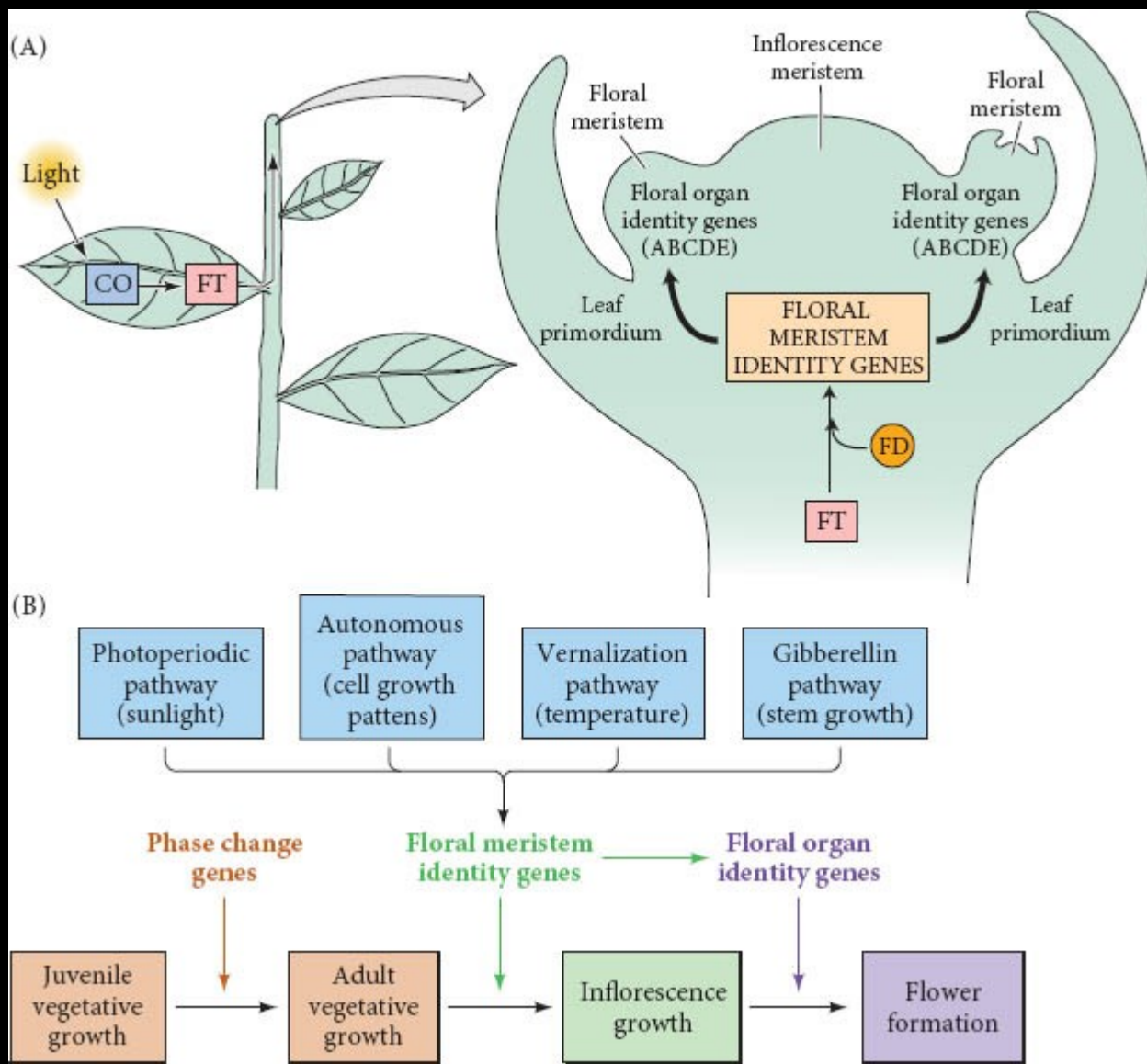
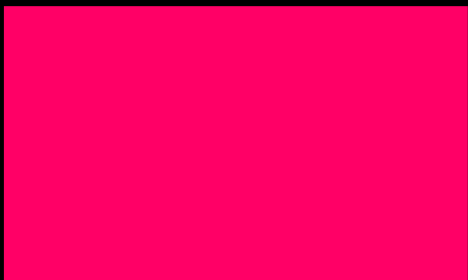


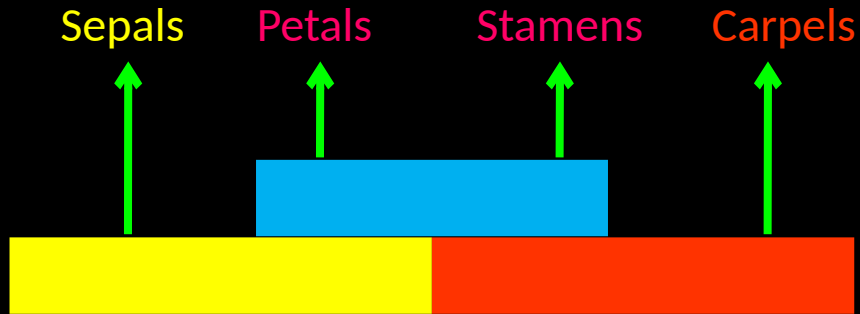
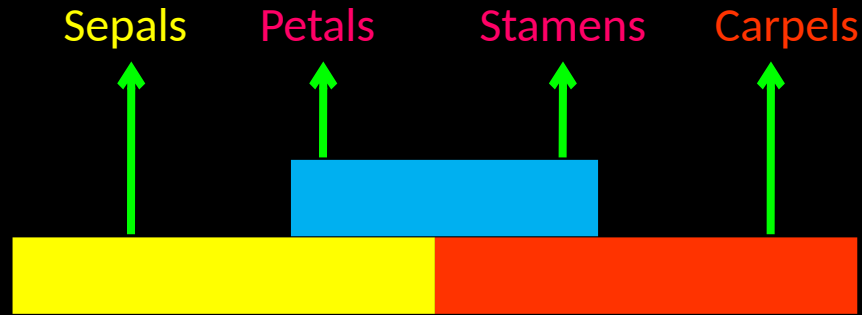
# MORPHOGENESIS & ORGANOGENESIS IN PLANTS

## What are MADS box genes?

- The MADS box is a **highly conserved sequence motif** found in a family of transcription factors.
- The conserved domain was recognized after the first four members of the family, which were **MCM1**, **AGAMOUS**, **DEFICIENS** and **SRF** (serum response factor). The name MADS was constructed from the "initials" of these four "founders".
- Length of the MADS-box reported by various researchers varies somewhat, *but typical lengths are in the range of 168 to 180 base pairs.*

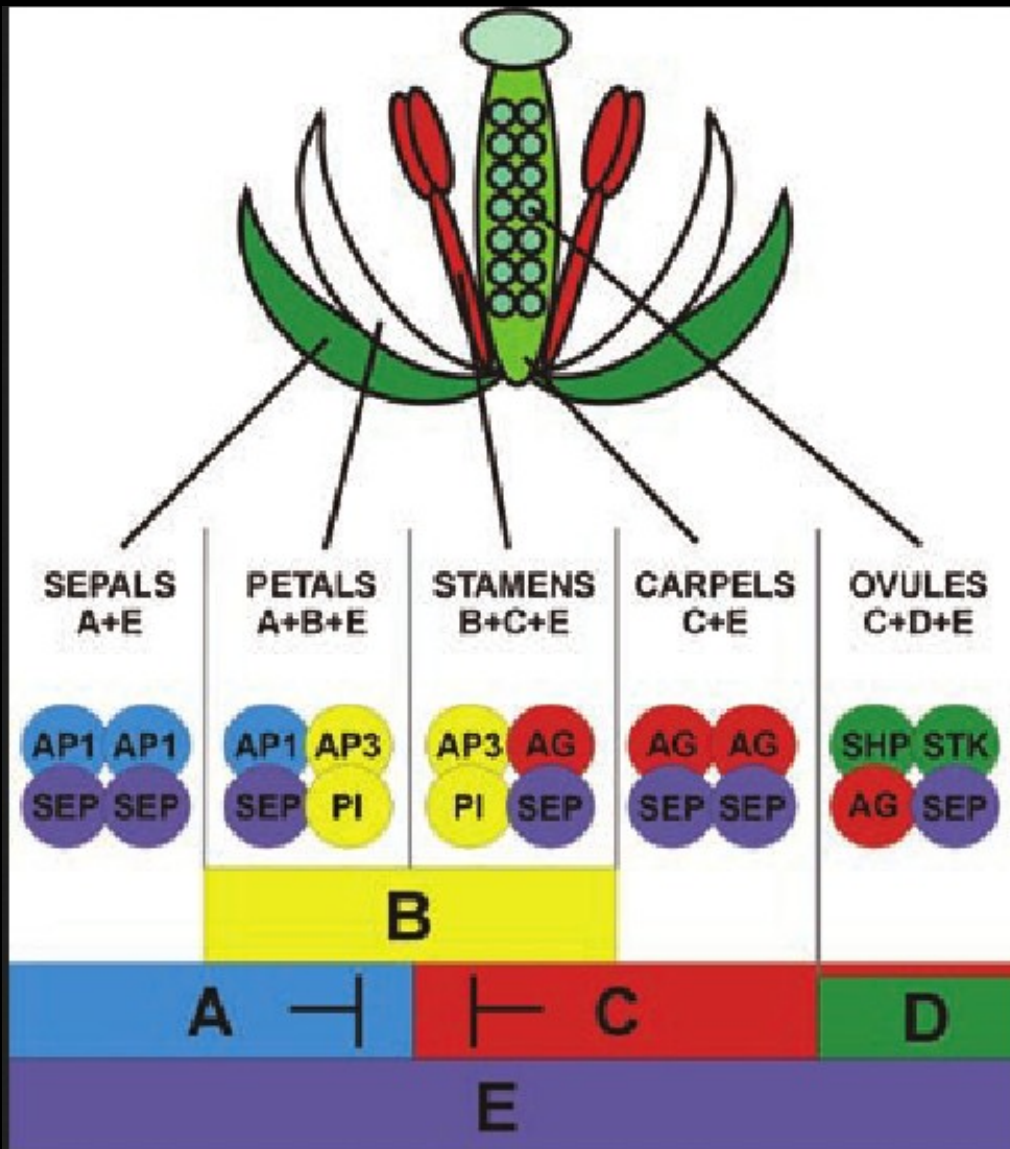






## Phenotypic Effects of Mutations in A, B or C Function Floral Identity Genes

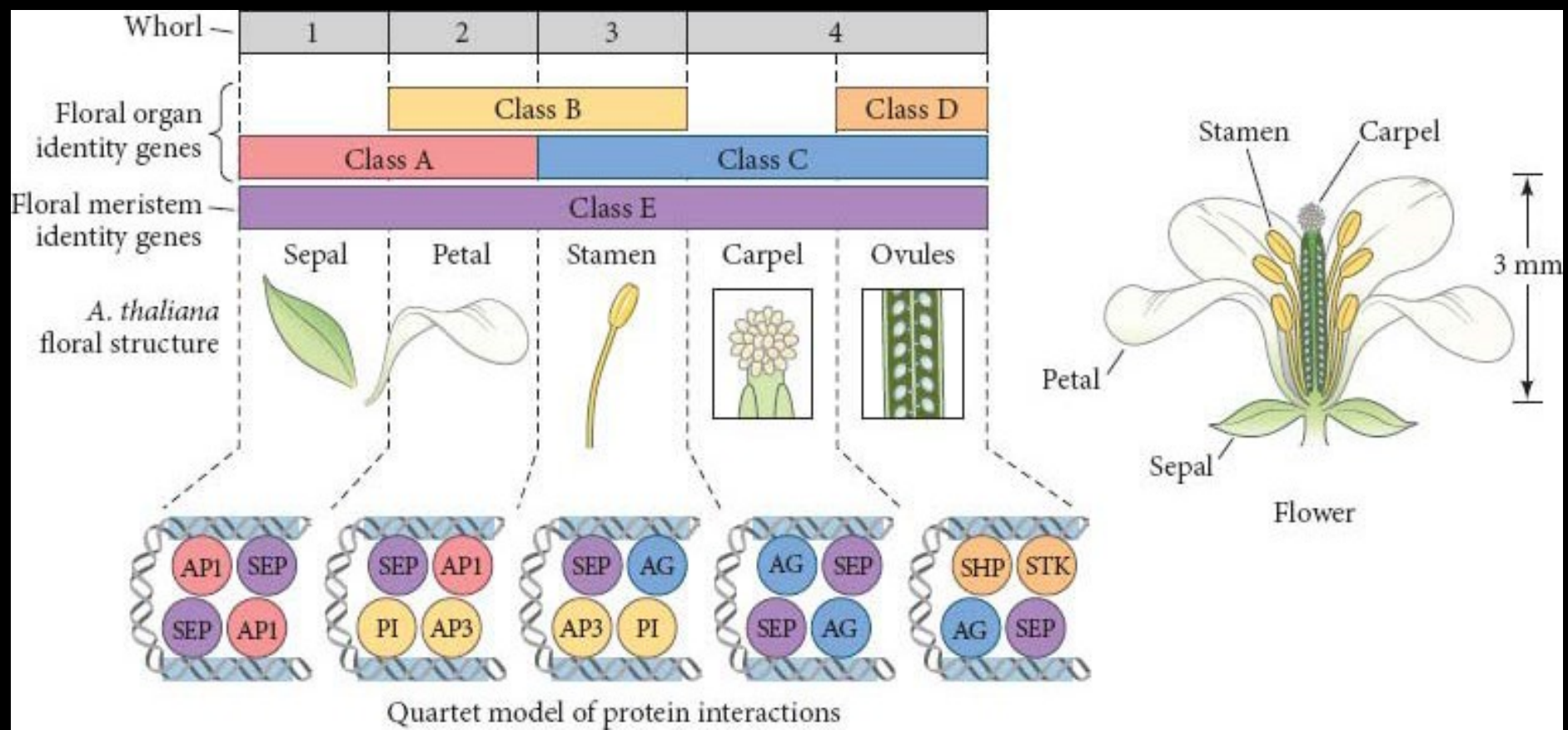
	Phenotype			
Mutation	Whorl 1	Whorl 2	Whorl 3	Whorl 4
Wild Type	Sepal	Petal	Stamen	Carpel
A Function	Carpel	Stamen	Stamen	Carpel
B Function	Sepal	Sepal	Carpel	Carpel
C Function	Sepal	Petal	Petal	New Flower



The ABC model has been gradually expanded to include class D- & E-function genes necessary for ovules & floral whorls.

