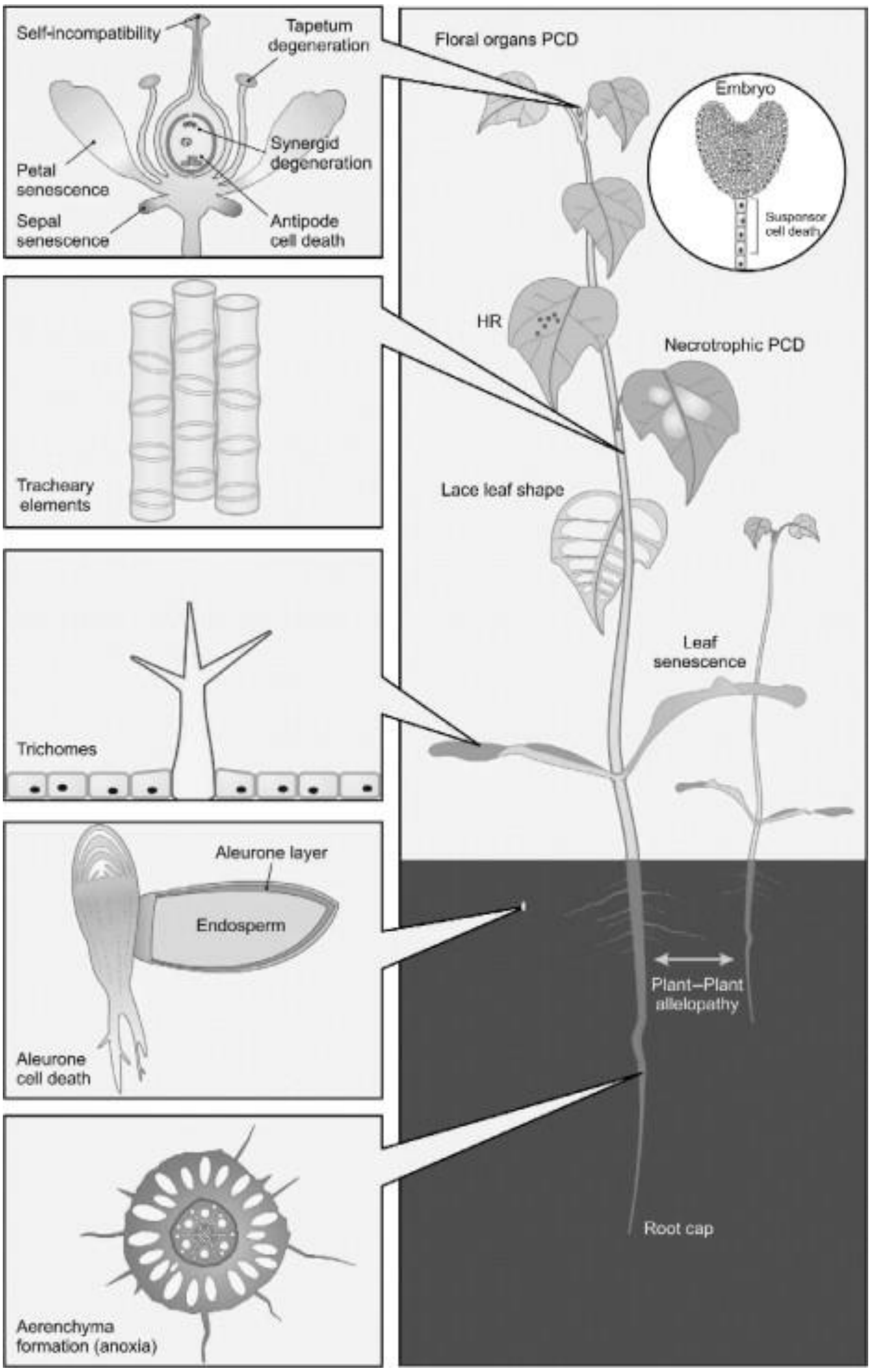

Figure 1. Programmed Cell Death in Plant Development (Gadjev et al., 2008).

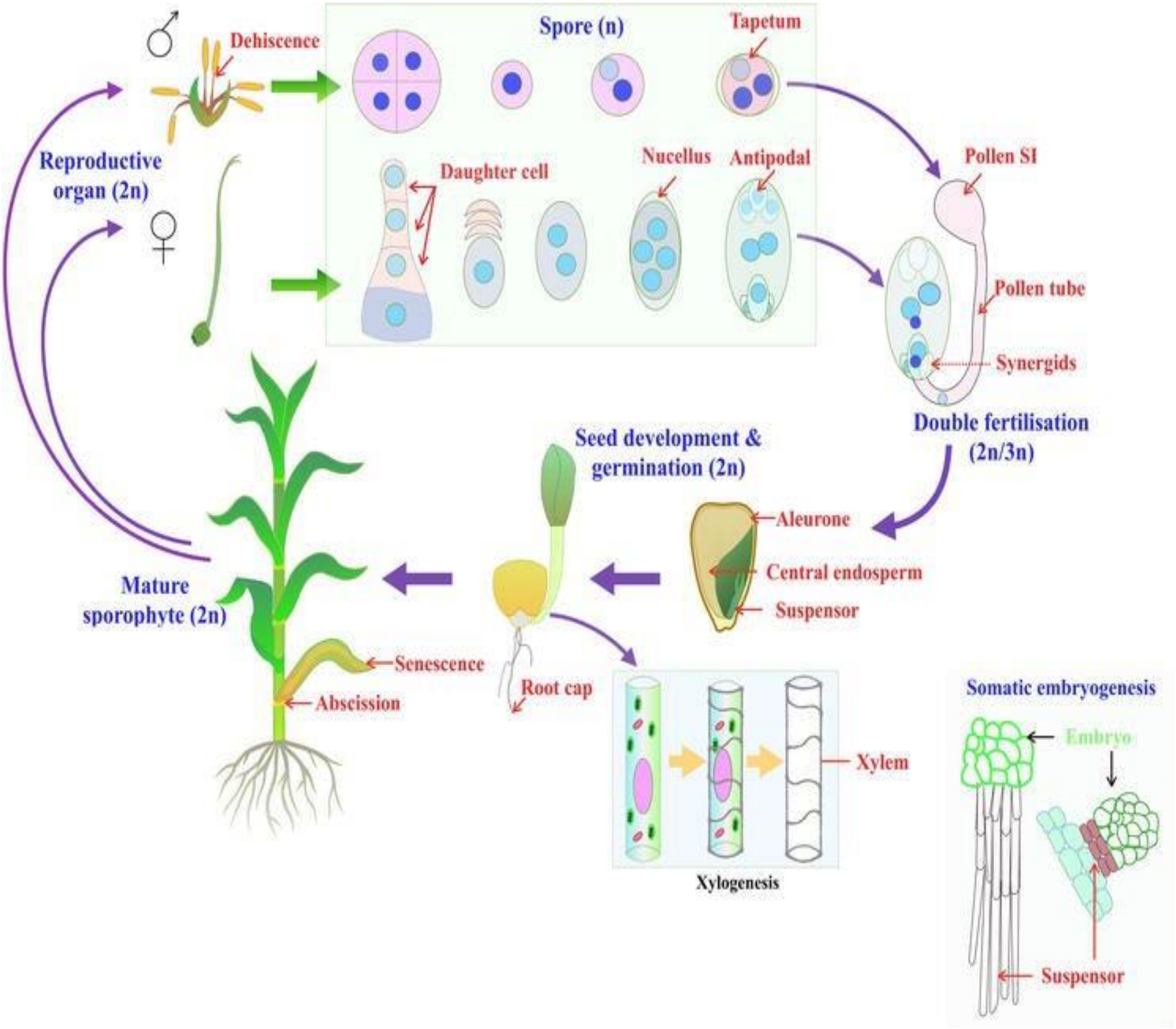

Figure 2. Central role of PCD across the plant life cycle (Mondal et al., 2021). Pre-zygotic and post-zygotic developmental changes such as tapetum layer degeneration, daughter cell degeneration, antipodal-synergids cell degeneration, pollen tube degeneration, aleurone layer, central endosperm, suspensor cell death are controlled by PCD. The process of xylogenesis is also influenced by PCD. During the differentiation of tracheary elements, vacuole swelling and rupture are coordinated with the thickening and restructuring of the cell wall. The final collapse of the vacuole immediately precedes nuclear DNA fragmentation, which occurs at the late stages of the cell-death process before the final autolysis of the cell. In mature sporophyte senescence, abscission and dehiscence are regulated by PCD. PCD is also observed during in vitro somatic embryogenesis. Symplastic cell-to-cell trafficking connection between the somatic embryo and mother explant is broken due to PCD. Degeneration of suspensor cell of somatic embryo mediated by PCD.

7.2. Molecular Mechanisms of Apoptosis in Plants

7.2.1 Caspase-like Proteases

While plants lack true caspases, they possess functionally similar proteases:

- **Metacaspases**: Plant-specific cysteine proteases involved in PCD execution.

- **Vacuolar Processing Enzymes (VPEs)**: Cysteine proteases with caspase-like activity.

Key Players:

- AtMC1 and AtMC2 are Arabidopsis metacaspases with opposing roles in PCD regulation.
- γVPE is involved in vacuole-mediated cell death during the hypersensitive response.

7.2.2 Mitochondrial Involvement

Plant mitochondria play a central role in PCD signaling and execution:

- **Cytochrome c Release**: Similar to animal systems, cytochrome c release from mitochondria can trigger PCD.
- **Mitochondrial Permeability Transition**: Changes in mitochondrial membrane permeability contribute to PCD initiation.

Molecular Mechanisms:

- The VDAC (Voltage-Dependent Anion Channel) proteins regulate mitochondrial permeability during PCD.
- The release of CYTOCHROME C from mitochondria activates a cascade of PCD-related events.

7.2.3 Reactive Oxygen Species (ROS)

ROS act as both signaling molecules and executioners in plant PCD:

- **ROS Production**: NADPH oxidases and mitochondrial electron transport chain are major sources of ROS during PCD.
- **ROS-Mediated Damage**: High levels of ROS can directly damage cellular components, leading to cell death.

Key Regulators:

- The RBOH (RESPIRATORY BURST OXIDASE HOMOLOG) gene family encodes NADPH oxidases crucial for ROS production during PCD.
- Antioxidant enzymes like SOD (Superoxide Dismutase) and CAT (Catalase) modulate ROS levels and PCD progression.

7.2.4 Calcium Signaling

Calcium acts as a second messenger in PCD signaling cascades:

- **Calcium Influx**: Increased cytosolic Ca2+ levels can trigger PCD-related processes.
- **Calmodulin and CDPKs**: Calcium-dependent protein kinases mediate calcium-triggered PCD responses.

Molecular Players:

- The TPC1 (TWO-PORE CHANNEL 1) gene encodes a vacuolar calcium-release channel involved in stress-induced PCD.
- CPK5 (CALCIUM-DEPENDENT PROTEIN KINASE 5) mediates calcium signaling during pathogen-induced PCD.

7.2.5 Phytohormone Regulation

Plant hormones play crucial roles in modulating PCD responses:

- **Ethylene**: Generally promotes senescence-associated PCD.
- **Abscisic Acid (ABA)**: Can induce PCD under stress conditions.
- **Salicylic Acid (SA)**: Important for pathogen-induced PCD and SAR.
- **Jasmonic Acid (JA)**: Modulates PCD responses, often antagonistically to SA.

Regulatory Mechanisms:

- The EIN2 (ETHYLENE INSENSITIVE 2) gene is a central regulator of ethylene-mediated PCD responses.
- NPR1 (NONEXPRESSER OF PR GENES 1) integrates SA and JA signaling in PCD-related defense responses.

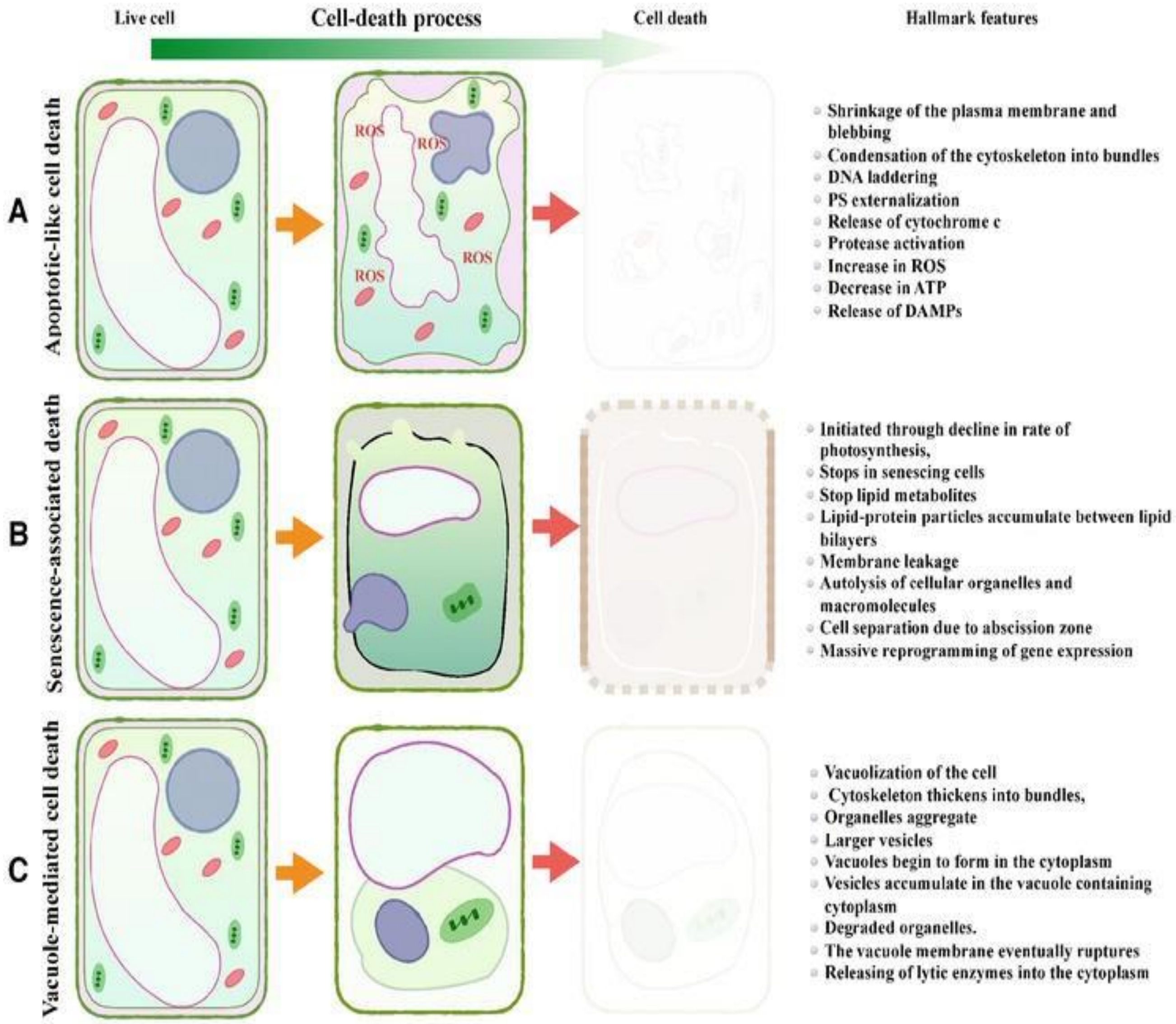

Figure 3. Morphological comparison, the hallmark features of types of cellular dysfunction in response to PCD (Mondal et al., 2021). (A) Apoptosis-like PCD mediated by shrinkage of the plasma membrane move away from the cell wall, membrane blebbing, condensation of the cytoskeleton into bundles, DNA laddering, PS externalization, cytochrome c release, protease activation, increase in ROS, decrease in ATP, the release of DAMPs. (B) Senescence-associated death initiated through the decline in the rate of photosynthesis, stops in senescing cells, stops lipid metabolites, lipid-protein particles accumulate between lipid bilayers, causing the membrane to become leaky. In the degenerative phase, autolysis of cellular organelles and macromolecules takes place. And in the terminal phase cell separation takes place at the abscission accumulation by massive reprogramming of gene expression. (C) Vacuole-mediated cell death or autophagic PCD can be characterized by vacuolization of the cell on a large scale. The cytoskeleton thickens into bundles, organelles aggregate, and larger vesicles and vacuoles begin to form in the cytoplasm. Vesicles accumulate in the vacuole containing cytoplasm and degraded organelles. The vacuole membrane eventually ruptures, releasing lytic enzymes into the cytoplasm and furthering cell death.