D-function genes: SEEDSTICK (STK) + SHATTERPROOF1 & 2 (SHP1 & SHP2)

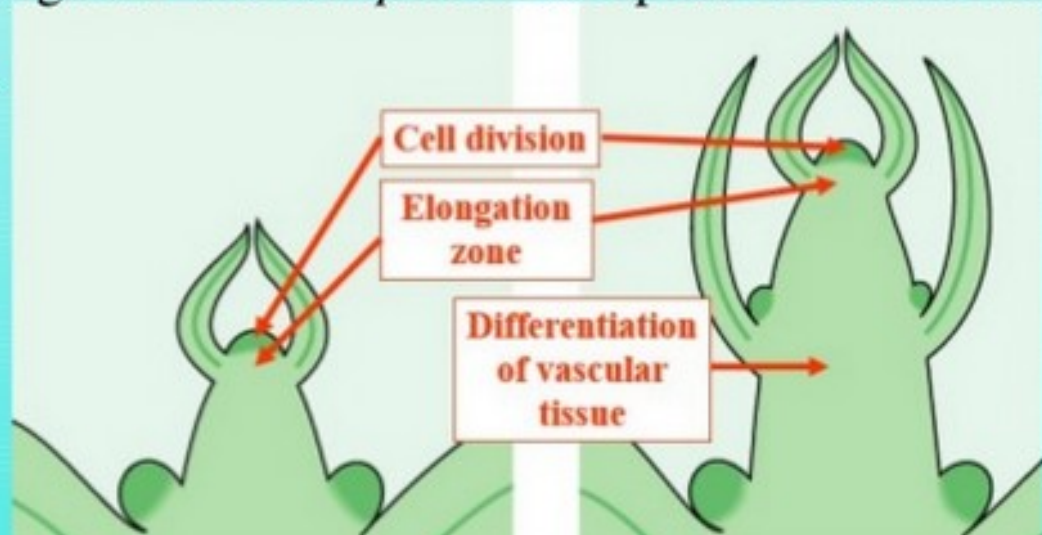
E-function genes requires at least one of the four SEPALLATA (SEP1, SEP2, SEP3 and SEP4)



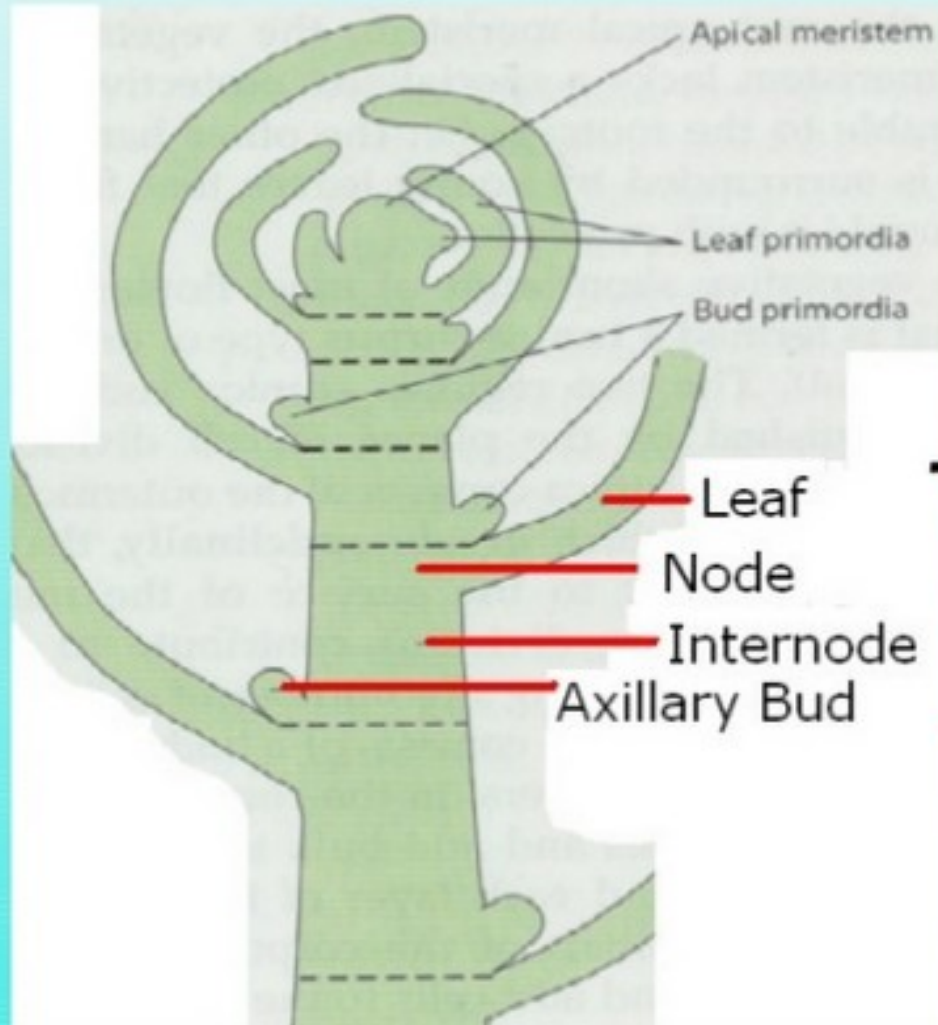
Quartet model of protein interactions

## Shoot Apical Meristem (SAM)

- The vegetative shoot apical meristem generates the stem, as well as the lateral organs attached to the stem (leaves and lateral buds).
- The shoot apical meristem typically contains a few hundred to a thousand cells, although the *Arabidopsis* shoot apical meristem has only about 60 cells.



## Shoot organization - Phytomeres



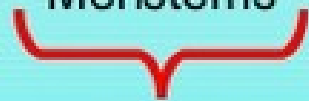
Phytomer =  
modular unit  
of the Shoot

# Shoot organization

Apical Meristem



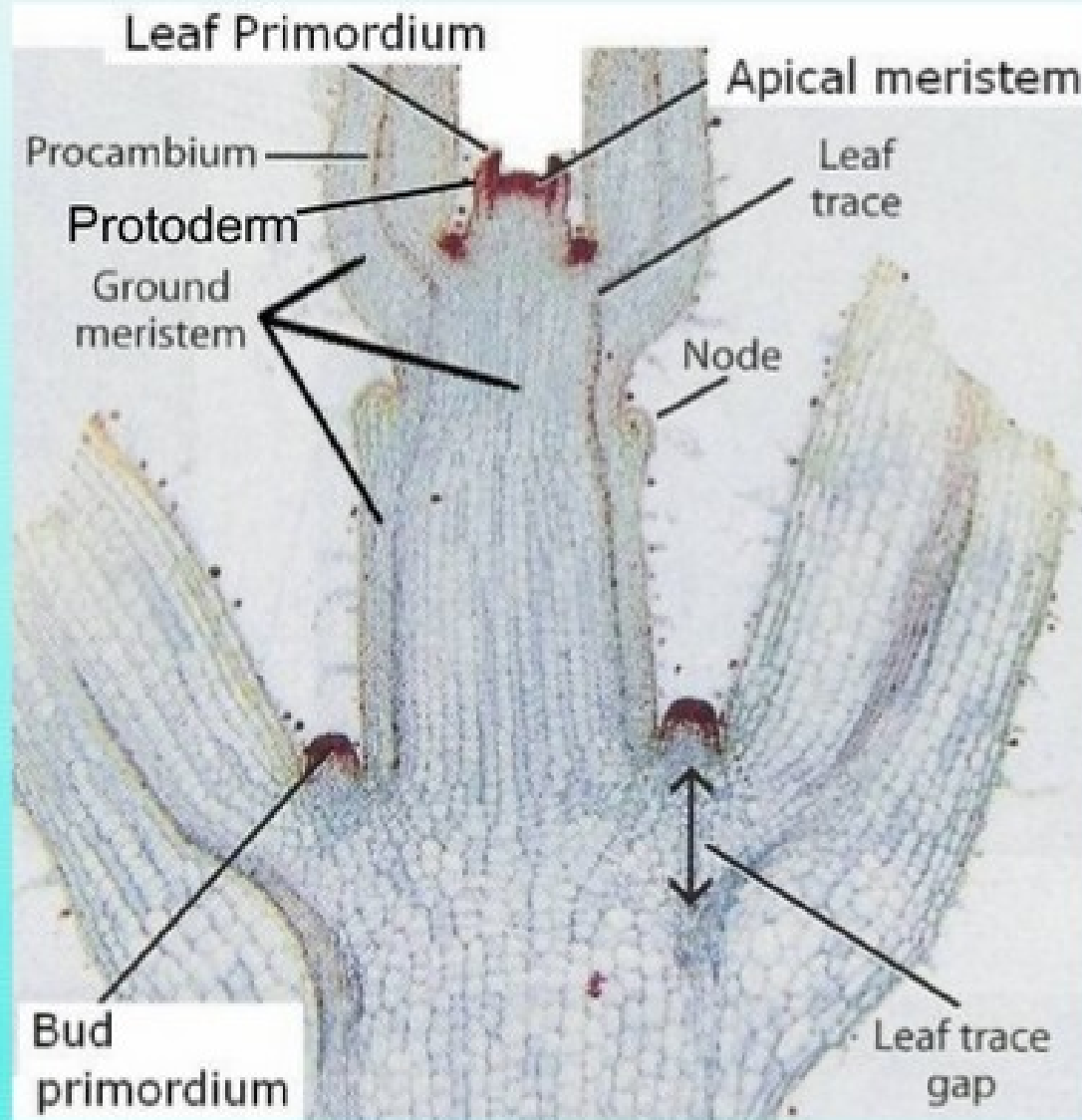
Primary Meristems



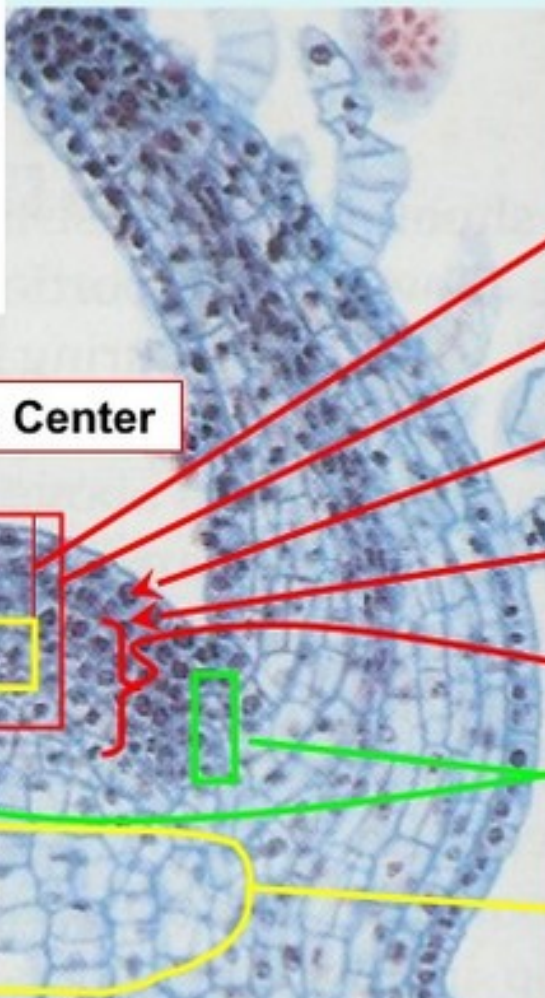
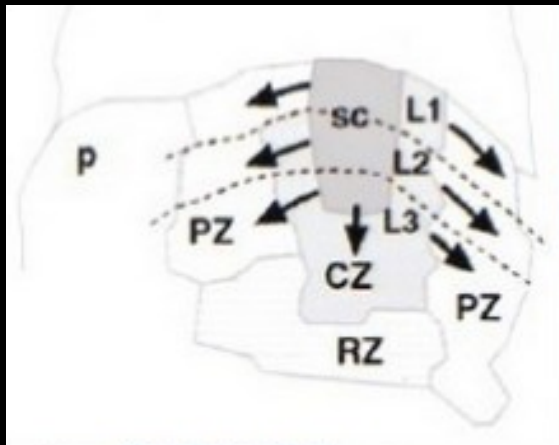
Protoderm