7.3. Physiological and Biochemical Characteristics of Plant PCD Types

Plant PCD can be categorized into different types based on their physiological and biochemical features:

1. **Apoptosis-like PCD**:
    - Physiological: Shrinkage of plasma membrane, membrane blebbing
    - Biochemical: DNA laddering, phosphatidylserine externalization, cytochrome c release, protease activation, ROS increase, ATP decrease
2. **Senescence-associated PCD**:
    - Physiological: Decline in photosynthesis rate, membrane leakage, cell separation at abscission zone
    - Biochemical: Lipid metabolite changes, accumulation of lipid-protein particles, massive gene expression reprogramming
3. **Vacuole-mediated (Autophagic) PCD**:
    - Physiological: Large-scale vacuolization, cytoskeleton thickening, organelle aggregation
    - Biochemical: Formation of vesicles containing degraded organelles, vacuole membrane rupture releasing lytic enzymes

7.4. Emerging Topics and Future Directions

Recent research has highlighted several exciting areas in plant PCD:

- **Autophagy and PCD**: The interplay between autophagy and apoptosis-like PCD in plants.
- **Epigenetic Regulation**: The role of histone modifications and DNA methylation in PCD regulation.
- **Small RNAs**: The involvement of miRNAs and siRNAs in modulating PCD-related gene expression.
- **Proteomics Approaches**: Large-scale identification of PCD-related proteins and their post-translational modifications.

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Part II.

Phenotypic Aspects of Plant Development

Course 8.

Embryogenesis and Body Plan Establishment in Plants

Plant embryogenesis is a critical stage in the plant life cycle, during which the single-celled zygote develops into a mature embryo with a basic body plan. This process involves a series of precisely coordinated cell divisions, cell fate specifications, and patterning events that lay the foundation for the future plant body.

8.1. Patterns of Embryo Development

Plant embryogenesis follows a relatively conserved pattern across species, with some variations. The model organism Arabidopsis thaliana has been extensively studied and serves as a reference for understanding this process.

8.1.1 Zygote Formation

The process begins with the fusion of male and female gametes during double fertilization:

- The egg cell fuses with one sperm cell to form the zygote.
- The central cell fuses with the other sperm cell to form the endosperm.

Molecular Regulation:

- The FERONIA receptor-like kinase is crucial for pollen tube reception and gamete fusion.
- The SHORT SUSPENSOR (SSP) gene is paternally contributed and activates YODA MAP kinase signaling in the zygote.

8.1.2 Asymmetric Cell Division

The zygote undergoes an asymmetric division, a critical step in establishing embryo polarity:

- The smaller apical cell will give rise to most of the embryo proper.
- The larger basal cell will form the suspensor and contribute to the root meristem.

Molecular Mechanisms:

- The WRKY2 transcription factor and WOX8/9 genes are involved in zygote polarization.
- The MAPKKK YODA pathway regulates this asymmetric division.

8.1.3 Embryo Patterning

Subsequent cell divisions and specifications lead to the formation of distinct embryonic structures:

1. **Octant Stage**: The apical cell undergoes three rounds of division, forming eight cells.
2. **Dermatogen Stage**: Tangential divisions separate the protoderm (future epidermis) from inner cells.
3. **Globular Stage**: Further divisions establish the ground tissue and vascular precursors.
4. **Heart Stage**: Cotyledon primordia emerge, and the shoot apical meristem is established.
5. **Torpedo Stage**: The embryo elongates, and organ systems continue to develop.

Key Regulators:

- The WUSCHEL-RELATED HOMEOBOX (WOX) gene family plays crucial roles in early patterning events.
- The PLETHORA (PLT) genes are essential for root meristem specification.

8.1.4 Embryo Axis Formation

The establishment of the embryonic axes is fundamental for proper body plan development:

- The apical-basal axis is initiated by the first asymmetric division of the zygote.
- The radial axis is established through the specification of concentric tissue layers.

- The shoot-root axis is defined by the positioning of the shoot and root apical meristems.

Molecular Control:

- Auxin gradients, established by PIN-FORMED (PIN) auxin efflux carriers, are crucial for axis formation.
- The MONOPTEROS (MP) and BODENLOS (BDL) genes mediate auxin responses in embryo patterning.

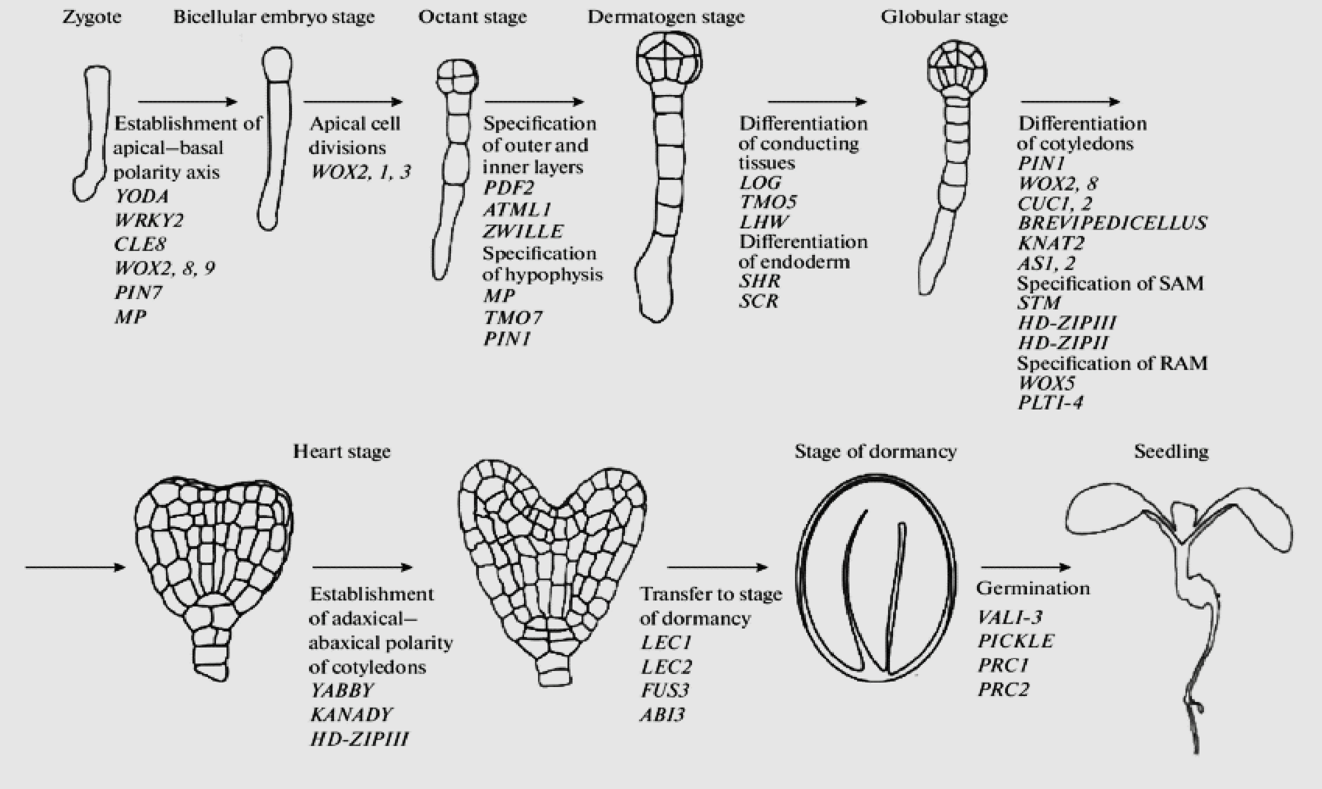

Figure 1. General pattern of embryonic development of Arabidopsis thaliana (Ten Hove et al., 2015). Main processes of differentiation of embryonic cells and genes involved in the processes are indicated under arrows. The stages of the embryo development (except the torpedo stage) are also specified.

8.2. Establishment of the Body Plan

The embryonic patterning events lay the foundation for the plant's overall body plan, which includes the primary root and shoot systems, and the organization of major tissue types.

8.2.1 Apical-Basal Patterning

The apical-basal axis is fundamental to the plant body plan:

- The apical domain gives rise to the shoot apical meristem and cotyledons.
- The central domain develops into the hypocotyl and embryonic root.
- The basal domain forms the root meristem and root cap.

Key Players:

- The HOBBIT gene is involved in root meristem formation and basal cell fate.
- The CUP-SHAPED COTYLEDON (CUC) genes define boundaries between cotyledons and the shoot meristem.

8.2.2 Radial Patterning

Radial patterning establishes the concentric tissue layers of the plant body:

- Protoderm: Gives rise to the epidermis.
- Ground tissue: Develops into cortex and endodermis.
- Vascular tissue: Forms the central stele (xylem and phloem).

Molecular Mechanisms:

- The SCARECROW (SCR) and SHORT-ROOT (SHR) genes are crucial for ground tissue patterning.
- The CLASS III HD-ZIP genes regulate vascular tissue development.

8.2.3 Dorsoventral Patterning

Dorsoventral patterning is particularly important for leaf and flower development:

- Establishes the adaxial (upper) and abaxial (lower) sides of lateral organs.
- Crucial for the formation of flat leaf blades and proper organ positioning.

Key Regulators:

- The PHABULOSA (PHB) and PHAVOLUTA (PHV) genes promote adaxial identity.
- The KANADI gene family promotes abaxial identity.

8.2.4 Meristem Establishment

The formation of apical meristems is critical for post-embryonic development:

- Shoot Apical Meristem (SAM): Responsible for above-ground organ formation.
- Root Apical Meristem (RAM): Drives root growth and development.

Molecular Control:

- The WUSCHEL (WUS) and CLAVATA (CLV) genes regulate SAM maintenance.
- The PLETHORA (PLT) and SHORTROOT (SHR) genes are crucial for RAM organization.

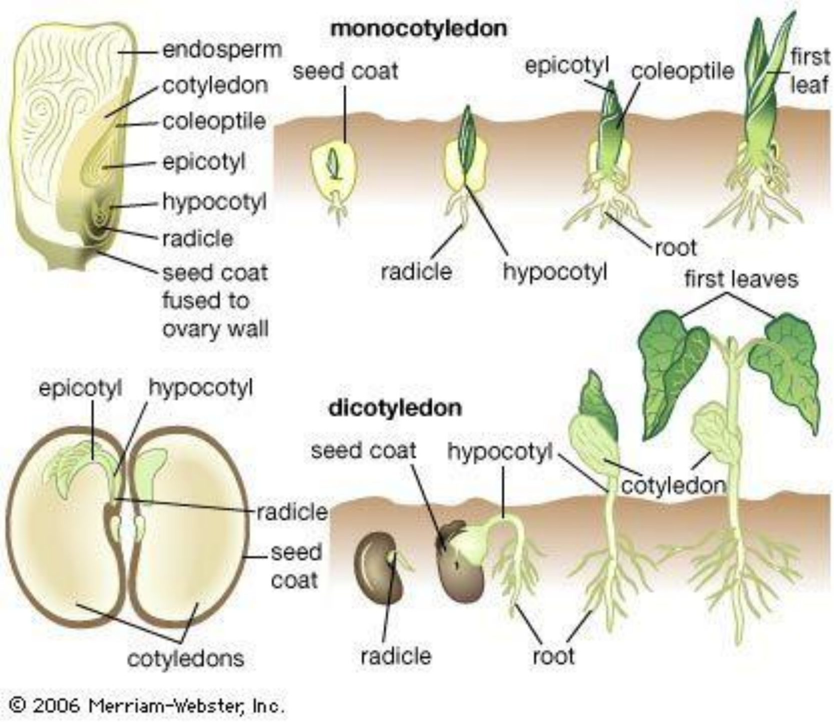

Figure 2. Establishment of the plant body plan during embryogenesis (https://www.britannica.com/science/germination)

8.3. Molecular Networks and Signaling Pathways

The precise coordination of embryo development and body plan establishment involves complex molecular networks:

8.3.1 Transcription Factor Networks

- The LEAFY COTYLEDON (LEC) genes are master regulators of embryo identity.
- The AINTEGUMENTA-LIKE (AIL) family regulates various aspects of embryo development.

8.3.2 Hormone Signaling

- Auxin: Crucial for embryo patterning and organ initiation.
- Cytokinin: Involved in cell division and meristem maintenance.

- Gibberellins: Regulate embryo growth and germination.

8.3.3 Small RNA Regulation

- microRNAs like miR165/166 regulate dorsoventral patterning.
- siRNAs are involved in epigenetic regulation during embryogenesis.

8.3.4 Epigenetic Mechanisms

- DNA methylation and histone modifications play roles in embryonic gene regulation.
- Chromatin remodeling factors like PICKLE (PKL) regulate embryonic identity genes.

8.4. Comparative Embryogenesis

While the basic patterns are conserved, there are notable variations in embryogenesis across plant species:

- Monocots (e.g., maize) have a distinct embryo morphology with a single cotyledon (scutellum).
- Some plants (e.g., orchids) have underdeveloped embryos and rely on mycorrhizal associations for early development.

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Course 9.