Procambium

Ground Meristem



## Shoot apical meristem organization



Organizing Center

Stem Cells

Central Zone

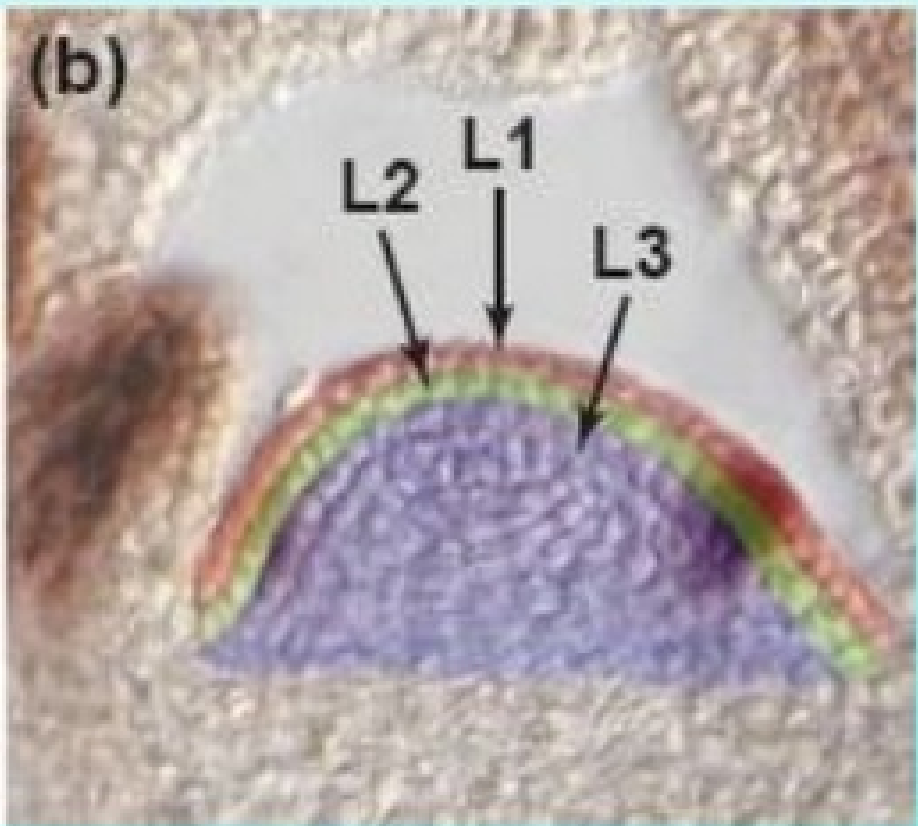
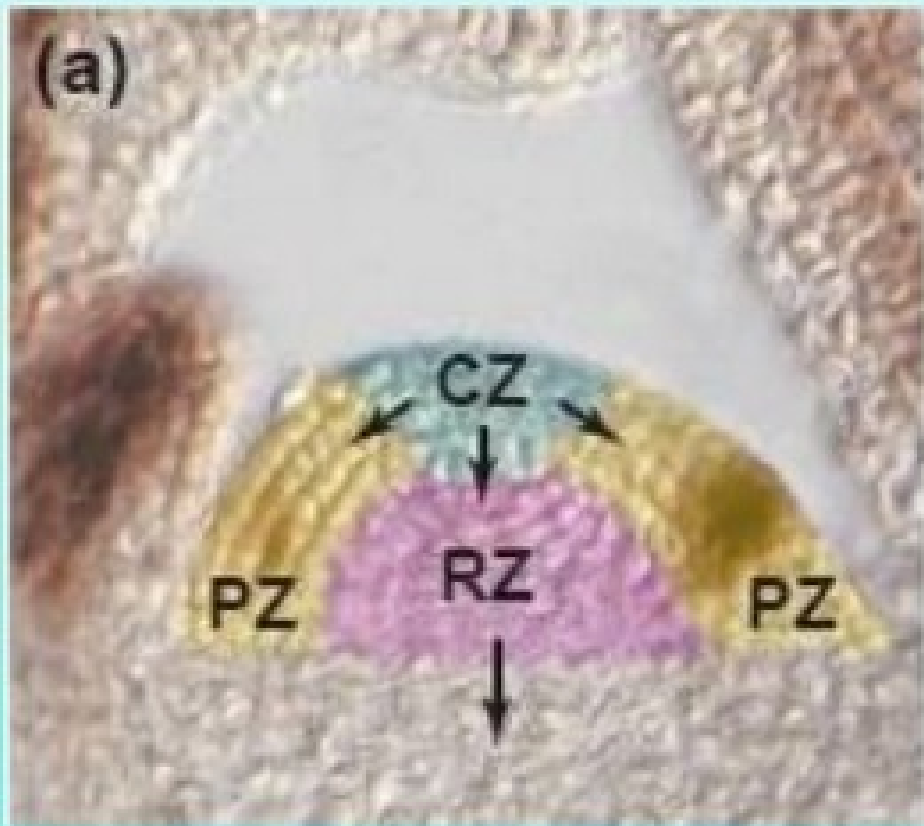
L1 = tunica

L2 = tunica

L3 = corpus

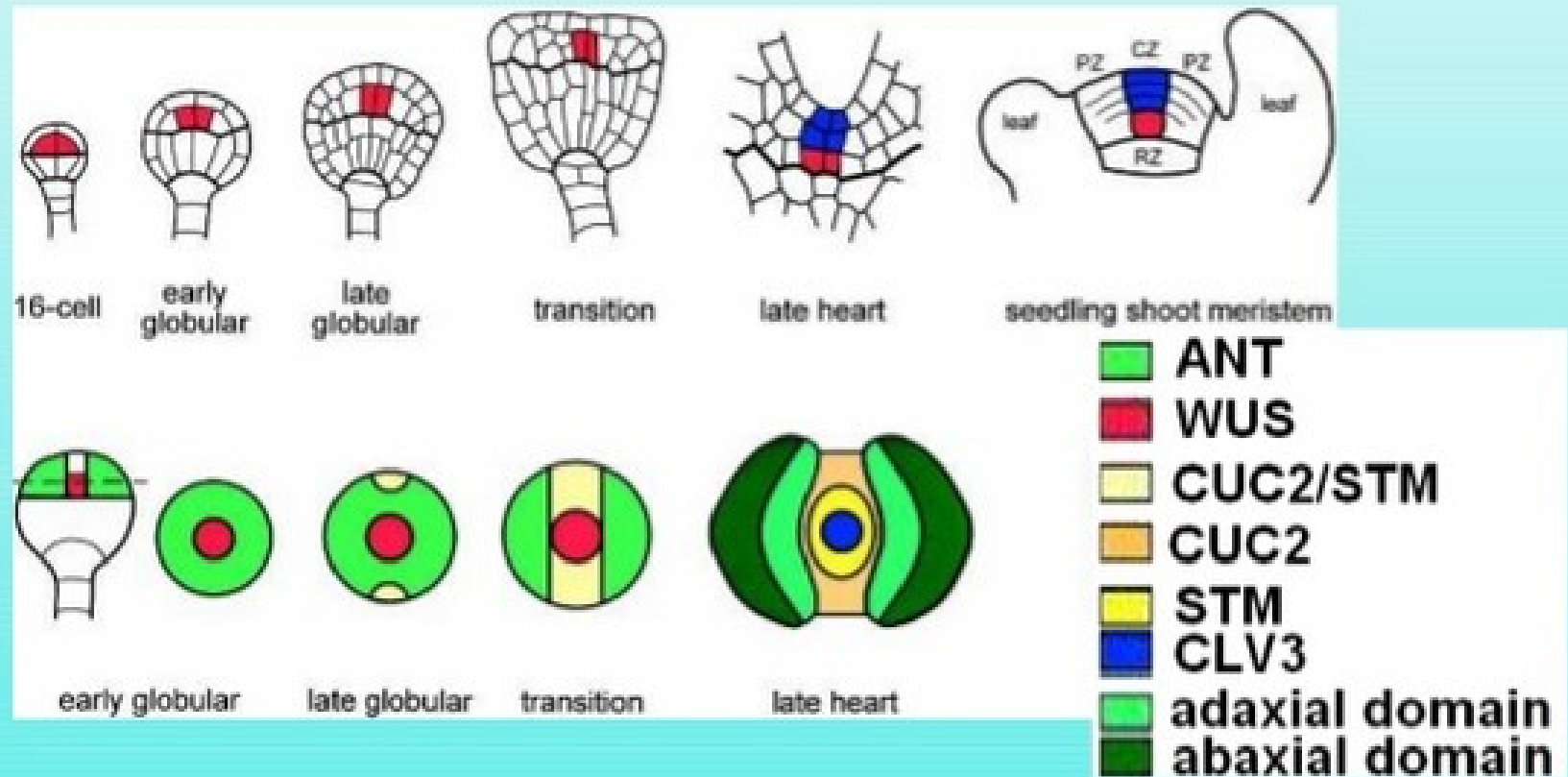
Peripheral Zone

Pith or Rib  
Meristem

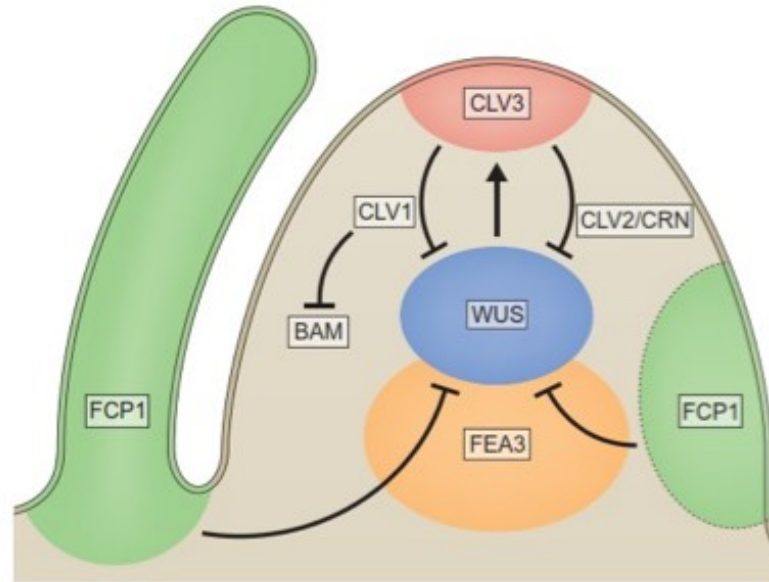


# Gene Expression in the Apical Embryo Domain

WUSCHEL (WUS), CLAVATA (CLV) AND SHOOT MERISTEMLESS (STM)

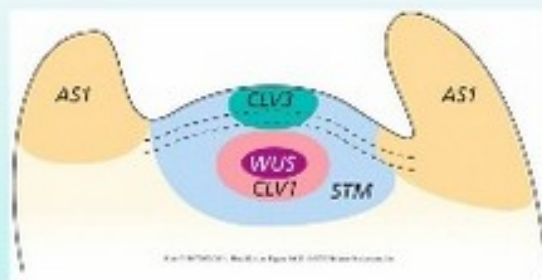


# Shoot Development Genes



**WUSCHEL (WUS)** → Stem cell promoting transcription factor

**CLAVATA3 (CLV3)** → Differentiation promoting peptide



WUS, CLV and STM expression in the shoot apex

### WUS gene

1. Organizing Center of Central Cells (just a few cells)
2. Molecular: Encodes homeodomain protein
3. Molecular Genetic: Induces Expression of CLV3
4. Developmental: WUS specifies stem cells of the SAM, i.e. maintains stem cells and maintains their identity.

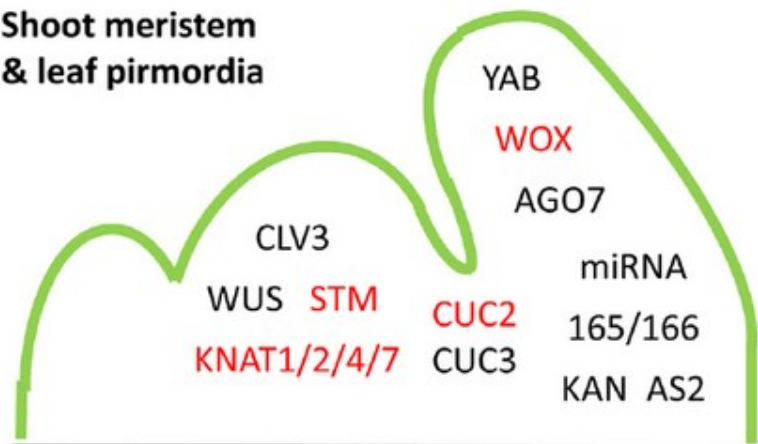
### CLV3 gene

1. Stem cells of Central Zone
2. Molecular: Encodes peptide secreted in extracellular space
3. Molecular Genetic: Inhibits WUS expression.
4. Developmental: CLV3 restricts size of Central Cells, i.e. CLV3 restricts size of the stem cell population.

### STM gene

1. Through SAM apical "dome" of cells: central zone and peripheral zone.
2. Molecular: Encodes homeodomain protein
3. Molecular Genetic: Blocks organ formation genes (AS1, AS2)
4. Developmental: Prevents premature differentiation of cells from Peripheral Zone... thus prevents premature organ initiation.

**Shoot meristem  
& leaf primordia**



**Flower organ**

AG PI AP1 AP3 SEP1  
SEP2 SEP3 SHP1  
SHP2 CRC SUP PTL



**Seed**

ABI3 LEC2 FUS3  
LEA7 OLEO4  
CRU3 CRA1  
SESA1 LTP



**Root**

PLT1 PLT2 ABI4  
PUCHI LAX3

**Architecture  
& cell elongation**

TCP BRC1 EXT3  
EXT4 EXPA7

**Hormone**

AUX ARF IAA PIN  
YUC CXXX EIR1  
GA20OX2 BSU1

**RNA silencing**

AGO3/5/7/9  
miR156/166/172/  
319/164



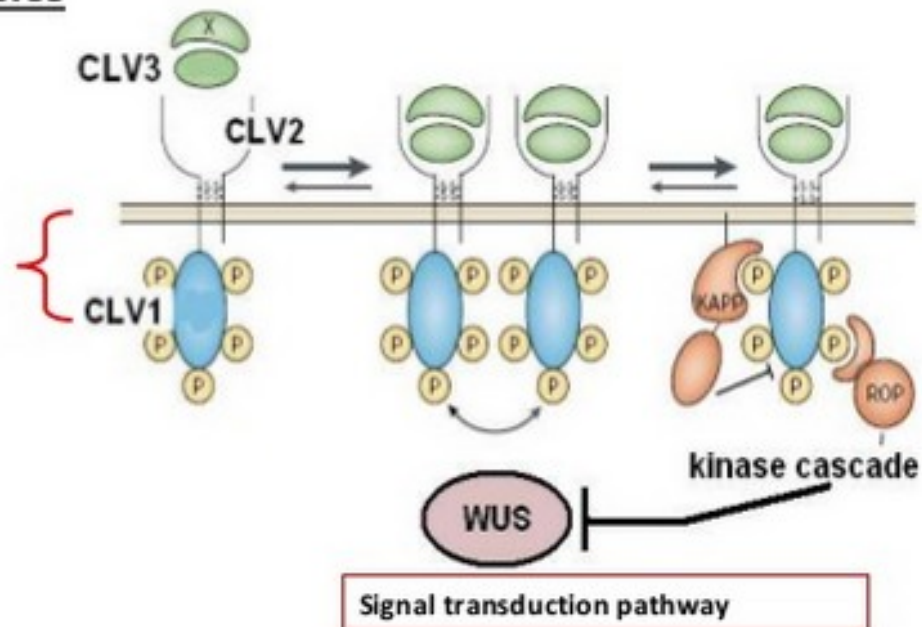
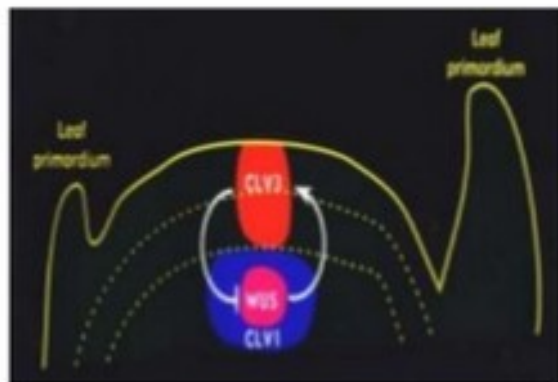
**Stomata**

SPCH MUTE  
FAMA



## Shoot Development : Genetics

### CLAVATA gene mechanism



### CLAVATA GENE Characteristics

CLV1 – Extracellular polypeptide: 96 amino acids. (*Ser/Thr*) kinase. Extracellular domain is leucine-rich repeats (LRRs)

CLV2 – Membrane-bound protein receptor with a protein-binding motif

CLV3 – Membrane-bound protein receptor with a protein-binding motif and **Restricted to L1, L2 of SAM Central Zone**

KAPP- The type-2C kinase-associated protein phosphatase

ROP-Ras GTPases are typically associated with cytosolic MAPK cascades

## Summary: Shoot Apical Meristem Genetic Influences on Development

1. Organizing Center (OC): Maintains Stem Cells
  - a. cells expressing WUS gene confers stem cell fate to overlying stem cells
  - b. cells above OC target stem cells by preferred connections through plasmodesmata
2. Stem Cells control boundaries of stem cells
  - a. Surgical expts. Demonstrate “release” from inhibition of differentiating “daughter” cells
  - b. CLV3 gene inhibits WUS gene expression
3. Daughter cells of stem kept in undifferentiated state
  - a. STM gene keeps daughter cells in an undifferentiated state.
  - b. Daughter cells increase to sufficient numbers before organ formation

## GENES ASSOCIATED WITH RAM

✓ *HOBBIT (HBT) genes*

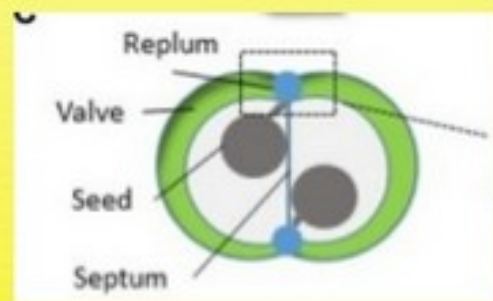
✓ *MONOPTEROS (MP) gene is required for formation of the embryonic primary root as well as vascular development*

✓ *SHORT ROOT (SHR) genes*

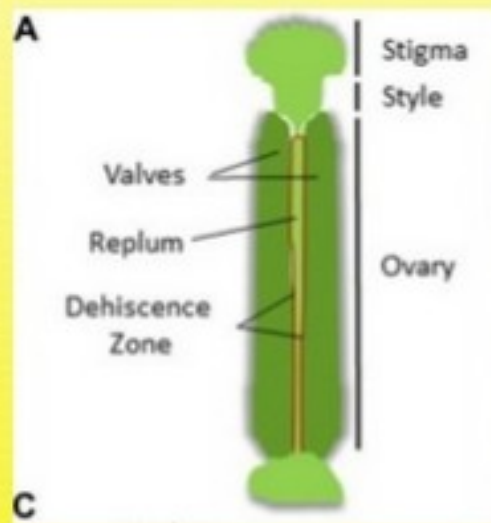
✓ *SCARECROW (SCR) genes*

# Genes

- Arabidopsis fruits develop from two fused carpels and are specialized capsules called siliques
- **FRUITFULL (FUL)** is necessary for proper valve development and represses SHATTERPROOF 1/2 (SHP 1/2)  
(Gu et al., 1998; Ferrándiz et al., 2000a).
- **SHATTERPROOF 1/2 (SHP1/2)** are necessary for valve margin development (Liljegren et al., 2000).
- **REPLUMLESS (RPL)** is necessary for replum development and represses SHP1/2 (Roeder et al., 2003)

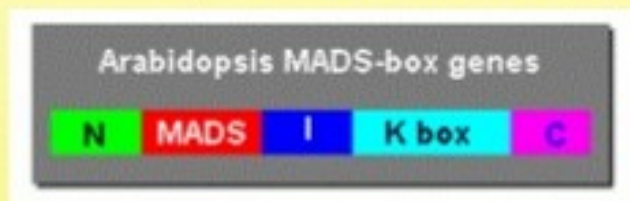


- SHP1/2 activate INDEHISCENT (IND) and ALCATRAZ (ALC), which are **both necessary for the differentiation of the dehiscence zone** between the valves and replum (Girin et al., 2011; Groszmann et al., 2011).
- FUL, SHP1/2, RPL, IND, SPT, and ALC all belong to large **transcription factor families**.
- **FUL and SHP1/2 belong to the MADS-box family** (Gu et al., 1998; Liljegren et al., 2000)

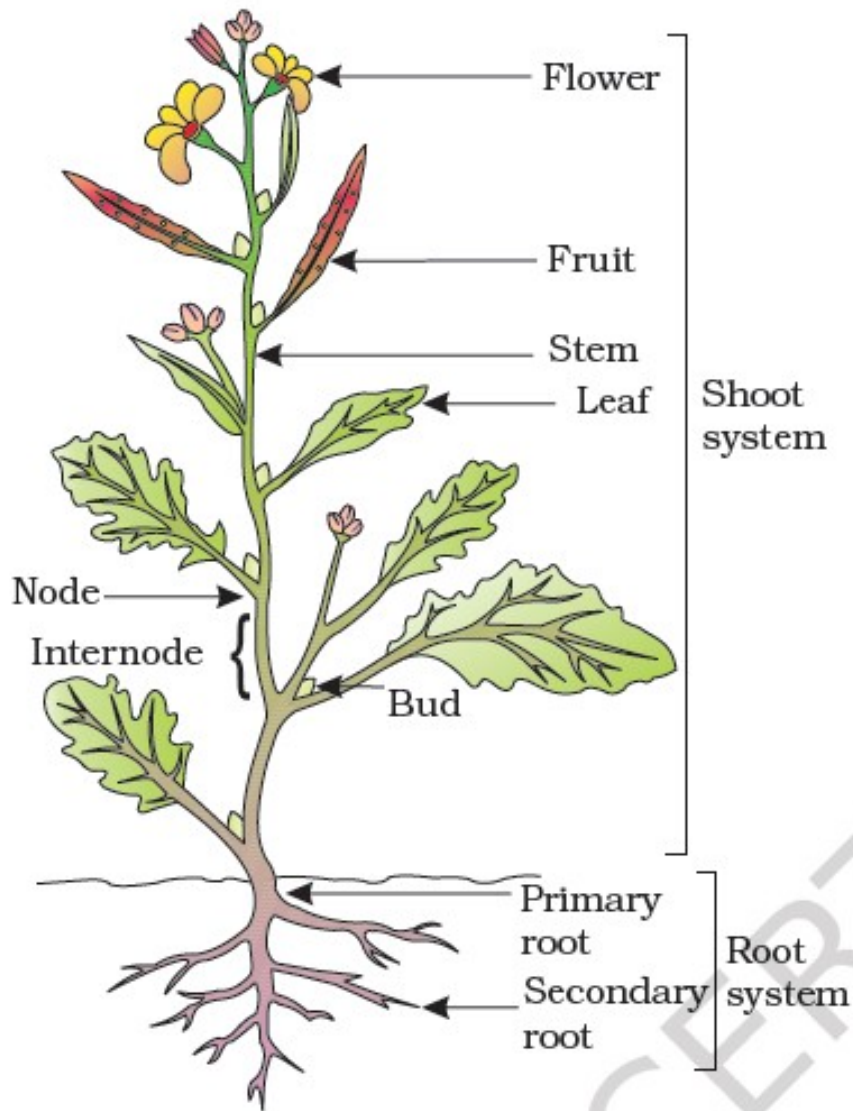


## MADS-box family

- MADS-box genes represent a highly conserved gene family of putative transcription factors in plants
- The proteins encoded by these genes are characterized by a highly conserved domain, which consists of 56 amino acids

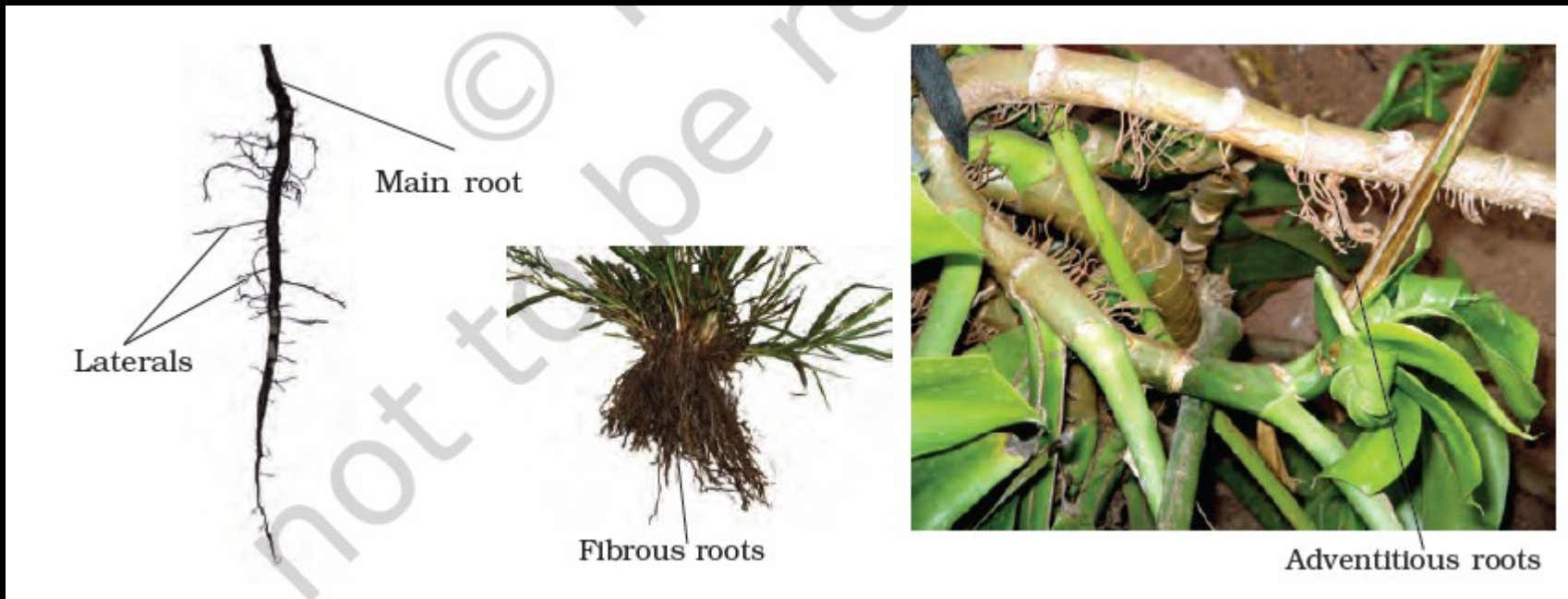


- **K-box** involved in protein-protein interactions.
- The MADS-box and K-box are separated by a weakly conserved **Intervening (I) region**, and a few MADS-box genes have an **amino-terminal extension (N)**. The **Carboxyl-terminal (C)** region may function as a **transcriptional activation domain**.



Dicotyledonous plants: direct elongation of radicle leads to the formation of primary root which grows inside the soil.

It bears lateral roots of several orders that are referred to as secondary, tertiary, etc.



Primary roots and its branches

Mustard



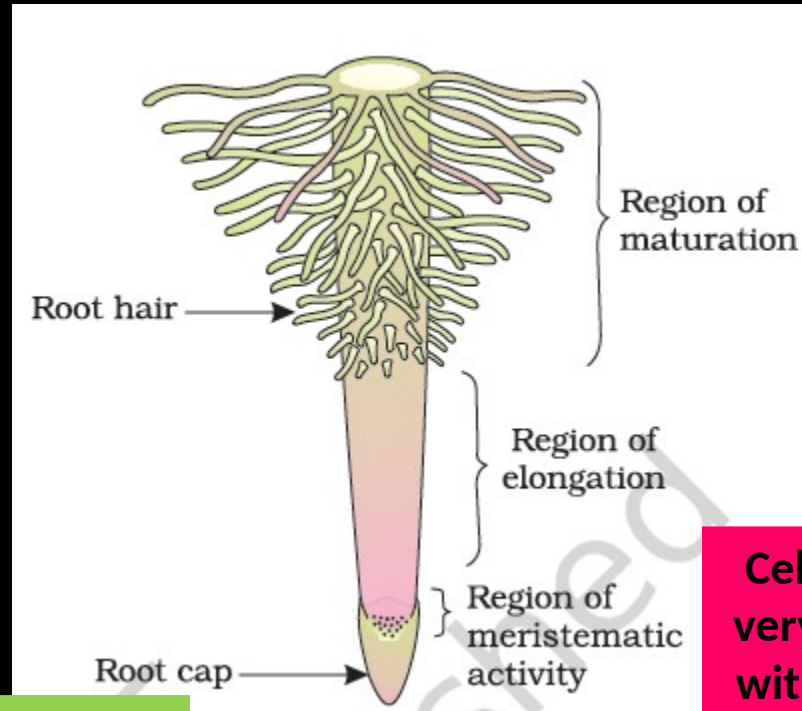
In monocots primary root is short lived & replaced by large no. of roots originating from the base of stem (fibrous)

wheat plant



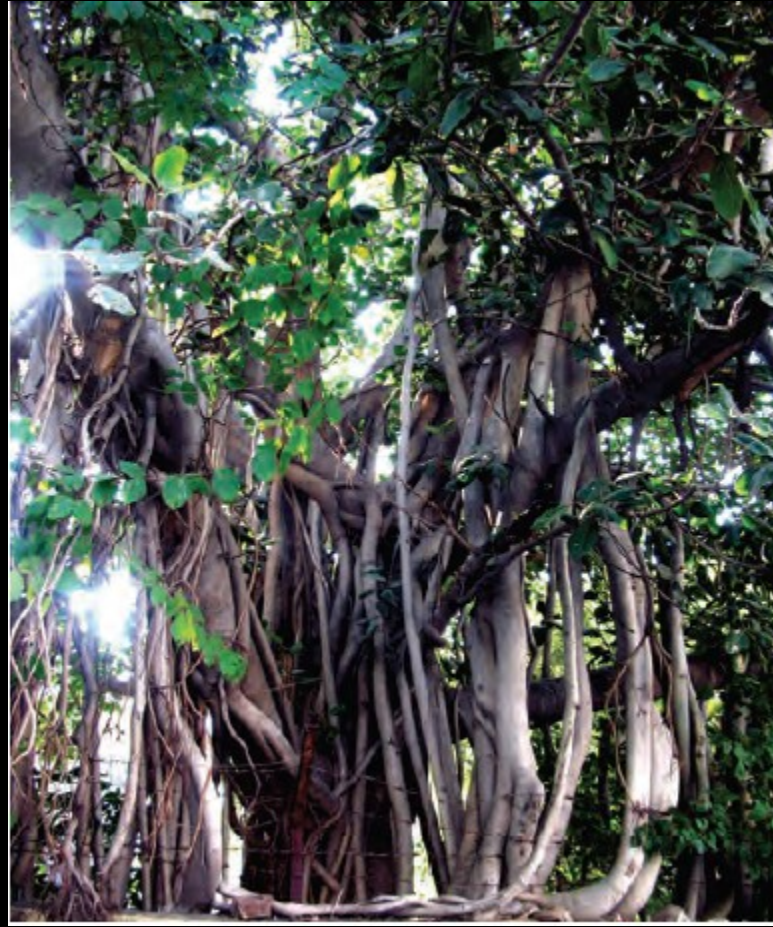
Roots arise from parts of the plant other than the radicle