Seed and Fruit Development in Plants

Seed and fruit development are crucial processes in the plant life cycle, ensuring successful reproduction and species dispersal. These processes involve complex interactions between various tissues and are tightly regulated by genetic and hormonal factors.

9.1. Seed Structure and Composition

A mature seed is a complex structure composed of several distinct components, each playing a vital role in the seed's function and future plant development.

9.1.1 Embryo

The embryo is the product of fertilization and represents the future plant:

- **Structure**: Consists of the embryonic axis (radicle and plumule) and cotyledon(s).
- **Development**: Undergoes stages from globular to heart-shaped to mature embryo.

Molecular Regulation:

- LEAFY COTYLEDON (LEC) genes are master regulators of embryo identity and maturation.
- ABSCISIC ACID INSENSITIVE 3 (ABI3) controls the acquisition of desiccation tolerance.

9.1.2 Endosperm

The endosperm is a nutritive tissue that supports embryo development:

- **Types**: Nuclear, cellular, or helobial, depending on the pattern of cellularization.
- **Function**: Provides nutrients and growth regulators to the developing embryo.

Key Players:

- MINISEED3 (MINI3) and IKU2 regulate endosperm proliferation and seed size.
- DNA methylation, regulated by MET1 and DME, controls endosperm development through genomic imprinting.

9.1.3 Seed Coat

The seed coat, derived from ovule integuments, plays protective and regulatory roles:

- **Layers**: Typically consists of multiple cell layers with specialized functions.
- **Functions**: Protection, water regulation, and control of dormancy/germination.

Molecular Mechanisms:

- TRANSPARENT TESTA (TT) genes regulate flavonoid biosynthesis in the seed coat.
- The MADS-box gene TRANSPARENT TESTA 16 (TT16) controls proper seed coat development.

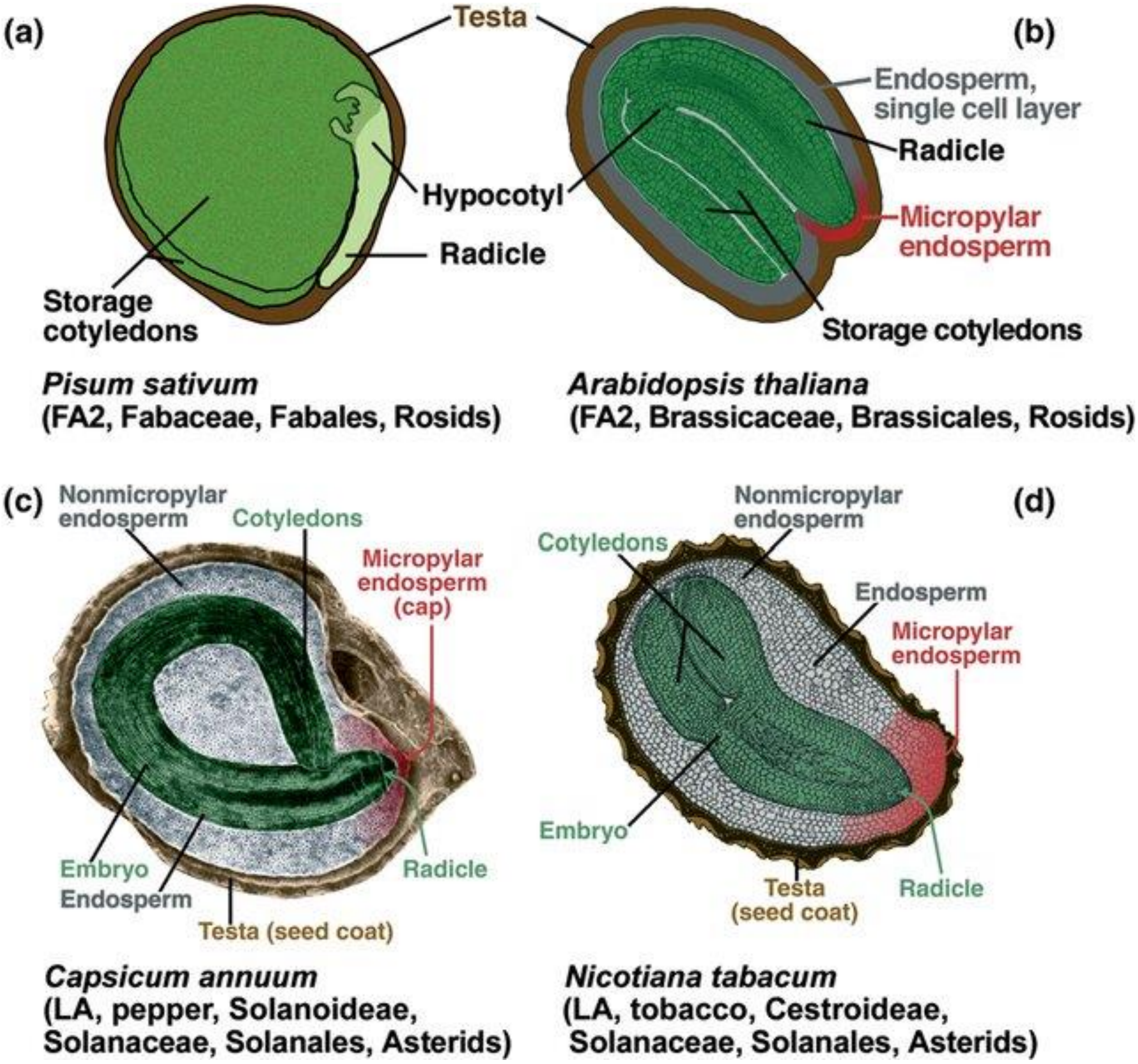
9.1.4 Seed Composition

Seeds store various compounds to support early seedling growth:

1. **Carbohydrates**: Mainly starch, stored in amyloplasts.
2. **Proteins**: Stored in protein bodies, often as specialized storage proteins.
3. **Lipids**: Stored as oil bodies, particularly abundant in oilseeds.

Regulation of Storage Compound Synthesis:

- WRINKLED1 (WRI1) transcription factor regulates fatty acid biosynthesis.
- The ABI3-FUSCA3-LEC2 network controls the accumulation of storage compounds.



Pisum sativum
(FA2, Fabaceae, Fabales, Rosids)

Arabidopsis thaliana
(FA2, Brassicaceae, Brassicales, Rosids)

Capsicum annuum
(LA, pepper, Solanoideae, Solanaceae, Solanales, Asterids)

Nicotiana tabacum
(LA, tobacco, Cestroideae, Solanaceae, Solanales, Asterids)

Figure 1. Biodiversity of the structure of mature seeds of angiosperms and the importance of the seed-covering layers (Finch-Savage and Leubner-Metzger, 2006).

The diploid embryo is surrounded by two covering layers: the triploid (in most species) endosperm (nutritive tissue; mostly living cells) and the diploid testa (seed coat; maternal tissue; mostly dead cells). In several species the endosperm is completely obliterated during seed development and the nutrients are translocated to storage cotyledons. Mature seeds of (a) pea (Pisum sativum) (without endosperm) and (b) Arabidopsis thaliana (single cell layer of endosperm) are characterized by embryos with storage cotyledons. The micropylar endosperm (several cell layers) is known to be a germination constraint of Solanaceae seeds (c, d). FA2 and LA are seed types. Part (c) is modified from Watkins & Cantliffe (1983) and reprinted with permission from the American Society of Plant Biologists. Parts (a), (b) and (d) are modified from 'The Seed Biology Place' (http://www.seedbiology.de).

9.2. Fruit Development and Ripening

Fruit development is a complex process that involves the transformation of the flower ovary into a mature fruit.

9.2.1 Fruit Set

Fruit set is the initial stage of fruit development following fertilization:

- **Pollination and Fertilization**: Triggers hormonal changes initiating fruit development.
- **Parthenocarpy**: Some fruits can develop without fertilization, either naturally or through genetic manipulation.

Molecular Control:

- Auxin and gibberellin signaling pathways play crucial roles in fruit set.
- The AUXIN RESPONSE FACTOR 8 (ARF8) gene regulates fruit initiation.

9.2.2 Fruit Growth

Fruit growth involves rapid cell division and expansion:

- **Cell Division Phase**: Characterized by intensive mitotic activity.
- **Cell Expansion Phase**: Cells enlarge, often accompanied by endoreduplication.

Key Regulators:

- FRUIT WEIGHT 2.2 (FW2.2) controls fruit size by regulating cell division.
- EXPANSIN proteins are involved in cell wall loosening during fruit growth.

9.2.3 Fruit Ripening

Ripening involves complex biochemical and physiological changes:

1. **Softening**: Cell wall degradation through the action of various enzymes.
2. **Color Changes**: Chlorophyll degradation and synthesis of new pigments.
3. **Flavor Development**: Accumulation of sugars and volatile compounds.
4. **Nutritional Changes**: Alterations in vitamin content and antioxidant levels.

Molecular Mechanisms:

- Ethylene biosynthesis and signaling are central to climacteric fruit ripening.

- The MADS-box transcription factor RIPENING INHIBITOR (RIN) is a master regulator of ripening in tomato.
- NON-RIPENING (NOR) and COLORLESS NON-RIPENING (CNR) genes also play crucial roles in the ripening process.

9.2.4 Hormonal Regulation of Fruit Development

Multiple hormones interact to control fruit development and ripening:

- **Auxins**: Promote fruit set and early growth.
- **Gibberellins**: Stimulate fruit set and cell expansion.
- **Cytokinins**: Regulate cell division and seed development.
- **Abscisic Acid**: Involved in seed maturation and stress responses.
- **Ethylene**: Key regulator of ripening in climacteric fruits.

Crosstalk and Integration:

- The DELLA proteins integrate multiple hormone signals during fruit development.
- Ethylene-auxin crosstalk fine-tunes the ripening process.

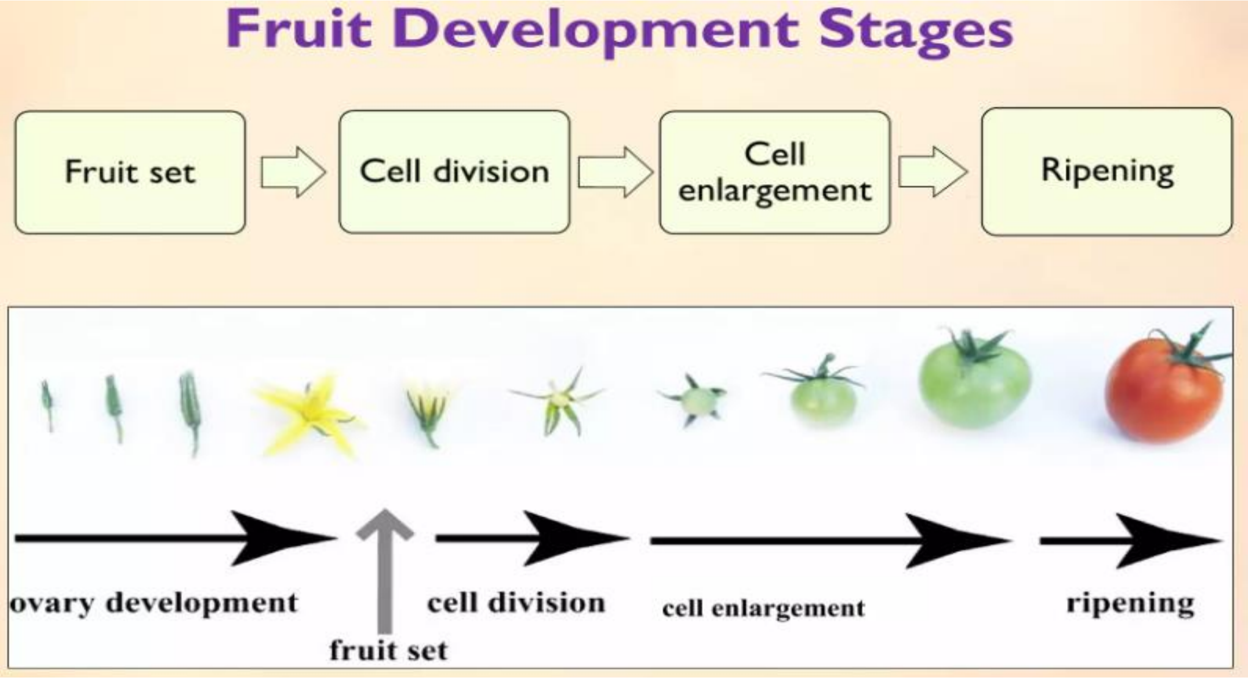


Figure 2. Stages of fruit development and ripening (https://fr.slideshare.net/slideshow/fruit-set-growth-developmental-stages-of-various-fruits/144113196).

9.3. Molecular Networks in Seed and Fruit Development

Complex genetic networks underlie seed and fruit development processes:

9.3.1 Transcription Factor Networks

- The NAC family transcription factors regulate various aspects of seed and fruit development.
- APETALA2 (AP2)-like factors control seed size and fruit ripening.

9.3.2 Epigenetic Regulation

- DNA methylation patterns change during seed development and fruit ripening.
- Histone modifications play roles in regulating seed maturation genes.

9.3.3 Small RNA Regulation

- miRNAs like miR156 and miR172 are involved in fruit development.
- siRNAs contribute to the regulation of seed size through genomic imprinting.

9.4. Environmental Influences on Seed and Fruit Development

Various environmental factors can impact seed and fruit development:

- **Temperature**: Affects the rate of development and the accumulation of storage compounds.
- **Water Availability**: Influences fruit growth and seed filling.
- **Light**: Impacts fruit pigmentation and nutritional quality.
- **Nutrients**: Mineral availability affects seed composition and fruit quality.

9.5. Biotechnological Applications

Understanding seed and fruit development has led to various biotechnological applications:

- Genetic engineering for improved seed composition (e.g., Golden Rice).
- Manipulation of fruit ripening for extended shelf life (e.g., FLAVR SAVR tomato).
- Enhancement of fruit nutritional quality through biofortification.
- Development of seedless fruits through parthenocarpy induction.

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Course 10.

Vegetative Development of Plants

Vegetative development in plants encompasses the growth and patterning of leaves, stems, and roots. This process is driven by the activity of specialized meristems and involves the integration of various genetic, hormonal, and environmental signals.

10.1. Shoot and Root Meristem Activities

The shoot and root apical meristems are the primary sites of continuous growth and organ initiation in plants. These meristems contain populations of undifferentiated, actively dividing cells that give rise to all aboveground and belowground organs, respectively.

10.1.1 Shoot Apical Meristem (SAM)

The SAM is responsible for the initiation and patterning of leaves, stems, and lateral shoots.

Structure and Organization:

- Central Zone (CZ): Contains slowly dividing stem cells
- Peripheral Zone (PZ): Site of organ initiation
- Rib Zone (RZ): Contributes to stem growth

Molecular Regulation:

- WUSCHEL (WUS) - CLAVATA (CLV) feedback loop maintains stem cell population:
    - WUS promotes stem cell identity
    - CLV3 peptide, produced by stem cells, restricts WUS expression
- SHOOTMERISTEMLESS (STM) prevents differentiation in the meristem
- KNOX genes maintain meristem indeterminacy

Hormonal Control:

- Cytokinin promotes cell division and WUS expression
- Auxin accumulation at the PZ triggers organ initiation

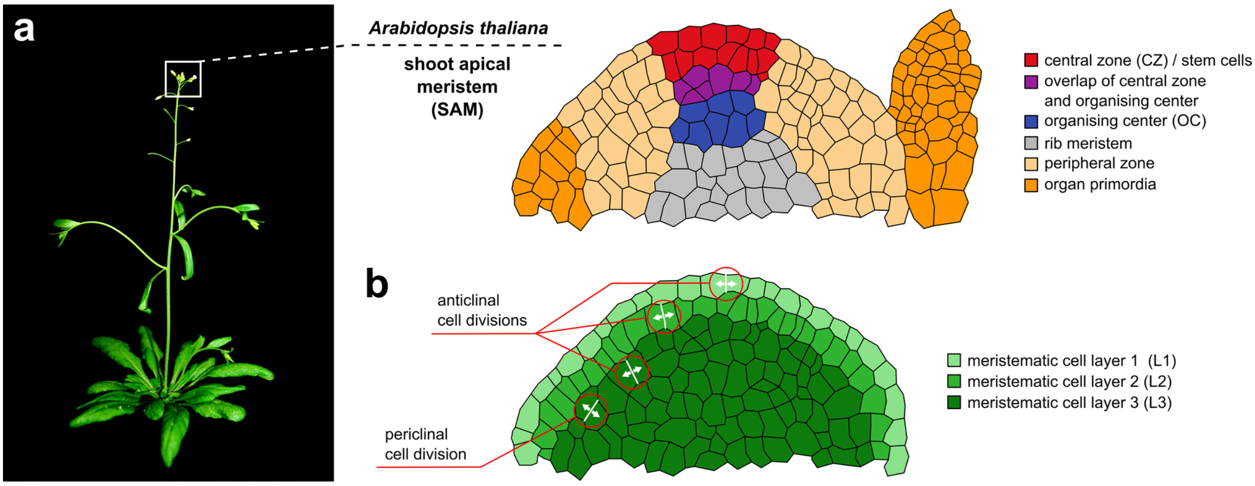

Figure 1. The shoot apical meristem of Arabidopsis thaliana (Fuchs and Lohmann, 2020). a Schematic representation of the shoot apical meristem (SAM) at the tip of the Arabidopsis shoot and of functional domains within the SAM. b Schematic representation of clonally distinct cell layers in the SAM. L1 and L2 originate from anticlinal cell divisions while cells in the L3 arise from anticlinal and periclinal divisions.

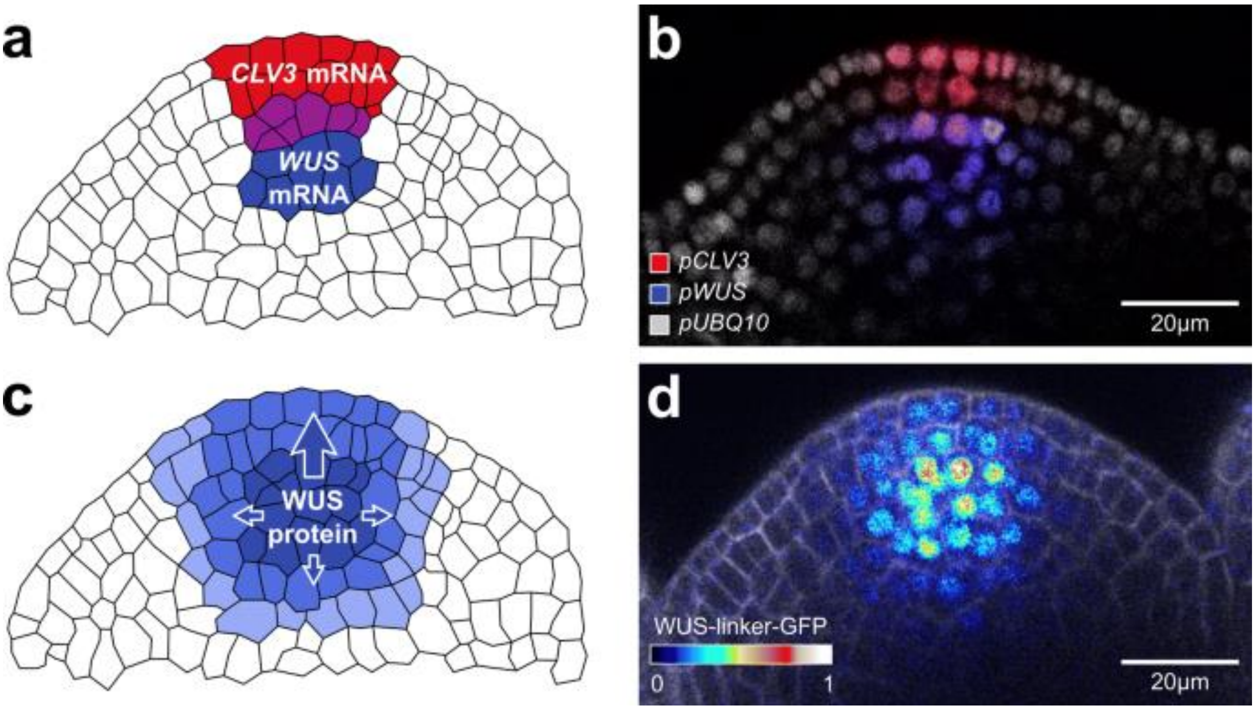

Figure 2. Localisation of key stem cell regulators in the SAM (Fuchs and Lohmann, 2020). **a** Schematic representation of the *CLV3* (red) and *WUS* (blue) mRNA expression domains. Note the overlap in the L3 (purple). **b** Confocal slice through the center of a *pCLV3* (red), *pWUS* (blue), *pUBQ10* (gray) triple reporter SAM. **c** Schematic representation of WUS protein localisation (intensity coded in blue). **d** Confocal slice through the center of a *pWUS::WUS-linker-GFP* rescue SAM. GFP was colour coded on a linear scale.

10.1.2 Root Apical Meristem (RAM)

The RAM drives the continuous growth and branching of the root system.

Structure and Organization:

- Quiescent Center (QC): Acts as an organizing center
- Surrounding stem cells: Give rise to different root tissues
- Proximal meristem: Zone of active cell division

Molecular Regulation:

- PLETHORA (PLT) genes form a gradient specifying stem cell niche
- SHORTROOT (SHR) and SCARECROW (SCR) regulate radial patterning
- WOX5 (WUSCHEL-RELATED HOMEOBOX 5) maintains QC identity

Hormonal Control:

- Auxin maximum at the QC is crucial for RAM organization
- Cytokinin antagonizes auxin to control the transition from cell division to differentiation

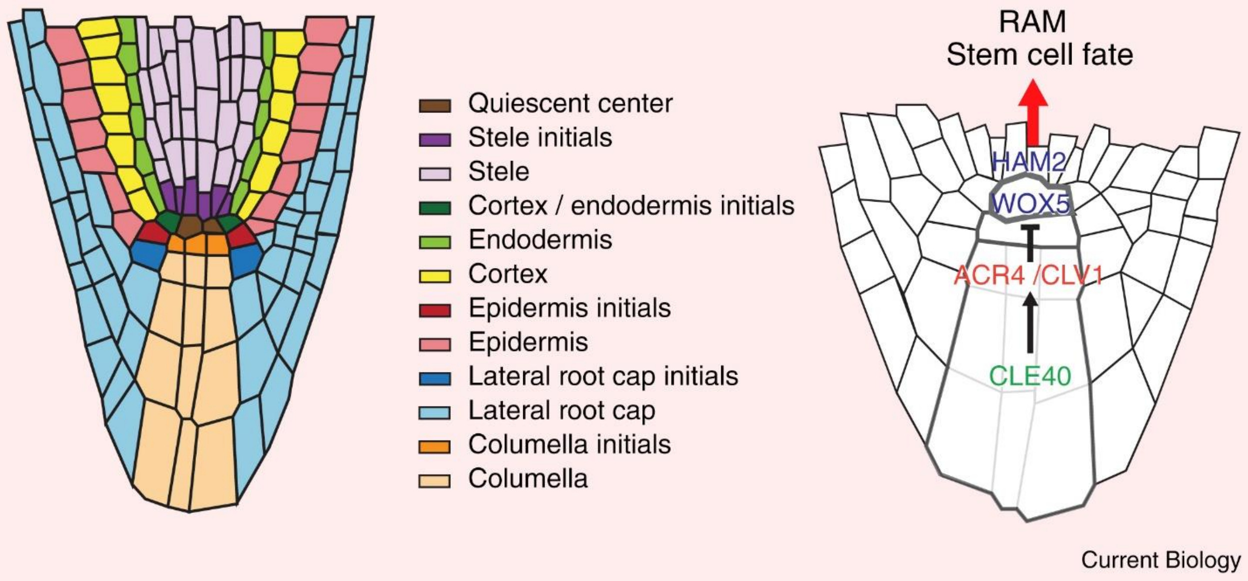

Figure 3. The root apical meristem (RAM) (Greb and Lohmann, 2016). A schematic outline of cell types found in the RAM is shown on the left, and the representation of one of the central regulatory loop maintaining RAM activity is shown on the right. Figure modified from Gaillochet and Lohmann (2015).

10.2. Organ Initiation and Growth

The initiation and subsequent growth of plant organs involve the coordination of cell division, expansion, and differentiation processes.

10.2.1 Leaf Development

Leaves are initiated at the flanks of the SAM and undergo complex patterning processes.

Initiation and Early Patterning:

- Auxin maxima specify sites of leaf primordium initiation
- ASYMMETRIC LEAVES1 (AS1) and AS2 genes promote leaf fate and repress KNOX genes
- Adaxial-abaxial polarity established by:
  - HD-ZIP III genes (PHB, PHV, REV) promote adaxial identity
  - KANADI and YABBY genes promote abaxial identity

Leaf Growth and Morphogenesis:

- GROWTH-REGULATING FACTOR (GRF) and GRF-INTERACTING FACTOR (GIF) promote cell proliferation
- TCP genes control leaf shape and curvature
- ANGUSTIFOLIA (AN) and ROTUNDIFOLIA3 (ROT3) regulate cell expansion

Vascular Patterning:

- MONOPTEROS (MP) and ATHB8 are key regulators of vascular development
- miR166-mediated regulation of HD-ZIP III genes influences vein patterning

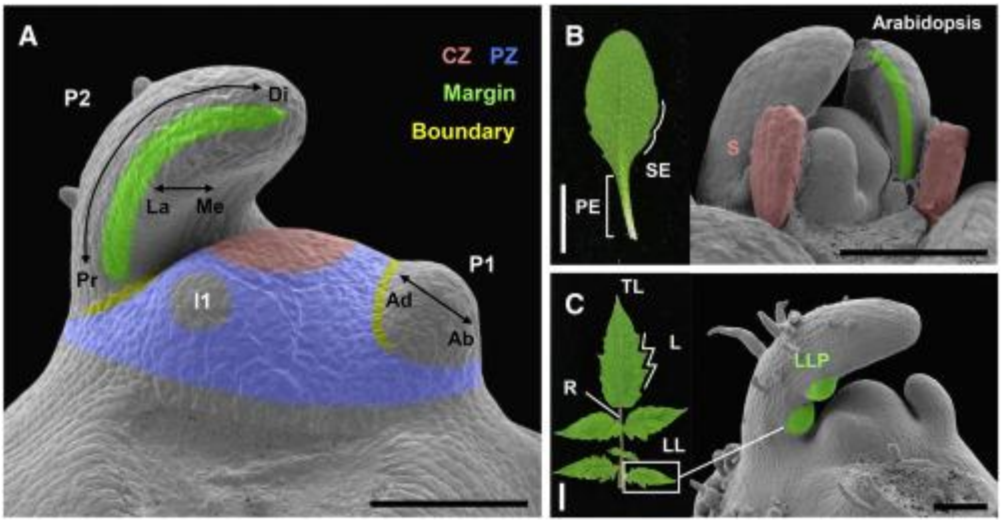

Figure 4. Morphology of Simple and Compound Leaves (Du et al., 2018).

(A) The organization of the shoot apex of tomato. Leaf primordia initiate from the peripheral zone (PZ), which surrounds the central zone (CZ) of the shoot apical meristem (SAM). The oldest incipient primordium (I1) marks the future initiation site, which cannot be distinguished in appearance from the SAM at this stage. Primordia are named according to the order of initiation; the youngest primordium that proliferates from the SAM is designated P1, the second youngest is P2, etc. A boundary forms following primordia initiation; this boundary separates the SAM and lateral organs. Leaf asymmetries are established in three axes marked by arrows: adaxial–abaxial axis (Ad–Ab), proximal–distal axis (Pr–Di), and medio—lateral axis (Me–La). The margin, covering the juxtaposition of the adaxial and abaxial leaf domains, initiates leaf blade outgrowth.
(B) Morphology of a simple leaf from *Arabidopsis*. Left: the mature rosette leaf displays serrations (SE) along the leaf margins and a petiole (PE) at the leaf base. Right: stipules (S) are generated beside young leaf primordia. Note that the leaf margins (green) of simple leaves are continuous.
(C) Morphology of a compound leaf from tomato. Left: the compound leaf is composed of a terminal leaflet (TL) and several lateral leaflets (LL) attached to a central rachis (R). Lobes (L) can be found in the margins of leaflets. Right: the lateral leaflet develops from the lateral leaflet primordium (LLP) along the discontinuous leaf margins.
Black scale bars, 100 µm. White scale bars, 1 cm.