Grass, Monstera, banyan tree



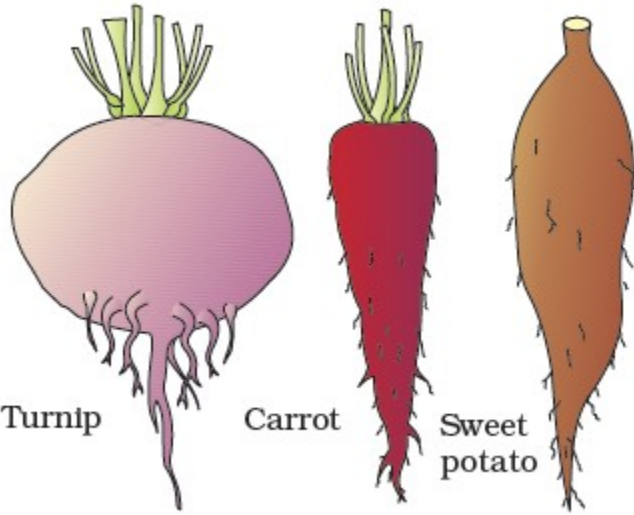
Protects the tender apex of the root as it makes its way through the soil

Cells of this region are very small, thin-walled, with dense protoplasm & divide repeatedly





Asparagus



Turnip

Carrot

Sweet potato



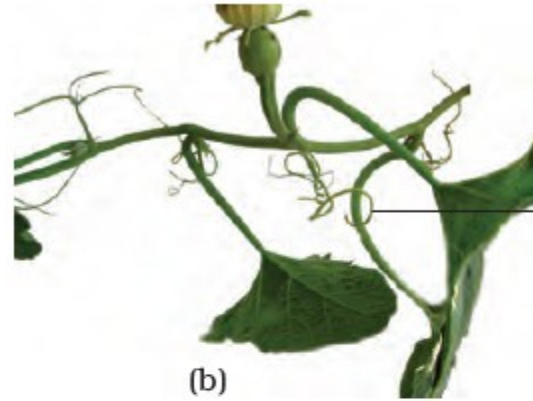


Ginger

Zaminkand

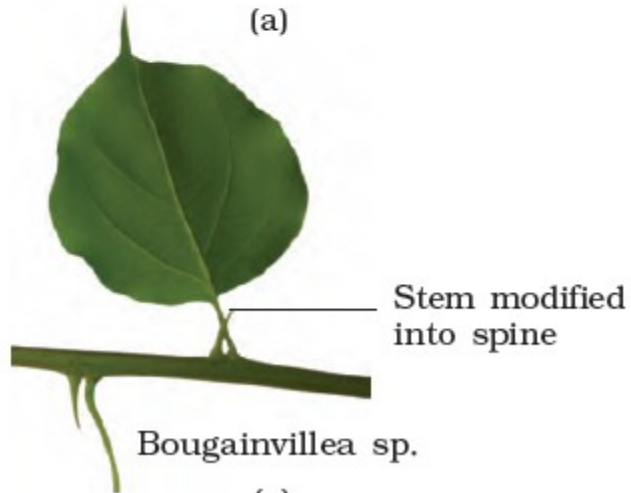
Potato

(a)



Axillary bud modified into tendril

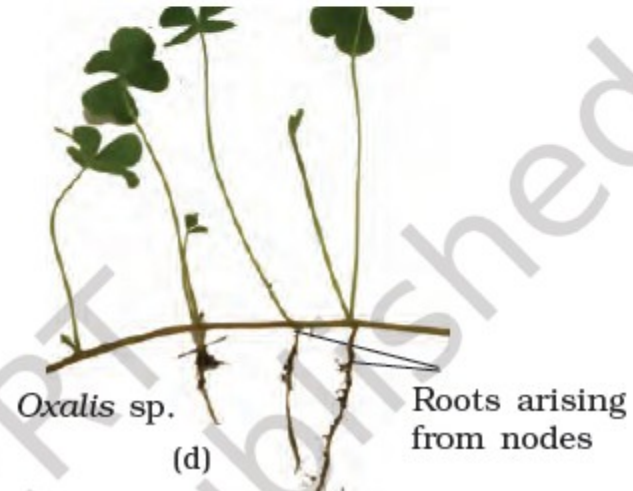
(b)



Stem modified into spine

Bougainvillea sp.

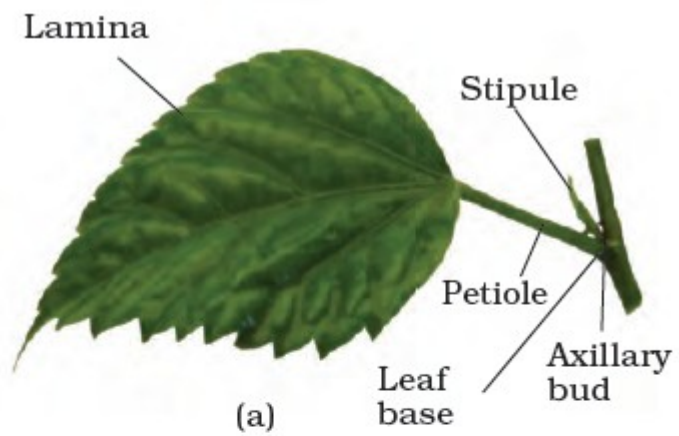
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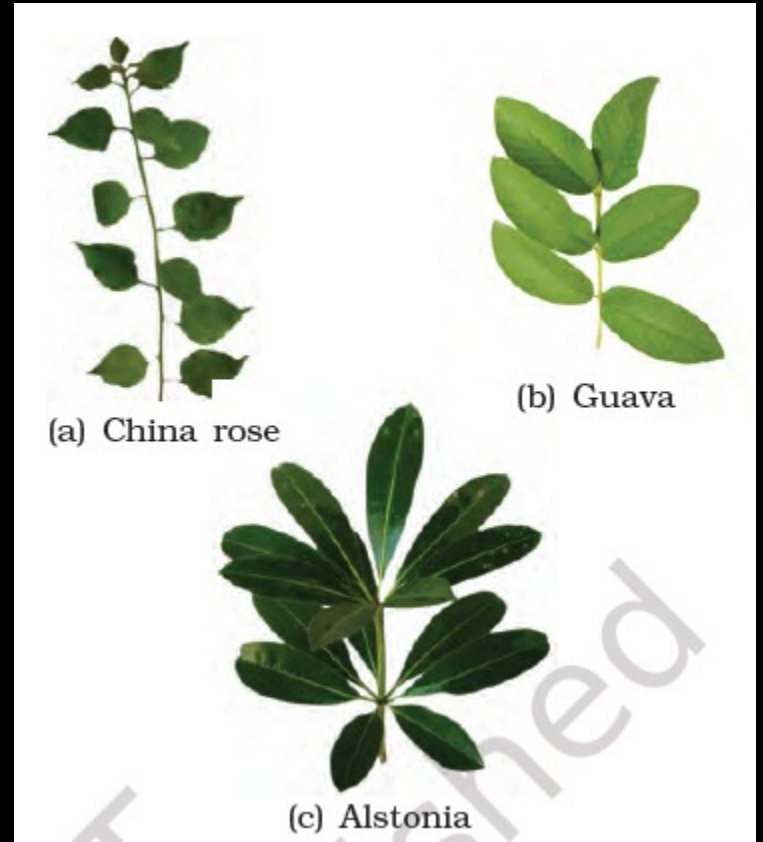
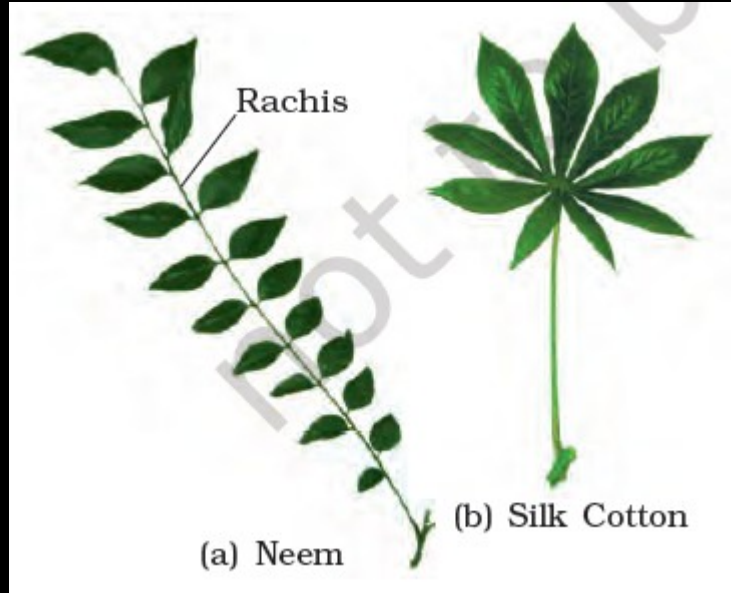


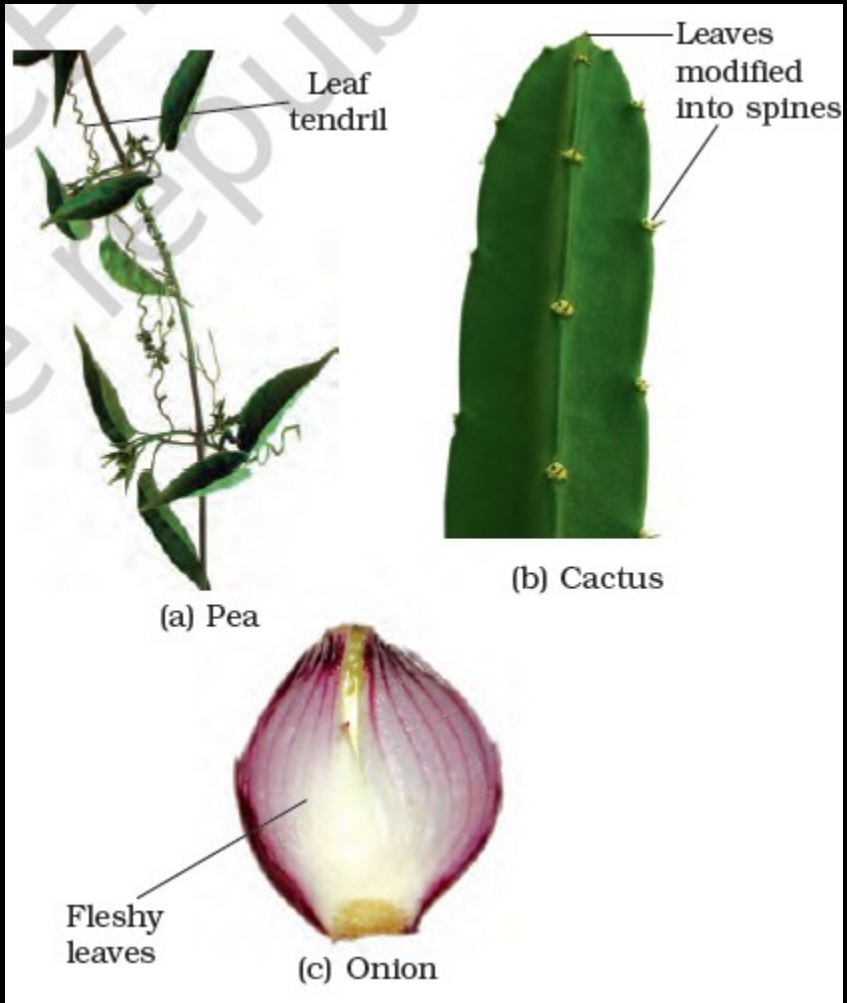
*Oxalis* sp.