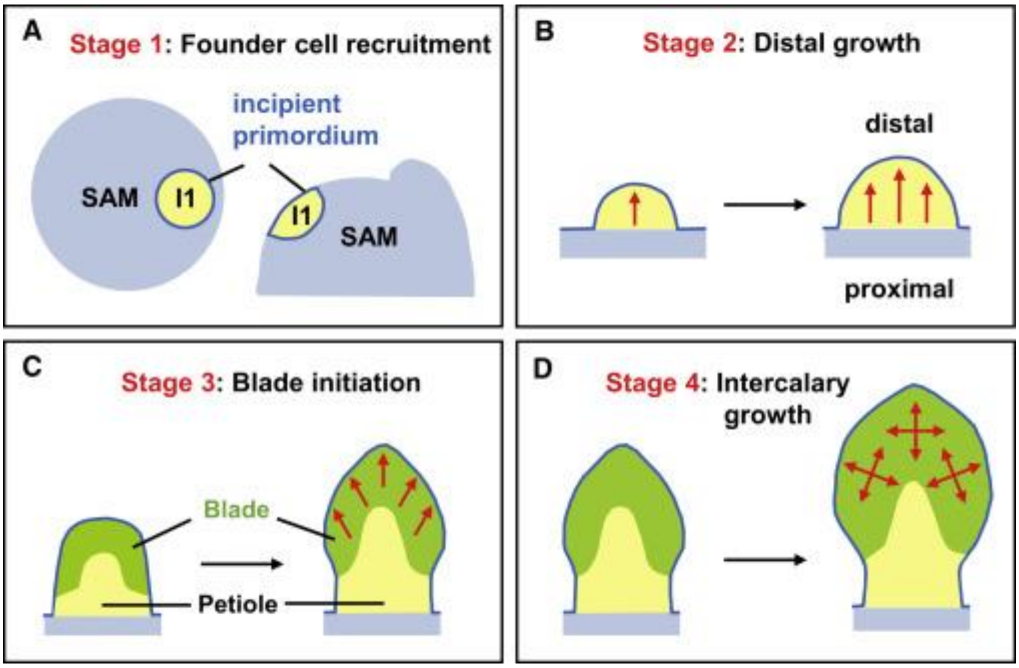

Figure 5. Schematic Illustration of Leaf Morphogenesis in Eudicots (Du et al., 2018).

(A) The founder cells are recruited from the peripheral zone of the SAM at the site of the incipient leaf primordium before initiation. I1: the oldest incipient leaf primordium. Left, top view; right, front view.
(B) Immediately following initiation, the leaf primordium grows predominantly in the distal direction.
(C) Subsequently, the blade and petiole regions are specified, and leaf growth and expansion occur largely at the margins during this stage.
(D) Finally, along with the termination of marginal meristem activity, cell proliferation and expansion occur in the entire blade, which leads to both distal and lateral leaf expansion.
Modified from Nakata and Okada (2013).

10.2.2 Stem Development

Stems are initiated from the SAM and undergo primary and secondary growth.

Primary Growth:

- Controlled by the activity of the apical and intercalary meristems
- DELLA proteins integrate multiple hormone signals to regulate stem elongation
- Gibberellins promote internode elongation by stimulating cell division and expansion

Secondary Growth:

- Vascular cambium produces secondary xylem (wood) and phloem
- VASCULAR-RELATED NAC-DOMAIN (VND) genes regulate xylem differentiation
- WUSCHEL-RELATED HOMEOBOX 4 (WOX4) maintains vascular cambium activity

Branching:

- Regulated by the activity of axillary meristems
- Strigolactones inhibit axillary bud outgrowth
- BRANCHED1 (BRC1) integrates multiple signals to control bud dormancy

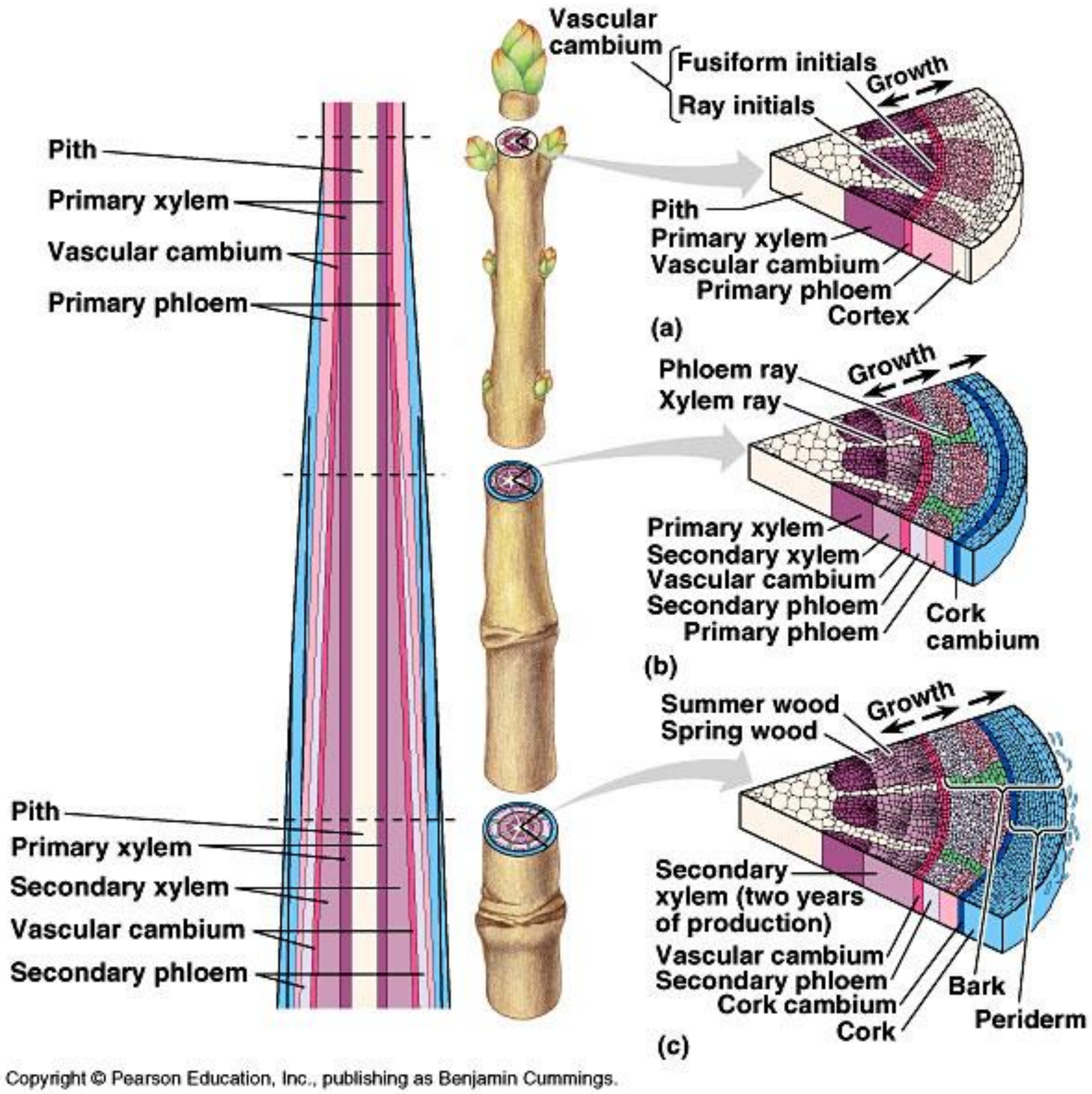

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Figure 6. Diagrammatic representations of meristems in plat body and their gradual differentiation in L.S. with corresponding transverse views in T.S. (https://adindart.wordpress.com/2011/09/28/pertanyaan-mengamati-struktur-akar-batang-dan-daun/).

10.2.3 Root Development

Root growth is driven by the RAM and involves complex interactions with the environment.

Primary Root Growth:

- Controlled by the balance between cell division in the meristem and cell elongation/differentiation

- UPBEAT1 transcription factor regulates the transition from proliferation to differentiation
- ROOT MERISTEM GROWTH FACTOR (RGF) peptides maintain root stem cell niche

Lateral Root Formation:

- Initiated from pericycle cells adjacent to xylem poles
- Auxin accumulation triggers lateral root founder cell specification
- LATERAL ORGAN BOUNDARIES-DOMAIN (LBD) genes are key regulators of lateral root formation

Root System Architecture:

- Highly plastic, responsive to environmental cues
- Phosphate starvation induces changes in root architecture through PHR1 transcription factor
- Nitrate availability modulates lateral root development via NRT1.1 transporter/sensor

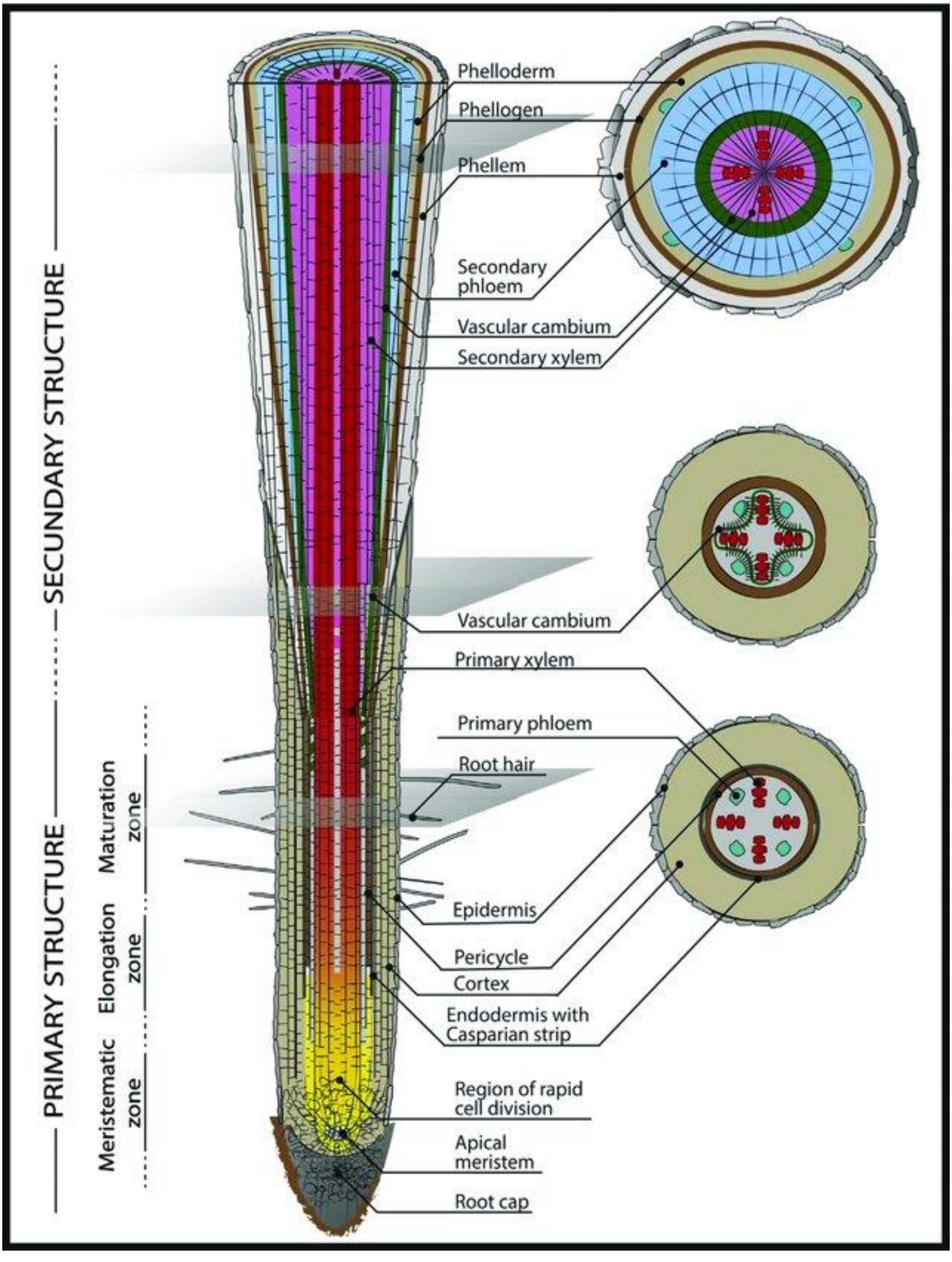

Figure 7. Longitudinal and transverse section of a terminal root (Centenaro et al., 2018).

10.3. Integration of Developmental Signals

Vegetative development involves the integration of multiple signaling pathways:

10.3.1 Hormone Crosstalk

- Auxin-cytokinin antagonism regulates meristem size and organ initiation
- Gibberellin-brassinosteroid synergy promotes stem elongation
- Strigolactone-auxin interactions control branching

10.3.2 Environmental Responses

- Phytochromes and cryptochromes mediate light responses affecting plant architecture
- DELLA proteins integrate environmental signals with GA responses
- ERECTA family receptor-like kinases modulate plant architecture in response to environmental cues

10.3.3 Nutrient Sensing

- TARGET OF RAPAMYCIN (TOR) kinase integrates nutrient status with growth signals
- NITRATE REGULATED1 (NLP7) transcription factor coordinates nitrogen responses with developmental programs

10.4. Biotechnological Applications

Understanding vegetative development has led to various applications:

- Manipulation of plant architecture for improved crop yield (e.g., semi-dwarf wheat varieties)
- Engineering of root system architecture for enhanced nutrient uptake and drought resistance
- Modification of leaf shape and arrangement for optimized light capture and photosynthetic efficiency
- Control of branching patterns for improved fruit production in horticultural crops

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Course 11.

Flowering and Floral Development in Plants

The transition from vegetative growth to reproductive development is a crucial event in the life cycle of flowering plants (angiosperms). This process, known as the floral transition, involves complex molecular mechanisms and is regulated by various environmental and endogenous factors. Understanding these mechanisms is essential for biodiversity conservation and crop improvement.

11.1 Molecular Mechanisms of Floral Transition

11.1.1 The FLOWERING LOCUS T (FT) Pathway

The FT protein, often referred to as "florigen," plays a central role in the floral transition:

1. **FT gene expression**: In Arabidopsis thaliana, the FT gene is expressed in leaf vasculature in response to inductive photoperiods.
2. **Protein transport**: The FT protein moves through the phloem to the shoot apical meristem (SAM).
3. **Interaction with bZIP transcription factor FD**: At the SAM, FT interacts with FD to form a complex.
4. **Activation of floral meristem identity genes**: The FT-FD complex activates genes such as APETALA1 (AP1) and LEAFY (LFY), which initiate the floral program.

11.1.2 The CONSTANS (CO) Pathway

CO is a key regulator of photoperiodic flowering:

1. **Circadian regulation**: CO expression is regulated by the circadian clock.
2. **Protein stabilization**: Under long-day conditions, CO protein is stabilized by light.
3. **FT activation**: Stabilized CO protein directly activates FT transcription.

11.1.3 Vernalization Pathway

Some plants require a period of cold exposure to flower:

1. **FLOWERING LOCUS C (FLC) repression**: FLC, a potent repressor of flowering, is epigenetically silenced during cold exposure.
2. **Histone modifications**: Vernalization involves repressive histone modifications at the FLC locus, including H3K27me3 deposition.
3. **VERNALIZATION INSENSITIVE 3 (VIN3)**: This gene is induced by cold and is crucial for initiating FLC silencing.