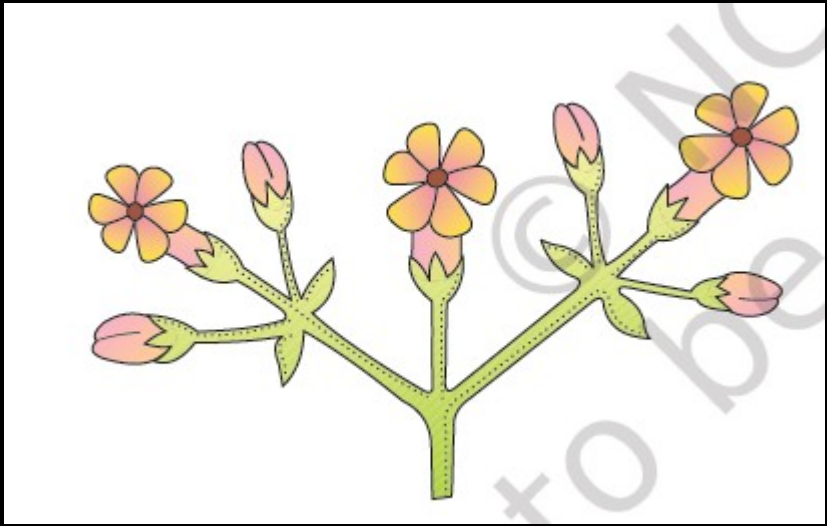
Roots arising from nodes

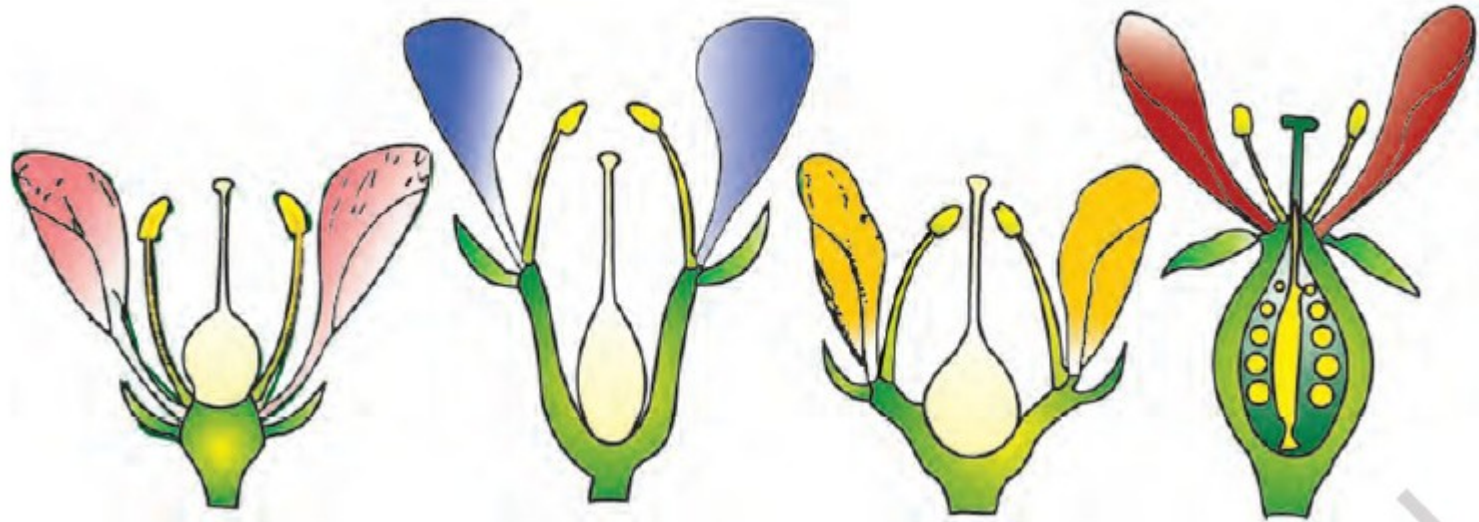
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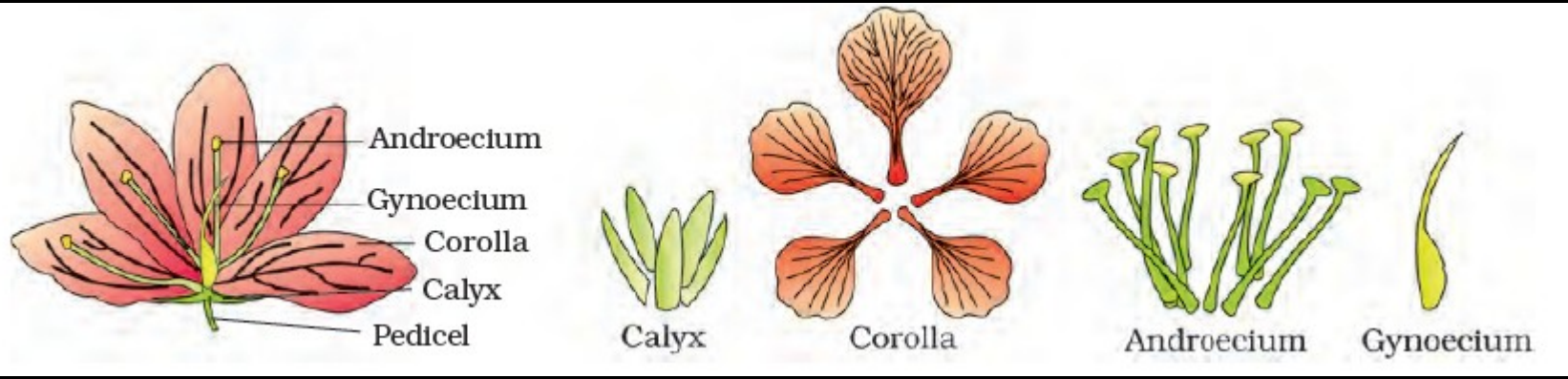


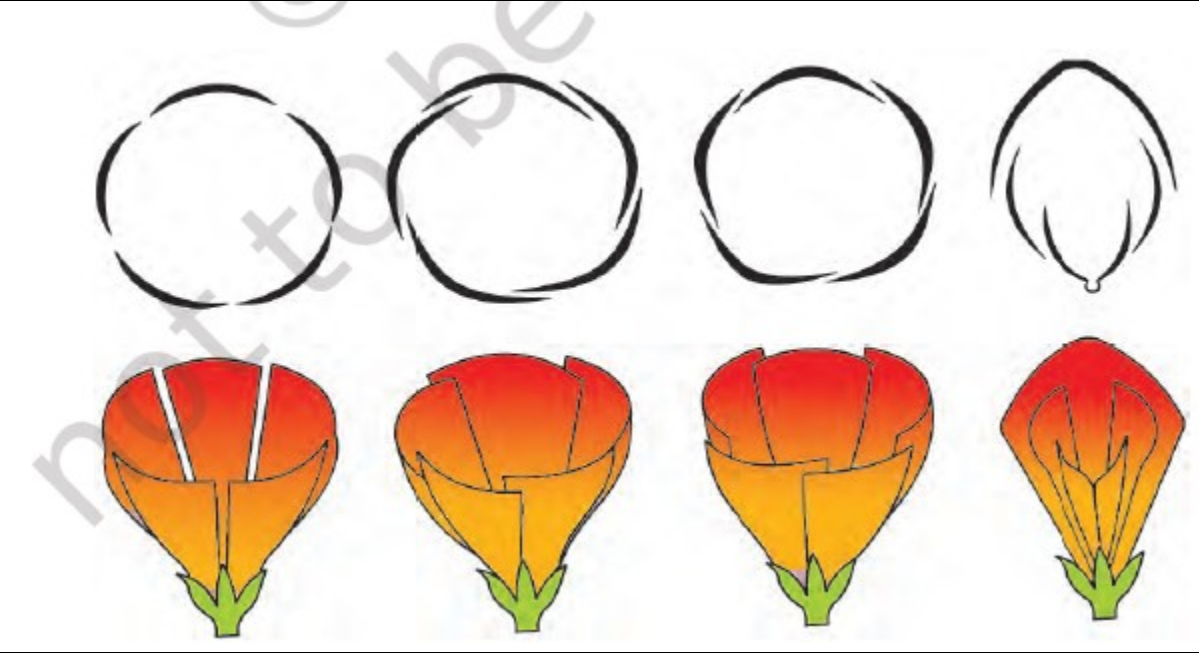


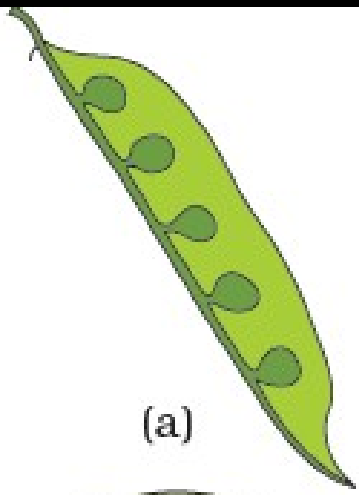




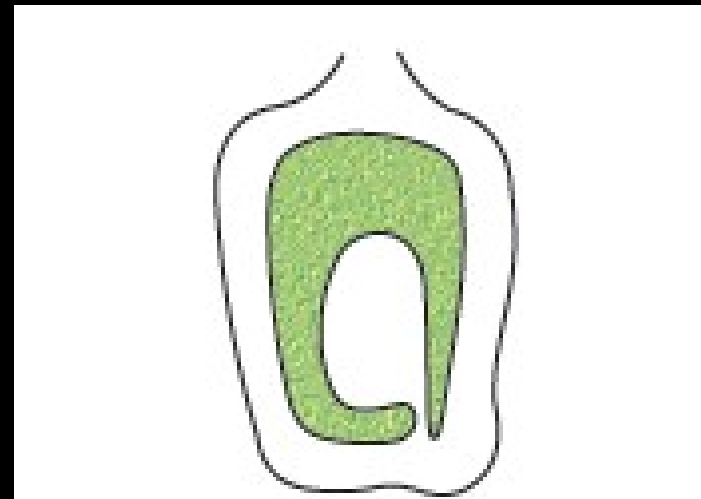
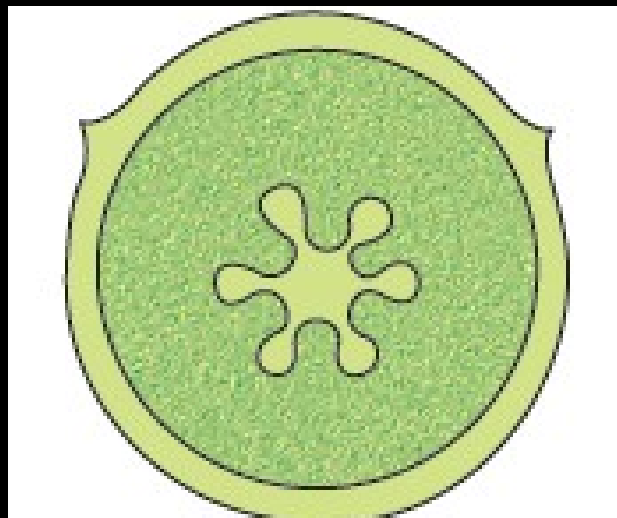
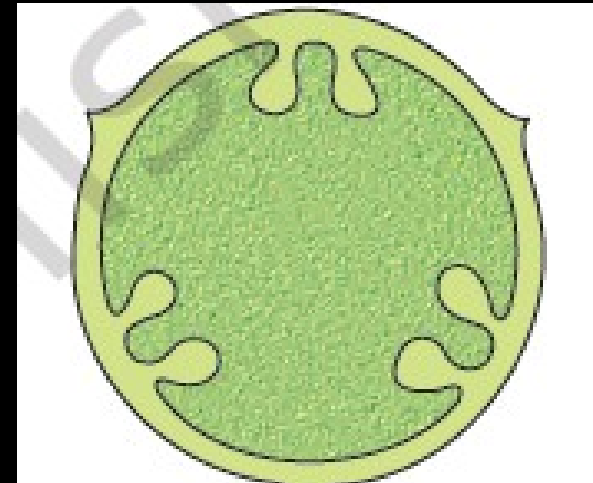
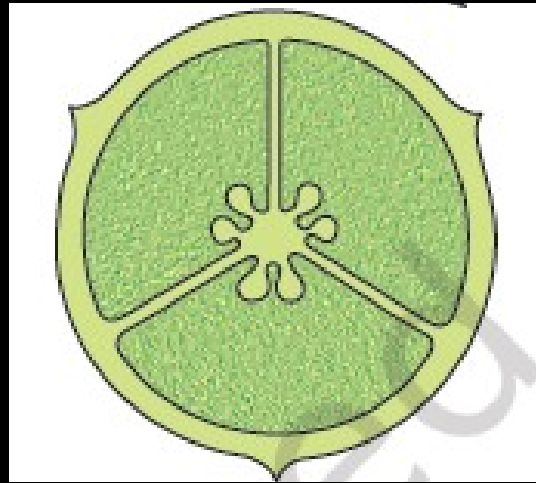


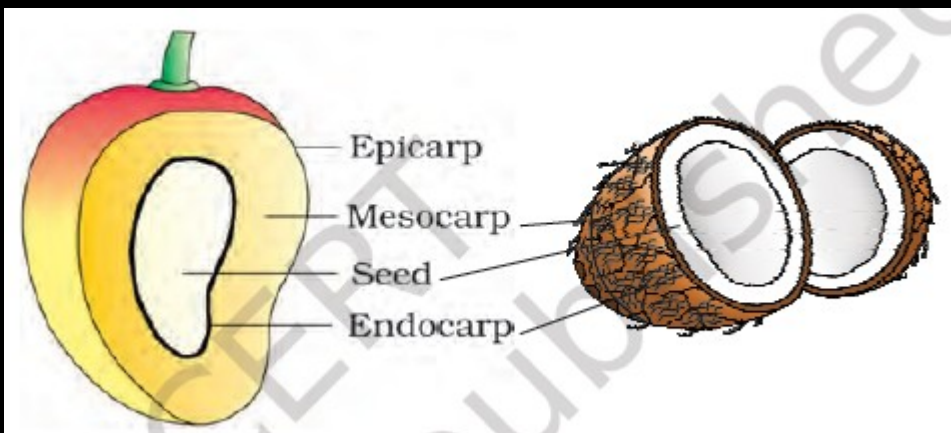


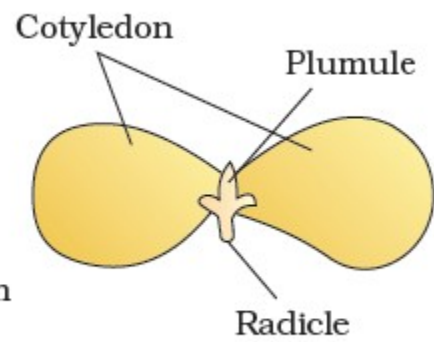
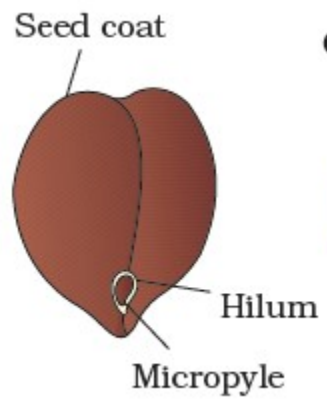