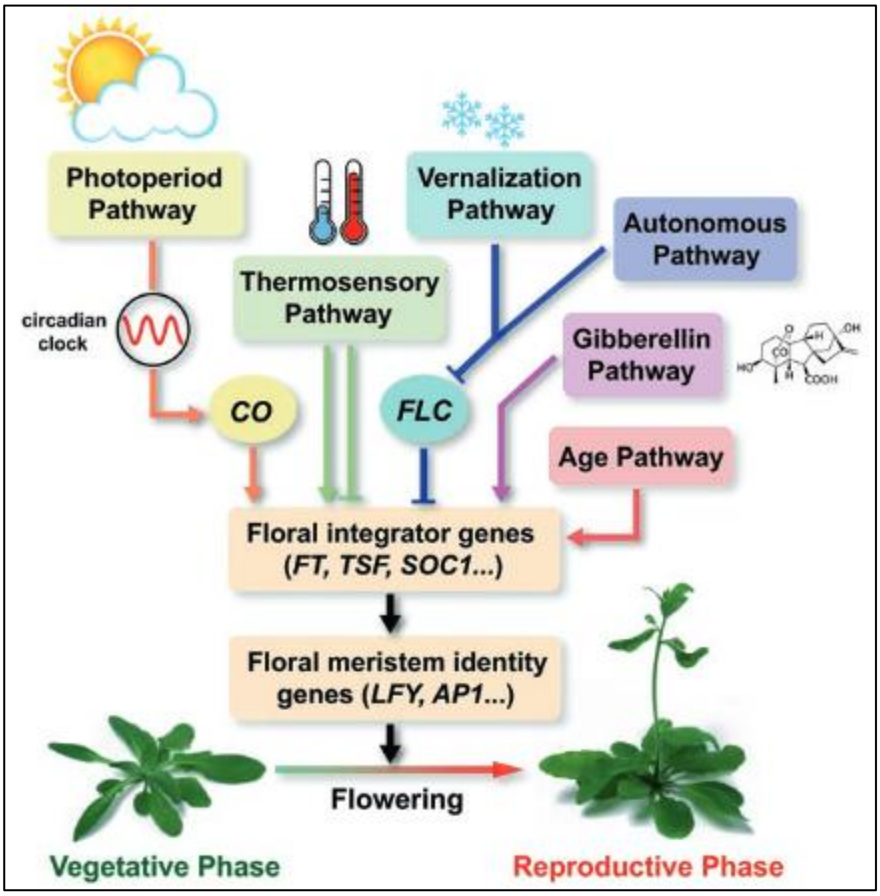


Figure 1A. Simplified genetic pathways that control flowering time in Arabidopsis (Wang et al., 2019). Six major genetic pathways that control flowering time have been characterized in Arabidopsis. The photoperiod, vernalization, and thermosensory pathways act in response to day length, winter temperature, and ambient temperature change, respectively, while the autonomous gibberellin (GA) and age pathways respond more to endogenous stimuli rather than environmental cues.

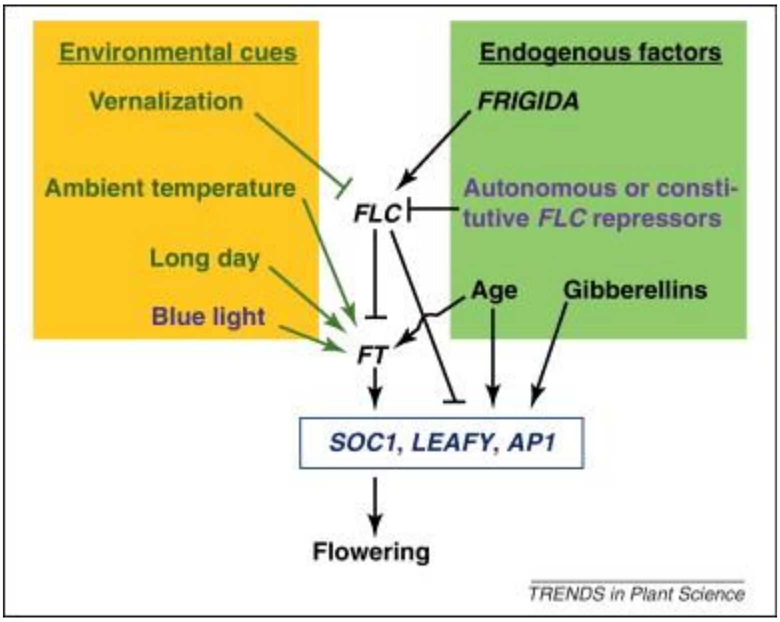


Figure 1B. Floral transition network in *Arabidopsis* (Chen and Li, 2022).). The main floral repressor *FLC* is activated by FRI supercomplex and this activation is counteracted by the autonomous pathway. FLC reduces the expression of the florigen *FT*, which is upregulated by the photoperiod pathway. FT initiates the floral-meristem identity genes *AP1* and *LFY* for flowering at proper conditions. In addition, ambient temperature, aging and gibberellin pathways modulate floral transition indirectly through *FT* or its downstream targets *AP1* and *LFY*. Arrows and bars indicate gene activation and repression, respectively, whereas, the solid and dotted lines represent for direct and indirect gene regulation.

11.2 Floral Meristem Identity and Organ Specification

11.2.1 ABCE Model of Floral Organ Identity

The ABCE model explains how floral organ identities are specified:

1. **A-function genes** (e.g., AP1, AP2): Specify sepals and contribute to petal identity.
2. **B-function genes** (e.g., AP3, PISTILLATA): Specify petals and stamens.
3. **C-function gene** (AGAMOUS): Specifies stamens and carpels.
4. **E-function genes** (SEPALLATA1-4): Act redundantly to specify all floral organs.

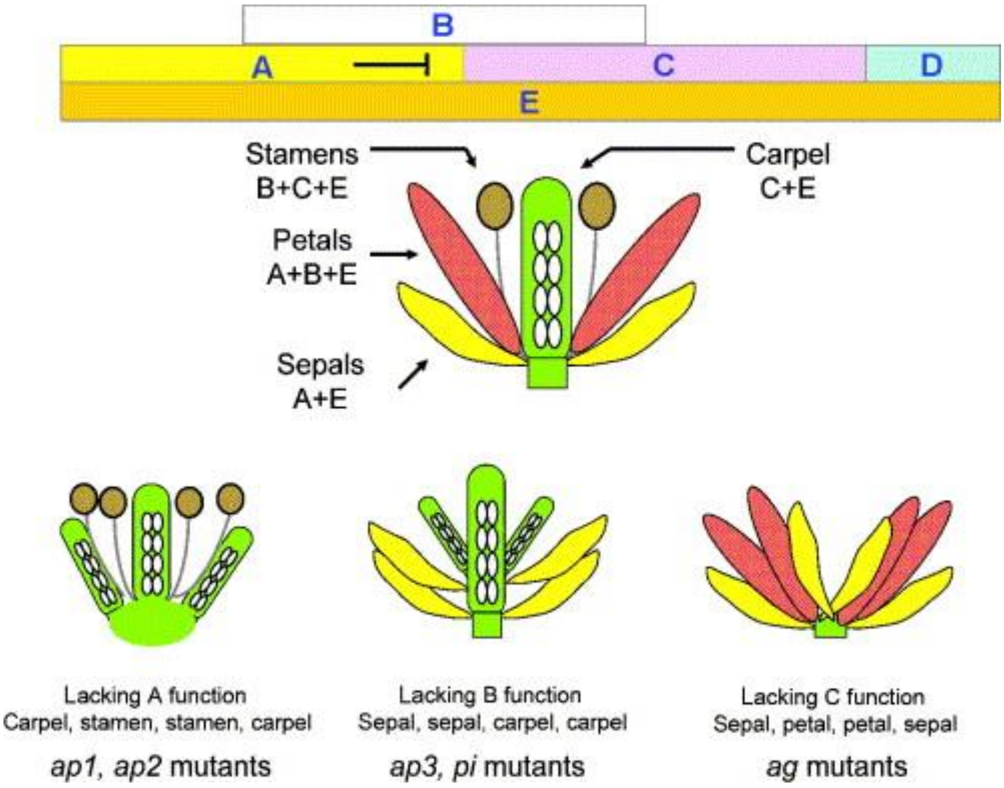
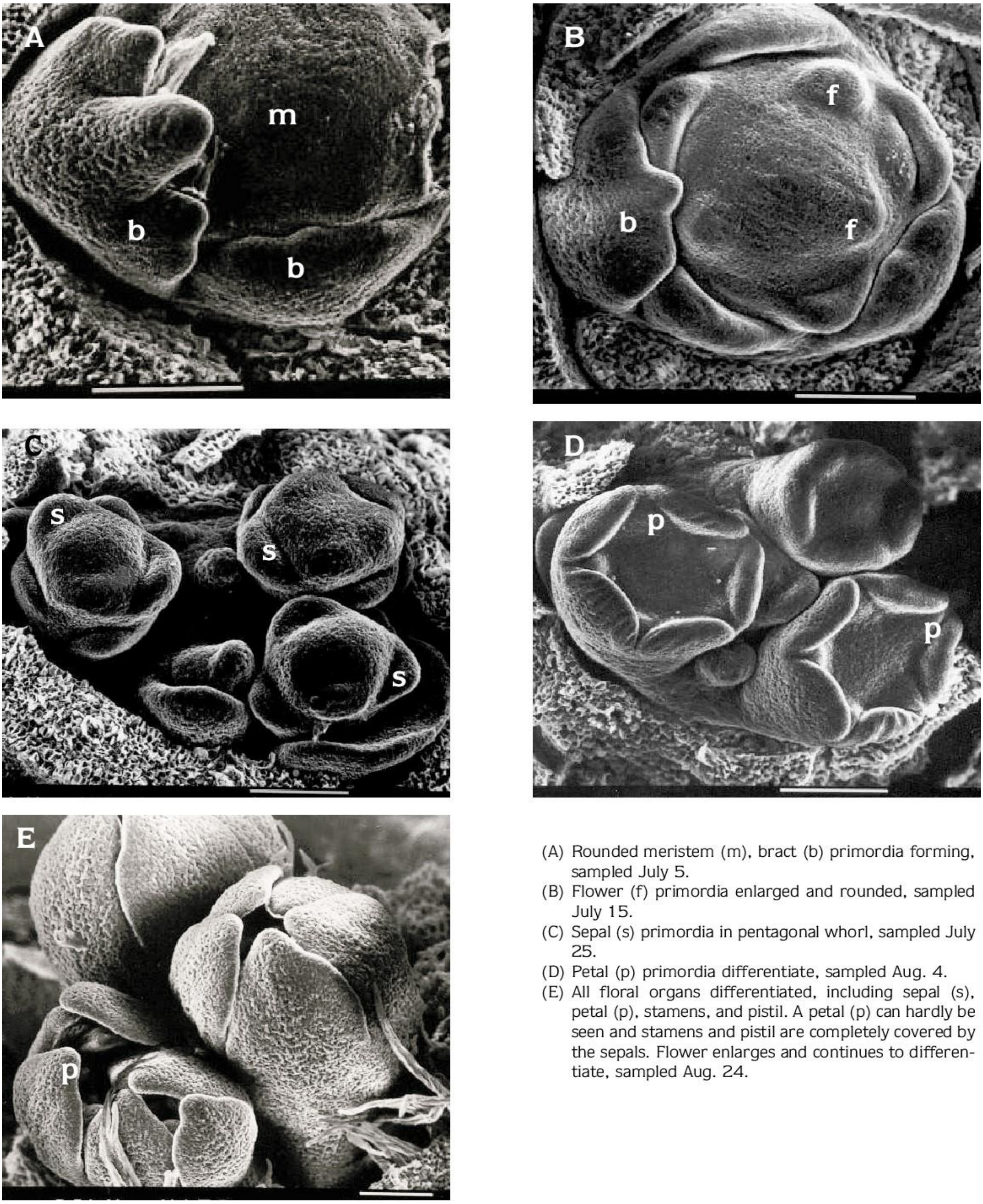


Figure 2. Beyond the ABC-model: regulation of floral homeotic genes (Zahn et al., 2006).



(A) Rounded meristem (m), bract (b) primordia forming, sampled July 5.
(B) Flower (f) primordia enlarged and rounded, sampled July 15.
(C) Sepal (s) primordia in pentagonal whorl, sampled July 25.
(D) Petal (p) primordia differentiate, sampled Aug. 4.
(E) All floral organs differentiated, including sepal (s), petal (p), stamens, and pistil. A petal (p) can hardly be seen and stamens and pistil are completely covered by the sepals. Flower enlarges and continues to differentiate, sampled Aug. 24.

Figure 3. SEM micrographs of 0900 Ziraat sweet cherry buds, showing developmental changes from initiation to differentiation. Bar = 100 µm. (ENGiN and Uenal, 2007).

11.2.2 Molecular Mechanisms of Floral Organ Development

1. **Protein interactions**: ABCE proteins form higher-order complexes to regulate target genes.
2. **Chromatin remodeling**: These complexes recruit chromatin modifiers to alter gene expression patterns.
3. **Downstream targets**: Include genes involved in cell division, expansion, and differentiation specific to each organ type.

11.3 Hormonal Regulation of Flowering

11.3.1 Gibberellins (GAs)

1. **Promotion of flowering**: GAs promote flowering, especially under non-inductive conditions.
2. **DELLA protein degradation**: GAs trigger the degradation of DELLA proteins, which are repressors of flowering.
3. **Interaction with other pathways**: GAs can promote flowering by activating genes like LEAFY and SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1).

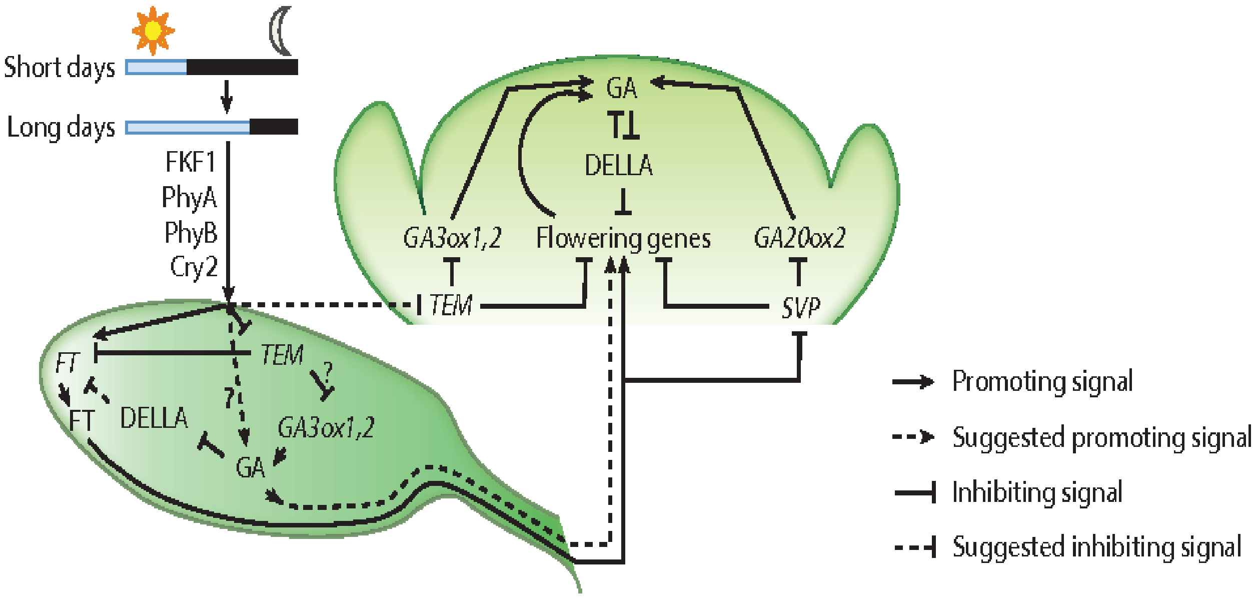


Figure 4. Gibberellic acid (GA) regulation during photoperiodic flowering (De Wit et al., 2016).