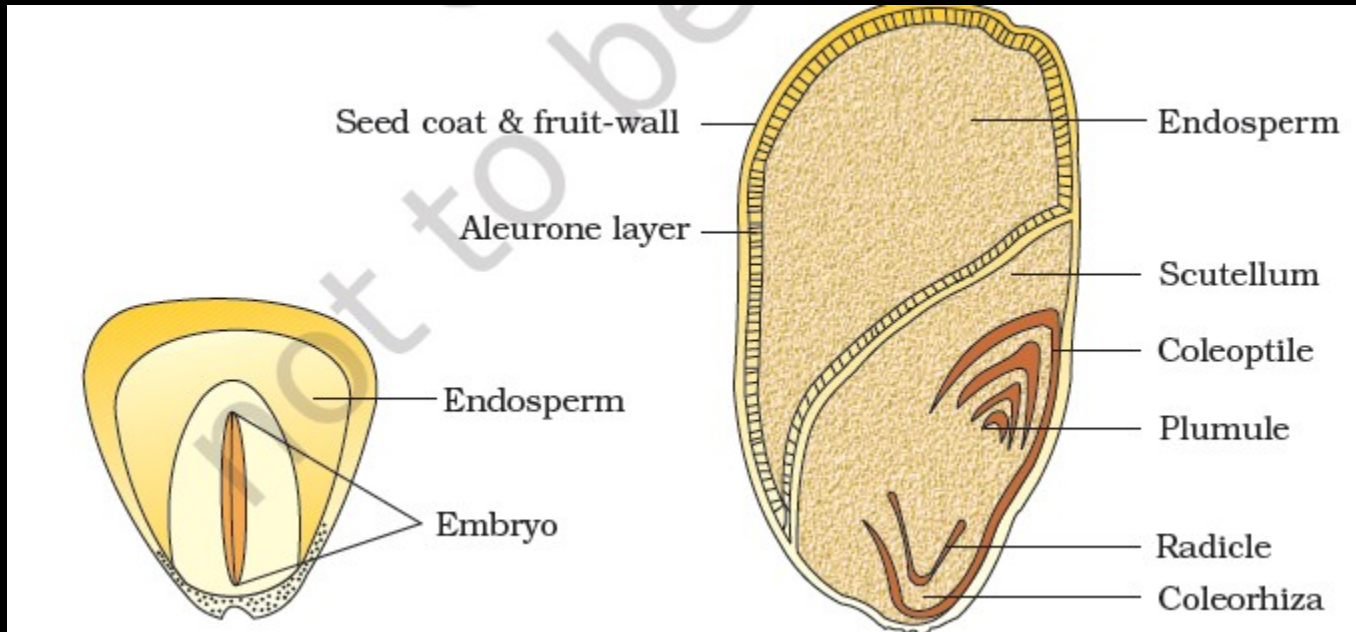


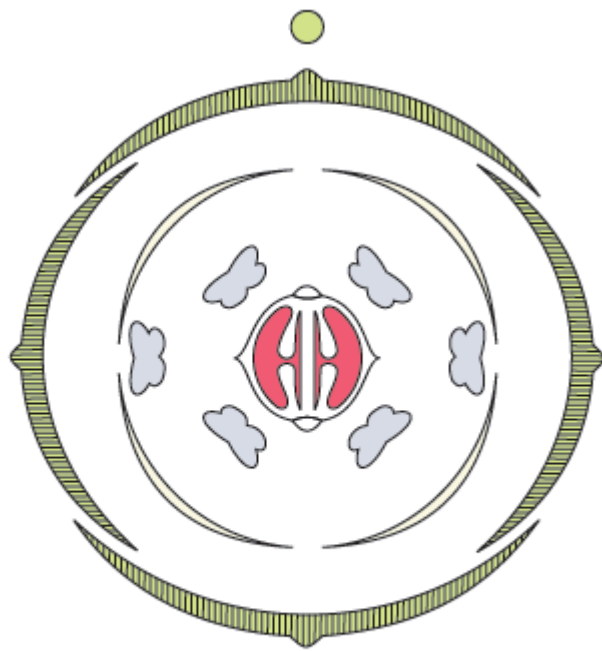
(a)



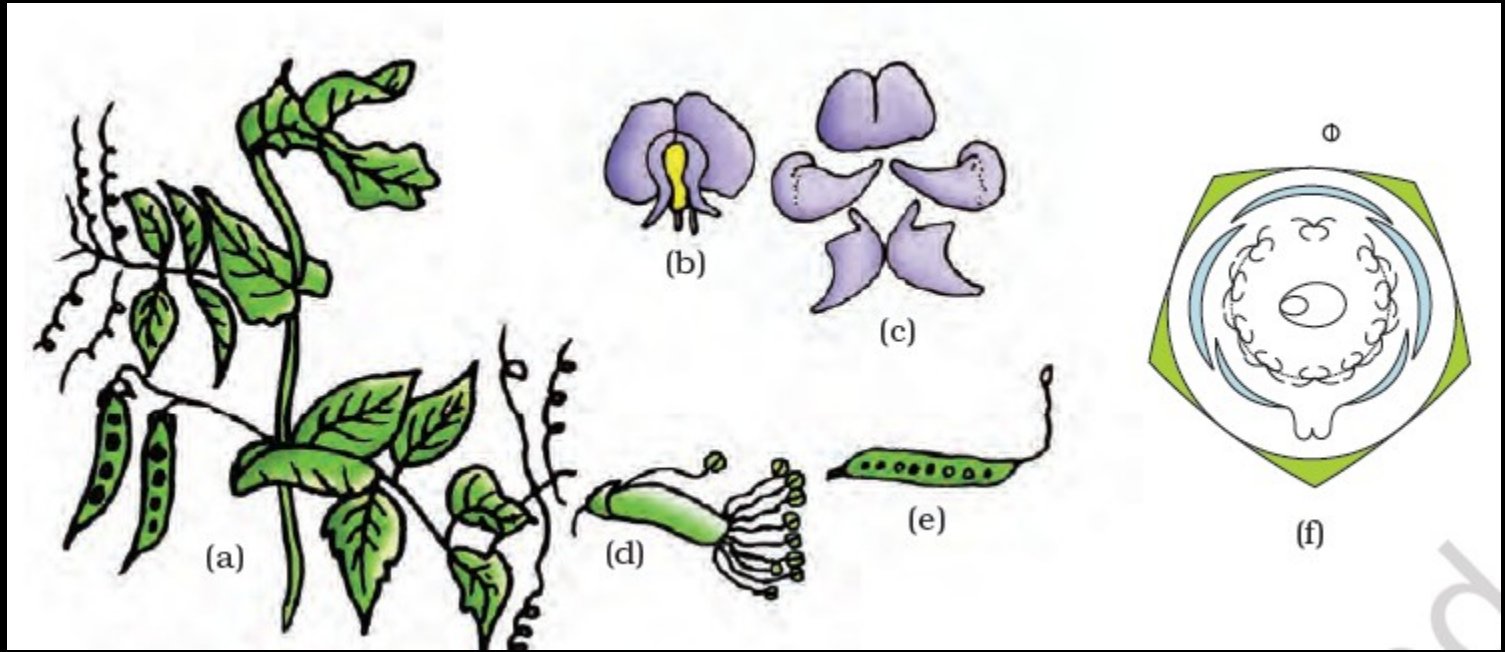








$$\oplus \begin{matrix} \text{♂} \\ \text{♀} \end{matrix} K_{2+2} C_4 A_{2+4} \underline{G}_{(2)}$$



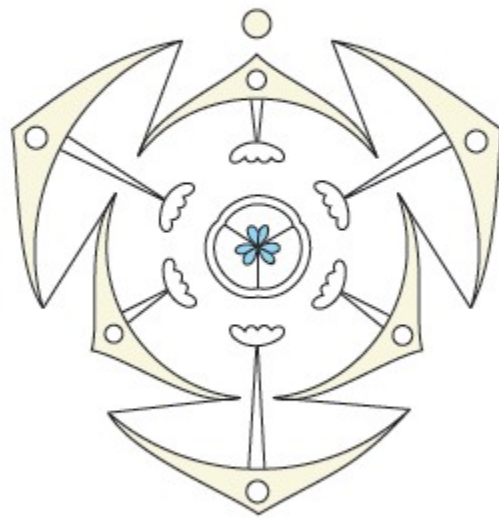




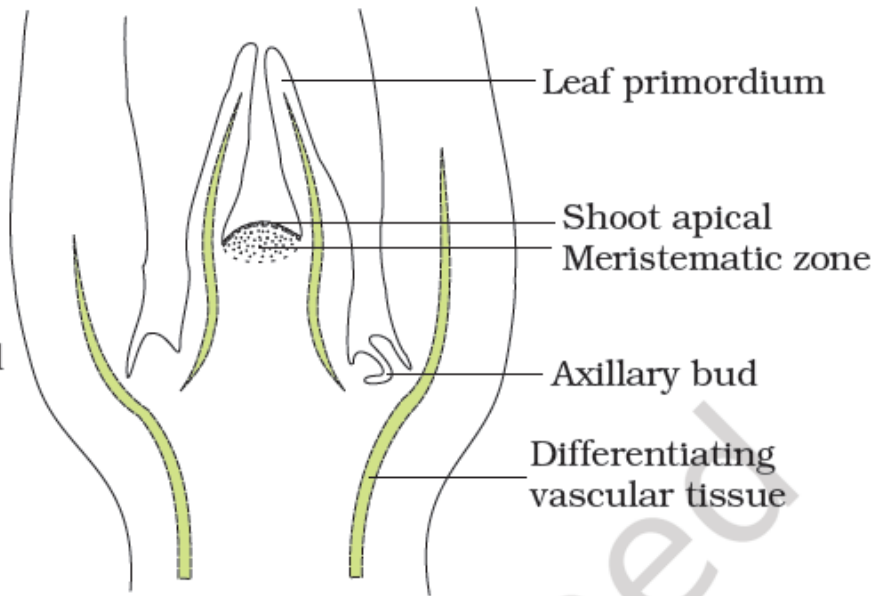
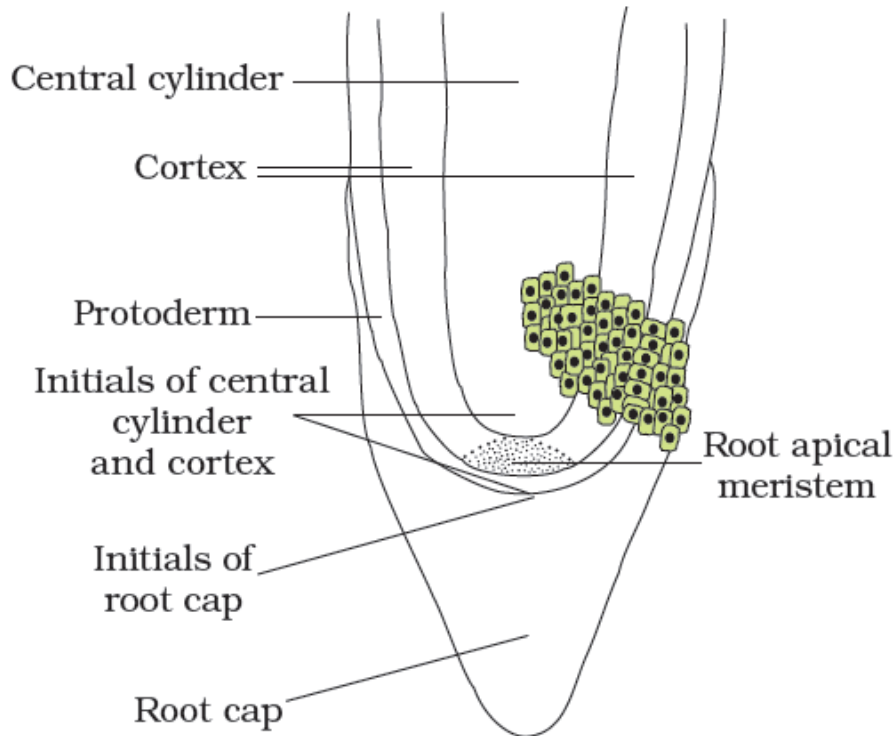
(b)

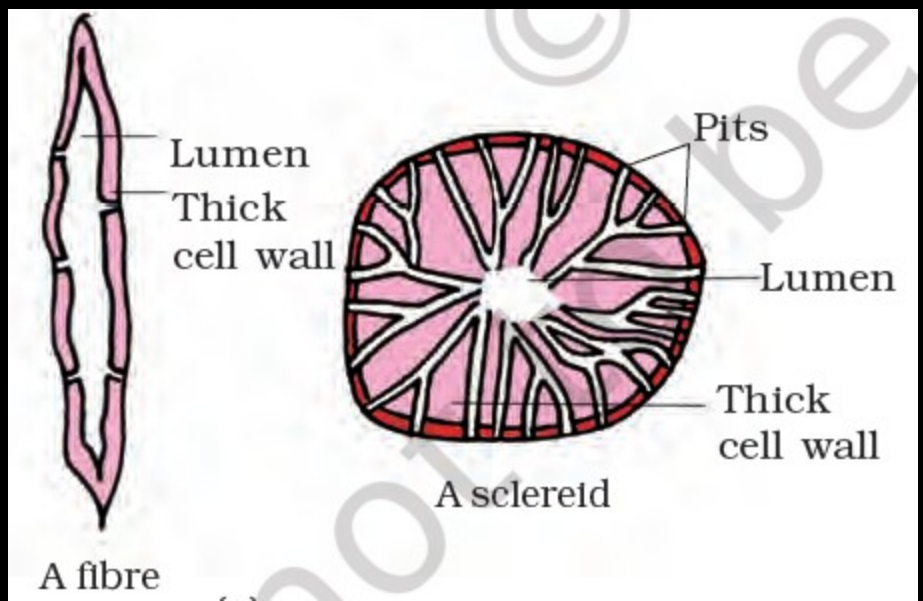
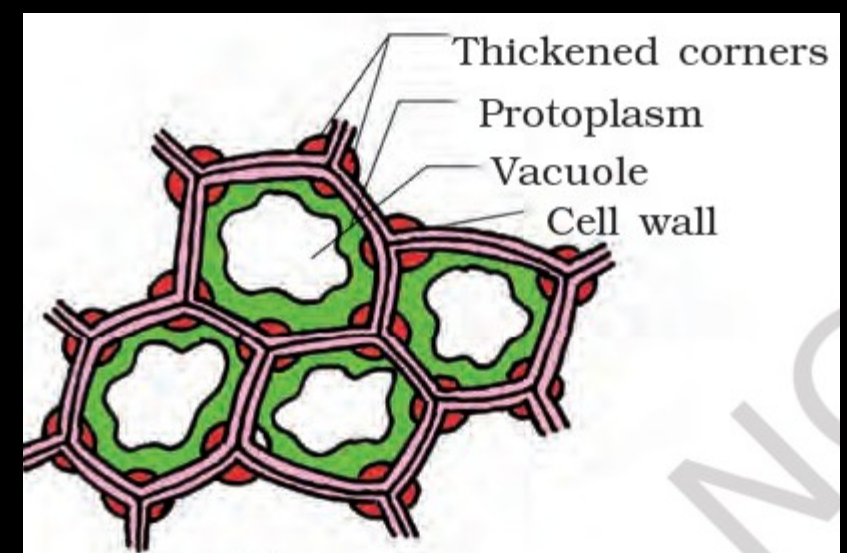
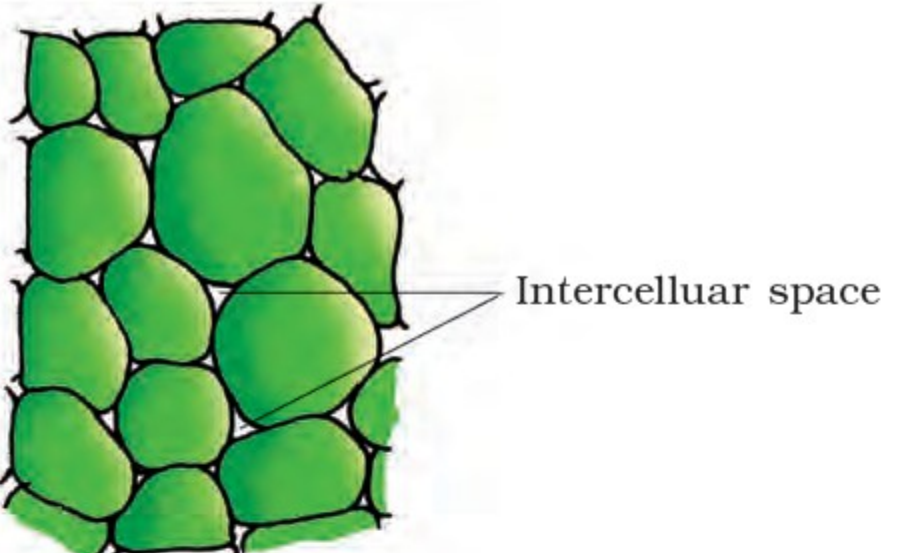