11.3.2 Auxin

1. **Floral primordium initiation**: Auxin maxima are crucial for the initiation of floral primordia.
2. **PIN1-mediated transport**: The auxin efflux carrier PIN1 is essential for establishing auxin maxima.
3. **Organ positioning**: Auxin gradients contribute to the proper positioning of floral organs.

11.4 Environmental Regulation of Flowering

11.4.1 Photoperiod

1. **Phytochrome and cryptochrome photoreceptors**: These proteins perceive day length and quality of light.
2. **Entrainment of circadian clock**: Light signals entrain the circadian clock, which regulates CO expression.
3. **Regulation of FT expression**: In long-day plants, FT expression peaks at the end of the long day, triggering flowering.

11.4.2 Ambient Temperature

1. **Thermosensory pathway**: Involves genes like PHYTOCHROME INTERACTING FACTOR 4 (PIF4) and FLOWERING LOCUS M (FLM).
2. **Alternative splicing**: Temperature changes can affect the splicing of key flowering regulators, altering their function.

11.5 Evolutionary Aspects of Flowering

1. **Conservation of key regulators**: Many flowering genes are conserved across angiosperms, suggesting a common evolutionary origin.
2. **Diversification of regulation**: Despite conservation, regulatory networks have diversified to adapt to different ecological niches.
3. **Genome duplications**: Whole genome duplications have contributed to the diversification of flowering pathways in many plant lineages.

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Course 12.

Self-Incompatibility in Plants

Self-incompatibility (SI) is a sophisticated genetic mechanism evolved by many flowering plants to prevent self-fertilization and promote genetic diversity through outcrossing. This process involves intricate molecular recognition systems, complex signaling cascades, and cellular responses that collectively prevent the growth of self-pollen tubes, thereby inhibiting self-fertilization.

12.1. Types of Self-Incompatibility Systems

There are two main types of SI systems in plants:

12.1.1. Gametophytic Self-Incompatibility (GSI)

- The incompatibility phenotype of the pollen is determined by its own haploid genotype.
- Examples: Solanaceae (e.g., tomato, potato), Rosaceae (e.g., apple, pear), Papaveraceae (e.g., poppy)

12.1.2. Sporophytic Self-Incompatibility (SSI)

- The incompatibility phenotype of the pollen is determined by the diploid genotype of its parent plant.
- Examples: Brassicaceae (e.g., cabbage, radish), Asteraceae (e.g., sunflower)

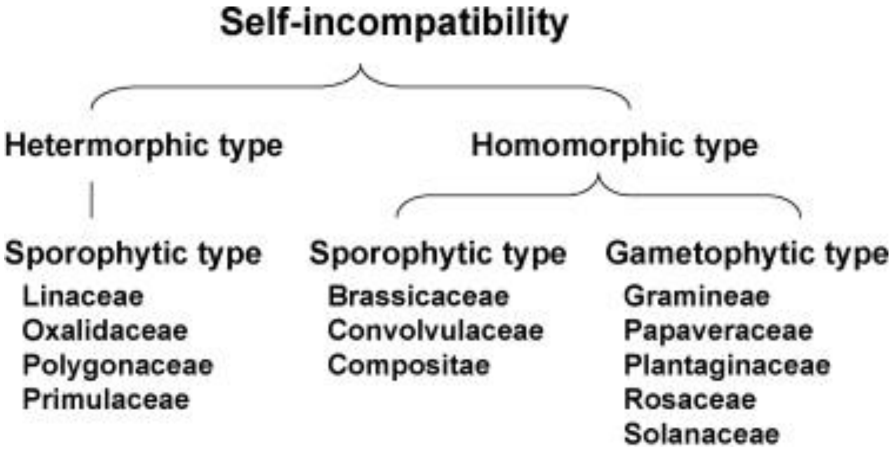

Figure 1. Types of Self-Incompatibility Systems (Tao and Iezzoni, 2010).

12.2. Molecular Mechanisms of Self-Recognition and Rejection

12.2.1. Gametophytic Self-Incompatibility (GSI)

12.2.1.1. S-RNase-based GSI (found in Solanaceae, Rosaceae, and Plantaginaceae)

1. **S-locus components**:
   - Female determinant: S-RNase (a cytotoxic ribonuclease)
   - Male determinant: S-locus F-box protein (SLF/SFB)
2. **Recognition mechanism**:
   - S-RNases enter all pollen tubes
   - In compatible pollen, SLF forms an E3 ubiquitin ligase complex that targets non-self S-RNases for degradation
   - In incompatible pollen, SLF cannot recognize self S-RNase, leading to RNA degradation and pollen tube growth inhibition
3. **Cellular responses**:
   - Disruption of tip-focused calcium (Ca^{2+}) gradient in incompatible pollen tubes
   - Actin cytoskeleton depolymerization
   - Vacuolar collapse and programmed cell death

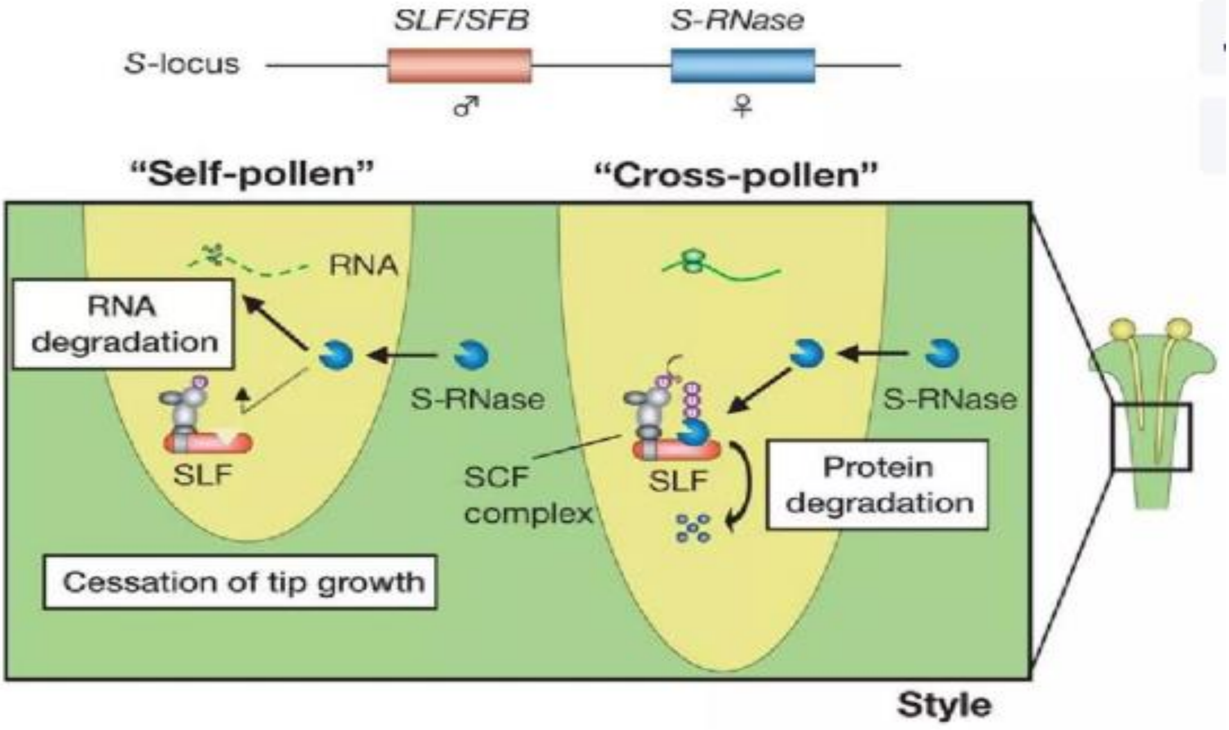

Figure 2. Gametophytic Self-Incompatibility (GSI)
(https://fr.slideshare.net/slideshow/self-incompatibility-)

12.2.1.2. Papaver GSI System (found in Papaveraceae)

1. **S-locus components**:
    - Female determinant: PrsS (Papaver rhoeas stigma S determinant)
    - Male determinant: PrpS (Papaver rhoeas pollen S determinant)
2. **Recognition mechanism**:
    - PrsS interacts with PrpS, triggering a Ca^{2+}-dependent signaling cascade in incompatible pollen
3. **Cellular responses**:
    - Rapid influx of Ca^{2+} and K^+ ions
    - Activation of mitogen-activated protein kinases (MAPKs)
    - Increase in reactive oxygen species (ROS)
    - Activation of programmed cell death pathways

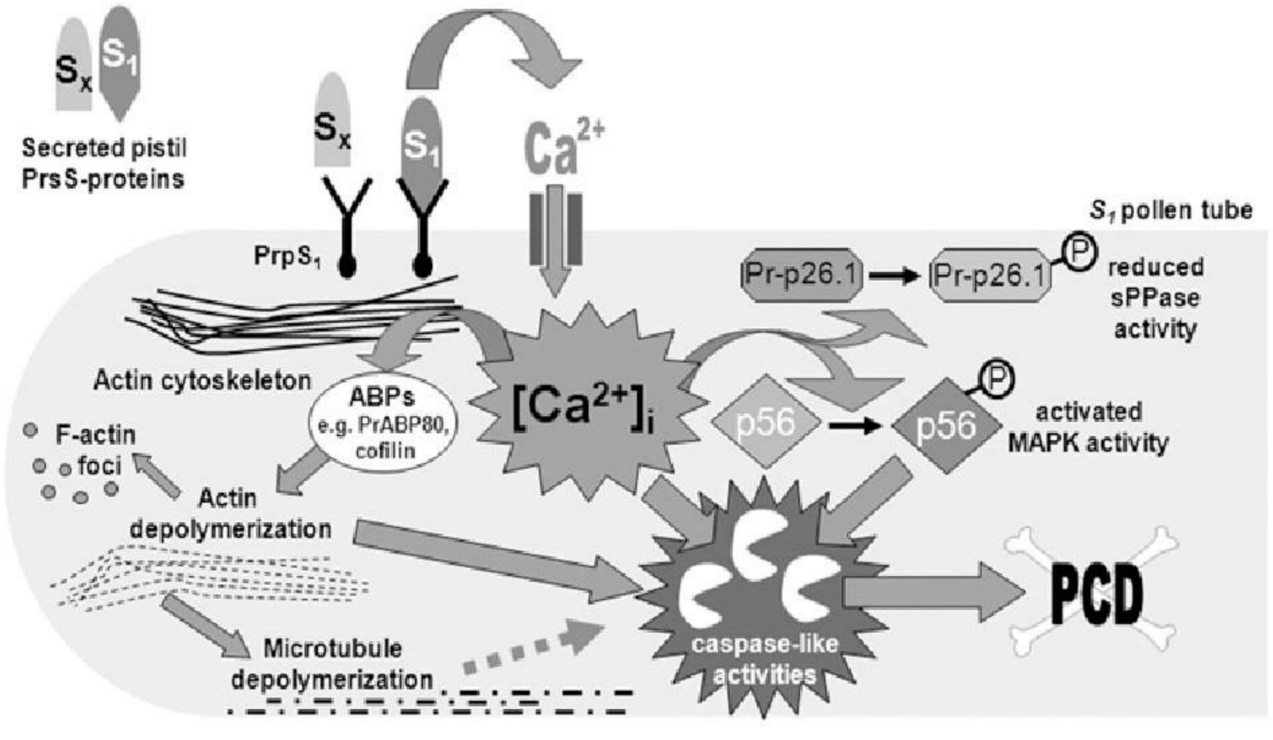

Figure 3. A model for the targets of the Papaver SI signalling network PrsS proteins secreted by the stigma interact with the pollen S-determinant PrpS in an S-specific interaction (Poulter et al., 2010). This triggers a Ca2+-mediated signalling cascade in incompatible pollen which targets several downstream components. The F-actin cytoskeleton is rapidly depolymerized, with the actin-binding proteins profilin and PrABP80 implicated in this process. Later in the SI response, the actin forms large punctate foci. The microtubule cytoskeleton is also rapidly depolymerized. Soluble inorganic pyrophosphatases, Pr-p26.1a/b, are

phosphorylated, inhibiting their activity and reducing the biosynthetic capability of the pollen. These events result in inhibition of pollen tube growth. An MAPK, p56, is also activated, and there is evidence that it signals to PCD. Several caspase-like activities are triggered, resulting in PCD of the pollen, ensuring that fertilization cannot occur in an incompatible situation. Figure adapted from Bosch and Franklin-Tong (2008) Self-incompatibility in Papaver: signalling to trigger PCD in incompatible pollen. Journal of Experimental Botany, 59(3), 481–490. c© 2008 Oxford University Press.

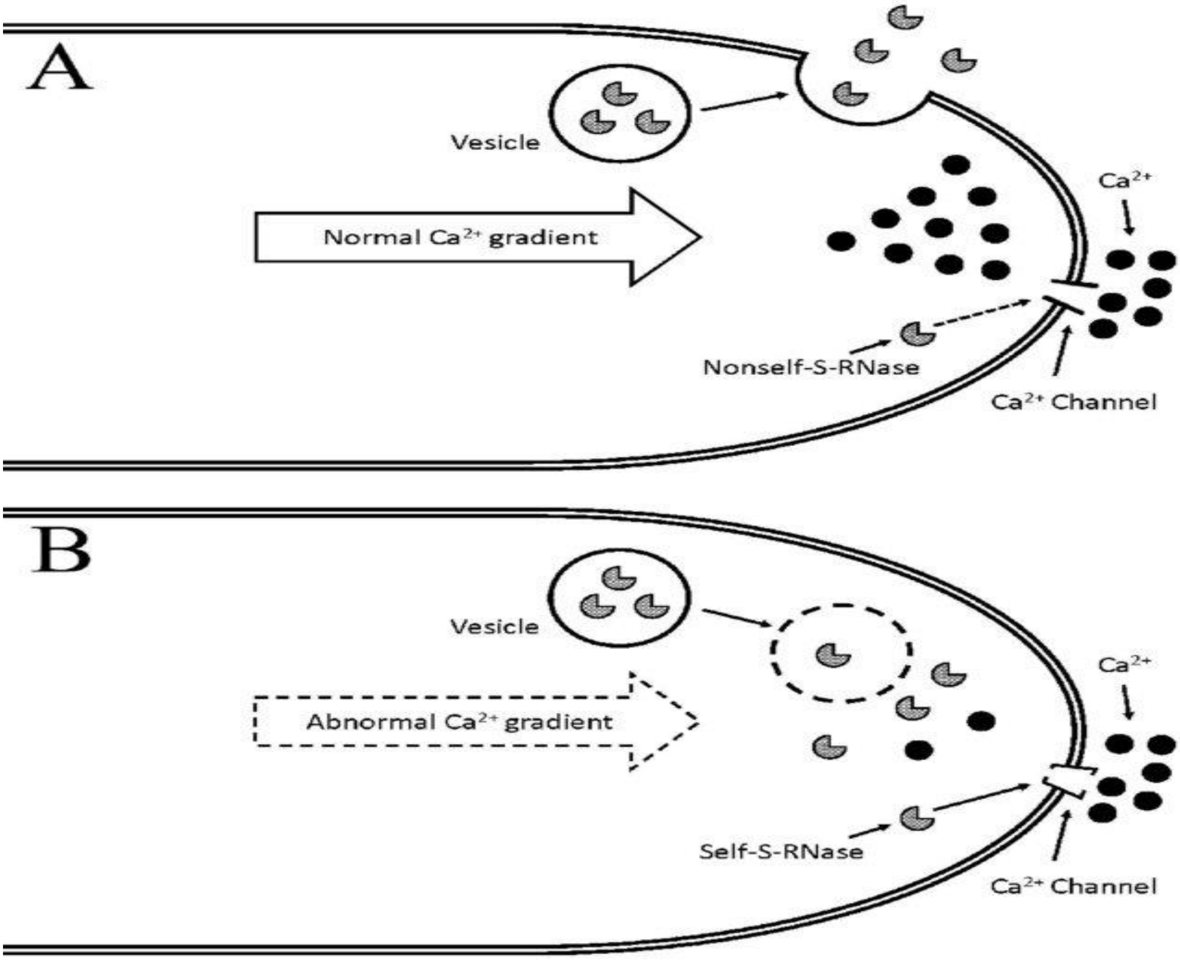

Figure 4. Gametophytic self-incompatibility in Rosaceae fruit trees (Ma and Qu, 2019). Model for the inhibition of pollen-tube growth by self-S-RNase through Ca 2+ transduction [Qu et al. 2016]. (A) Compatibility. (B) Incompatibility.

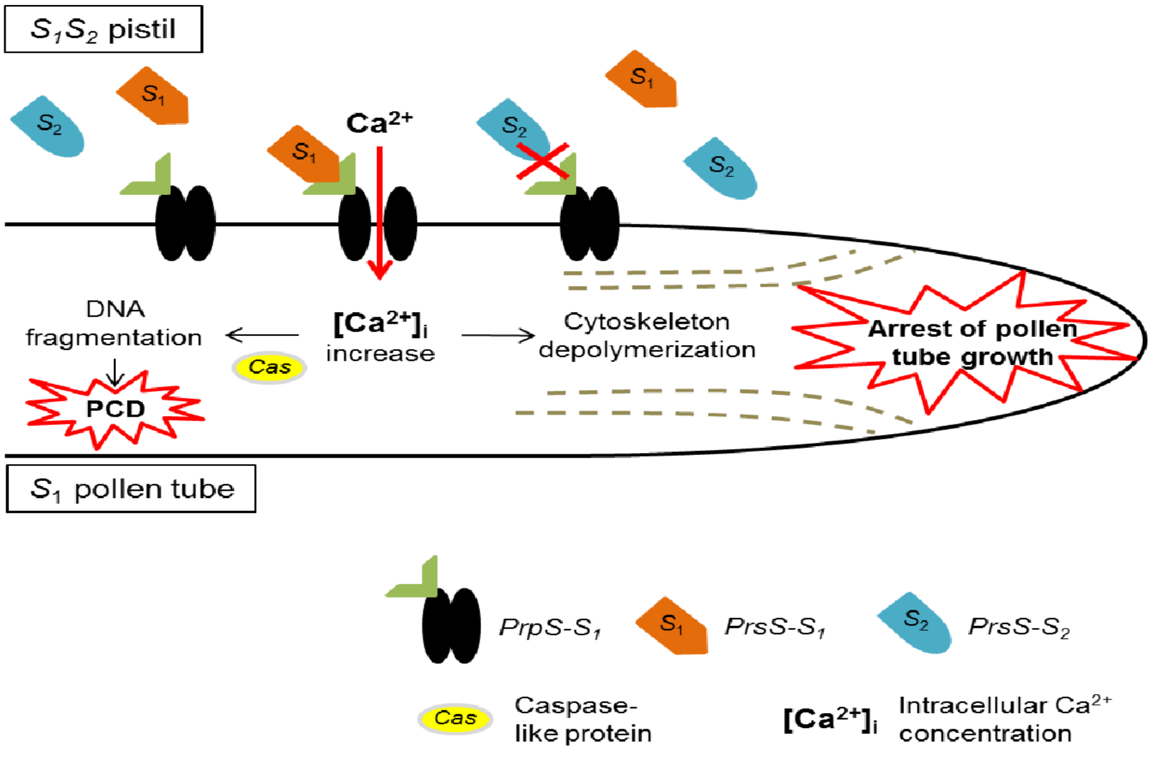

Figure 5. Model for the GSI S-glycoprotein system unique to the Papaveraceae (Manzanares, 2013). The SI system is a ligand gating type. The pistil S-specific component PrsS, secreted by the stigmatic cells into the extra cellular matrix, will be recognized by the pollen S-specific component, PrpS which is an ion channel or part of one. In a self-incompatible pollination, the complex PrsS-PrpS will lead to an intake of calcium by the pollen tube, resulting in an increase in [Ca 2+]i and therefore the loss of the gradient necessary to the pollen tube growth. Affected by the increase in [Ca 2+]i is the cytoskeleton with a depolymerisation of the F-actin and the DNA fragmentation, through caspase-3-like activity, leading to the PCD of the pollen tube. Figure adapted from Wheeler et al., 2010.

12.2.2. Sporophytic Self-Incompatibility (SSI)

12.2.2.1. Brassicaceae SSI System

1. **S-locus components**:
    - Female determinant: SRK (S-locus Receptor Kinase)
    - Male determinant: SCR/SP11 (S-locus Cysteine-Rich protein/S-locus Protein 11)
2. **Recognition mechanism**:
    - SCR/SP11 on the pollen coat interacts with SRK on the stigma surface
    - This interaction triggers a signaling cascade in incompatible stigma cells
3. **Cellular responses**:

- Activation of MLPK (M-locus Protein Kinase)
- Phosphorylation and activation of ARC1 (Armadillo Repeat-Containing 1) E3 ubiquitin ligase
- Ubiquitination and degradation of Exo70A1, a component of the exocyst complex involved in vesicle trafficking
- Inhibition of vesicle delivery to the pollen contact site, preventing pollen hydration and germination

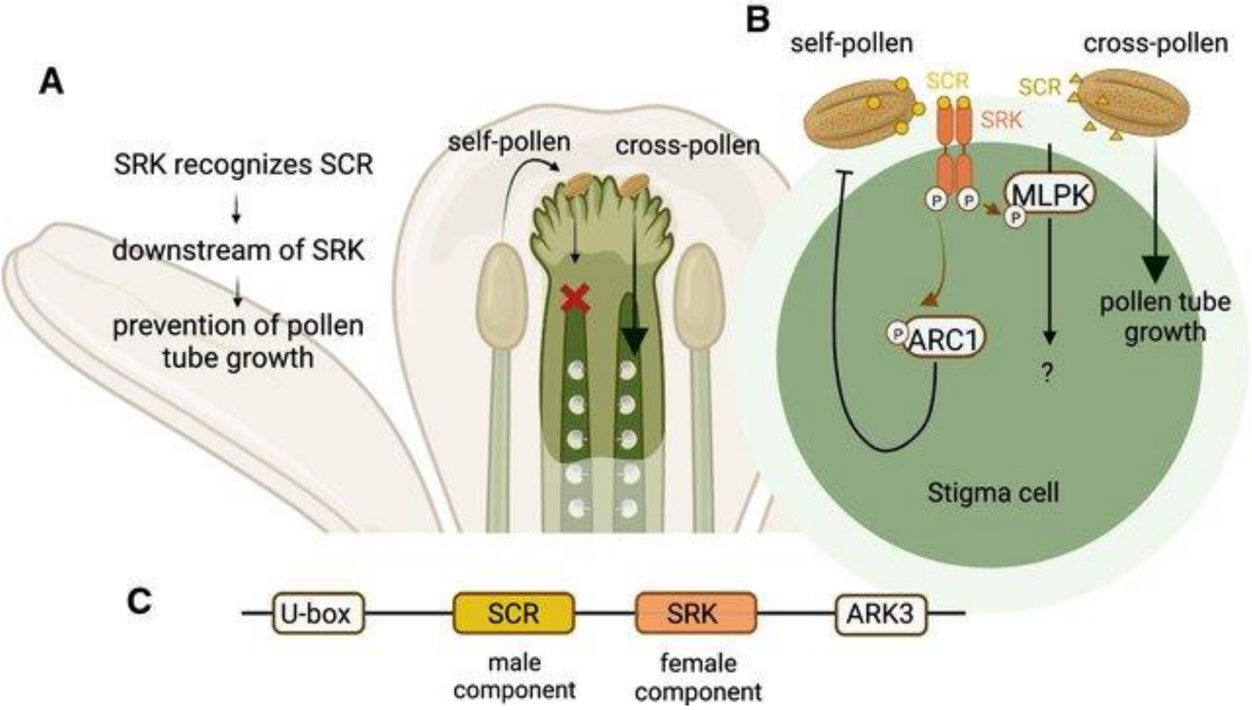

Figure 6. The mechanism of the sporophytic self-incompatibility system, typical for the Brassicaceae family (Novikova et al., 2023). **A** In a self-pollination attempt, the SRK receptor on the surface of the pistil will recognize the SCR ligand on the surface of pollen which will switch on a downstream signalling cascade leading to the prevention of pollen tube growth. **B** Recognition of SCR ligand by SRK receptor results in formation of a heterotetrameric structure (Ma et al. 2016) and induces autophosphorylation of SRK. ARC1 (arm repeat containing 1) and MLPK (M-locus protein kinase) interact with SRK and positively regulate the downstream reaction, as knockout of these genes can also lead to self-compatibility (Chen et al. 2019). ARC1 is an E3 ubiquitin ligase which activates proteasomal protein degradation (Stone et al. 2003; Samuel et al. 2008). Although Arabidopsis/Capsella and Brassica self-incompatibility systems share the same major players, some differences also exist (Yamamoto and Nishio 2014). For example, in Brassica SLG (S-locus glycoprotein) protein is also present in stigma, which enhances the self-incompatibility reaction upon SCR-SRK recognition (Takayama et al. 2001). **C** A schematic representation of the S-locus: genes coding for male (SCR in Arabidopsis or SCR/SP11 in Brassica) and female (SRK) components are strongly linked together, forming a haplotype typically flanked by U-box (U-box/ARM repeat protein or B80) and ARK3 (receptor kinase 3) genes (Kusaba et al. 2001; Hagenblad et al. 2006). SCR will be recognized as “self” by SRK from the same haplotype.

12.3. Genetic Basis of Self-Incompatibility

12.3.1. S-locus structure

- Highly polymorphic, with multiple alleles (sometimes >100) in a population
- Often contains several genes in tight linkage, forming an S-locus complex
- Low recombination rates within the S-locus, maintaining allelic specificities

12.3.2. Evolutionary aspects

- Balancing selection maintains high allelic diversity at the S-locus
- Trans-specific polymorphism: S-alleles can be more similar between species than within species
- Convergent evolution: Different SI systems have evolved independently multiple times

12.3.3. Dominance relationships

- In SSI systems, S-alleles can exhibit dominance hierarchies in pollen and/or stigma
- This affects the SI phenotype in heterozygous plants

12.4. Breakdown of Self-Incompatibility

12.4.1. Natural breakdown

- Some species have evolved self-compatibility from self-incompatible ancestors
- Often involves mutations in S-locus genes or other components of the SI pathway

12.4.2. Induced breakdown

- Bud pollination: Pollinating flowers before they open can sometimes bypass the SI response
- Temperature effects: Extreme temperatures can weaken the SI response in some species
- Chemical treatments: Compounds like CO_2, auxins, or protein synthesis inhibitors can sometimes overcome SI

12.5. Applications in Agriculture and Plant Breeding

12.5.1. Hybrid seed production

- SI can be used to ensure cross-pollination in hybrid breeding programs
- Understanding SI mechanisms helps in developing strategies to produce hybrid seeds efficiently

12.5.2. Genetic resource management

- Knowledge of SI systems is crucial for maintaining genetic diversity in seed banks and breeding populations

12.5.3. Crop improvement

- Manipulation of SI systems can be used to introduce desirable traits from self-incompatible wild relatives into cultivated crops

12.5.4. Molecular markers

- S-locus genes can be used as molecular markers for diversity studies and marker-assisted selection in breeding programs

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Annex

Program of the Subject matter

Intitulé de la matière : Biologie cellulaire et développement des plantes
Crédits : 7
Coefficients :3
Objectifs de l'enseignement (*Décrire ce que l'étudiant est censé avoir acquis comme compétences après le succès à cette matière – maximum 3 lignes).* Connaître les aspects génotypiques et phénotypiques du développement.

Connaissances préalables recommandées (*descriptif succinct des connaissances requises pour pouvoir suivre cet enseignement – Maximum 2 lignes).* Connaissance de base de biologie végétale, biologie cellulaire et biochimie.

Contenu

- Aspects génotypiques du développement : mutants, gènes dont l'expression varie au cours du développement, gènes régulateurs du développement. Mécanismes de croissance (en taille et en nombre) des cellules végétales (constituants de la paroi, voies de biosynthèse et analyse de mutants. Différenciation des stomates et des trichomes : analyse de mutants. Différenciation des gamètes, fécondation et formation de la graine : analyse de mutants. Mécanismes d'apoptose induits lors du développement des plantes.

- Aspects phénotypiques du développement : embryogenèse, graines et fruits, développement végétatif (feuilles, tiges racines), mise à fleur et développement floral, autoincompatibilité.

TD de protéomique, bioinformatique, application de la transgenèse et génomique fonctionnelle.

TP de génétique inverse, étude de mutants d'insertion.
TP : À cause du déficit au niveau des laboratoires « en générale » S'il vous plaît inclure des TP sur les coupes histologiques horizontale et longitudinale, pour montrer également les phénomènes : auxesis, meresis et aussi l'initiation proliférative des organes.

Mode d'évaluation : Exposés, Micro-Interrogations, Comptes rendus des TP, Examen écrit.