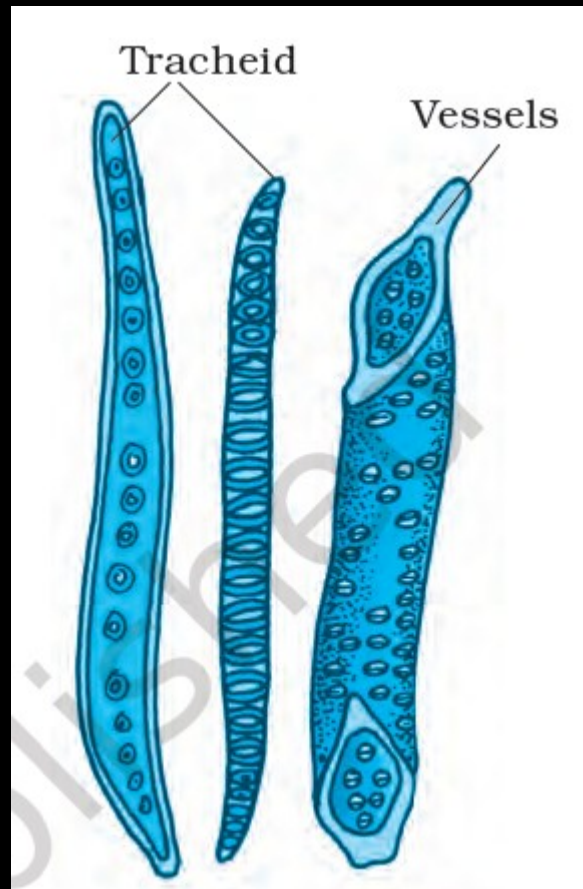
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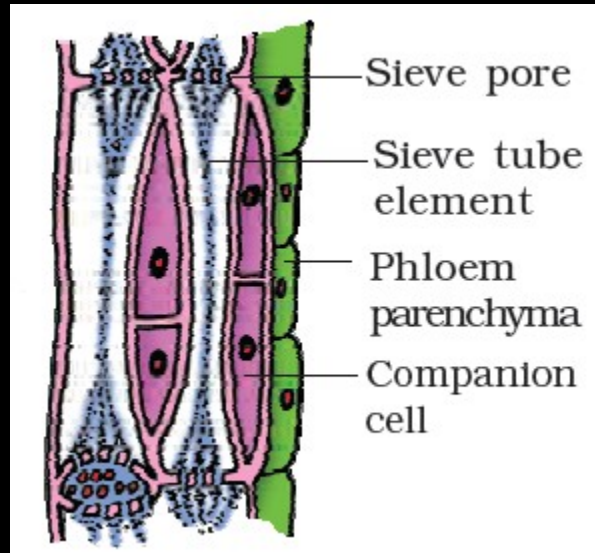


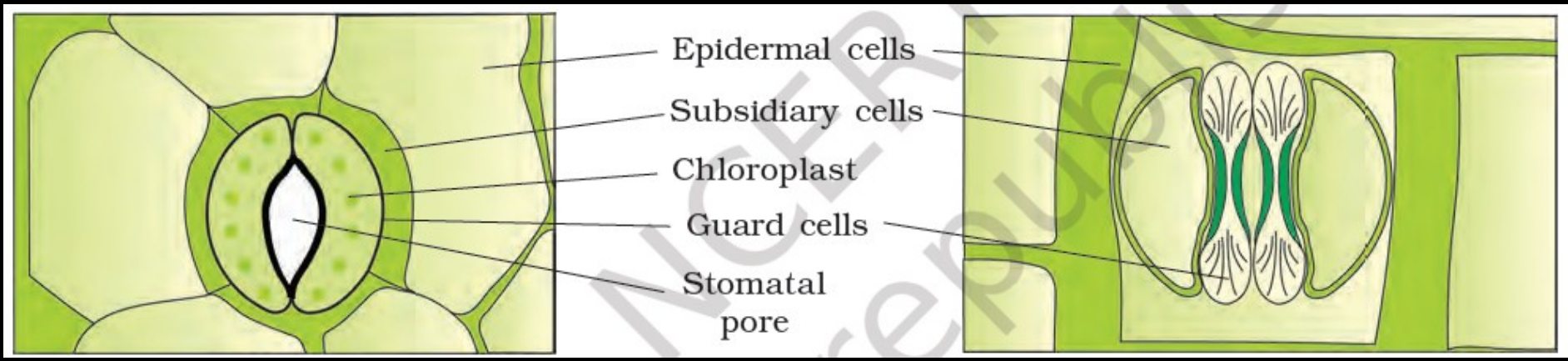
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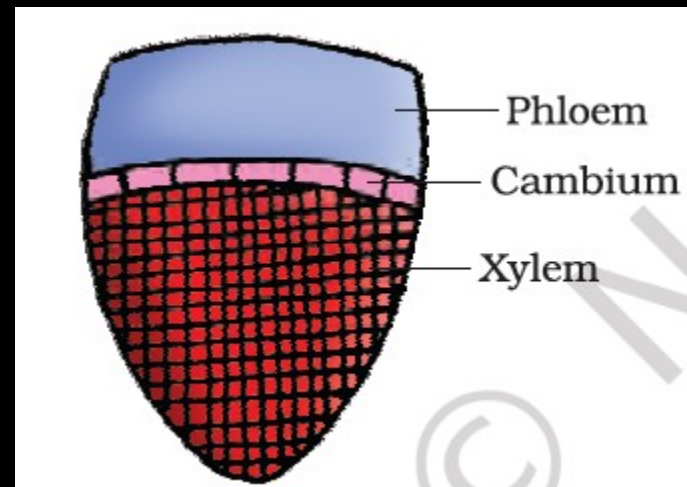
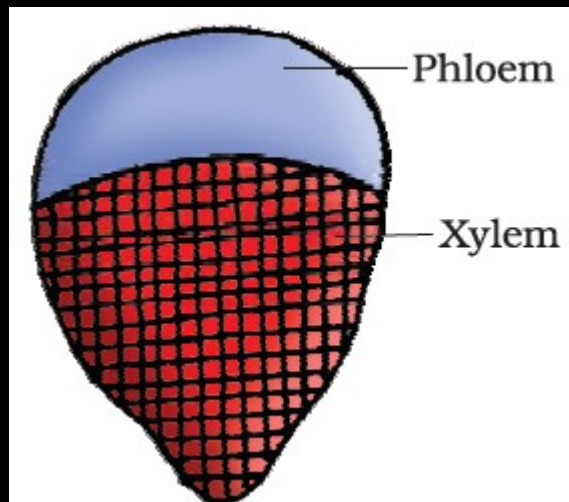
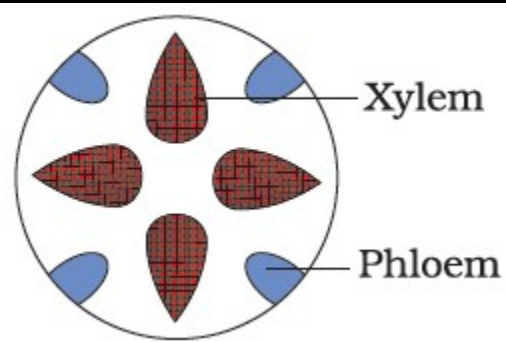


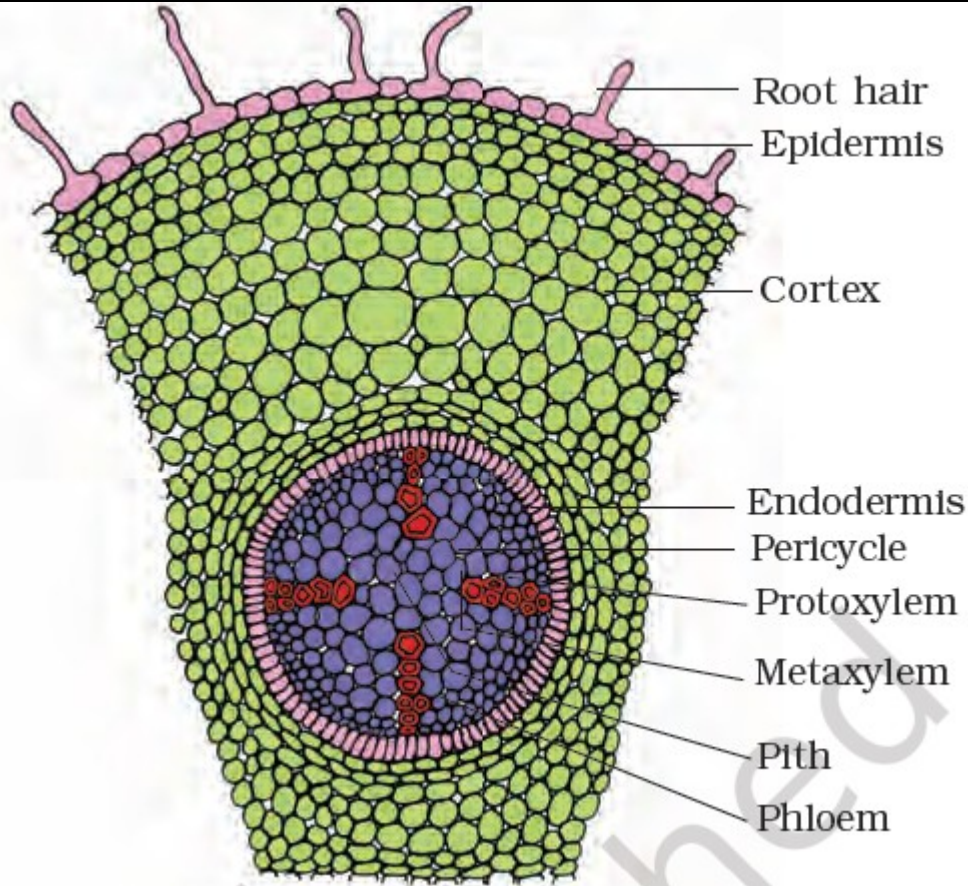


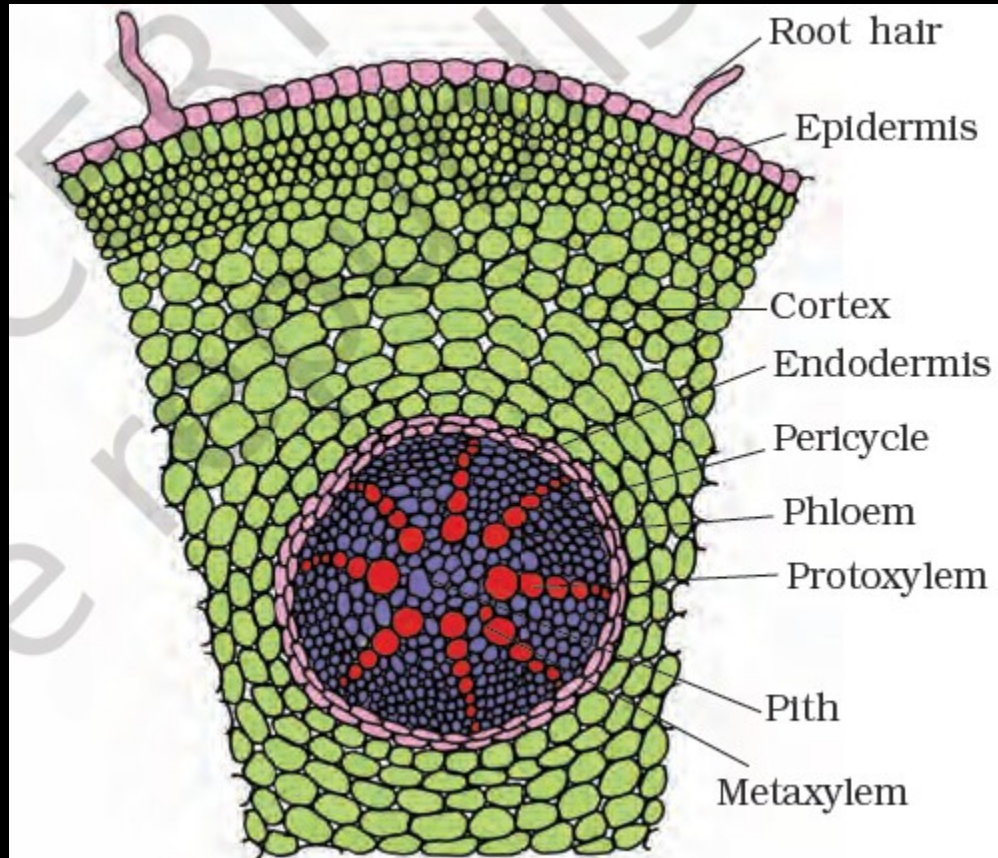


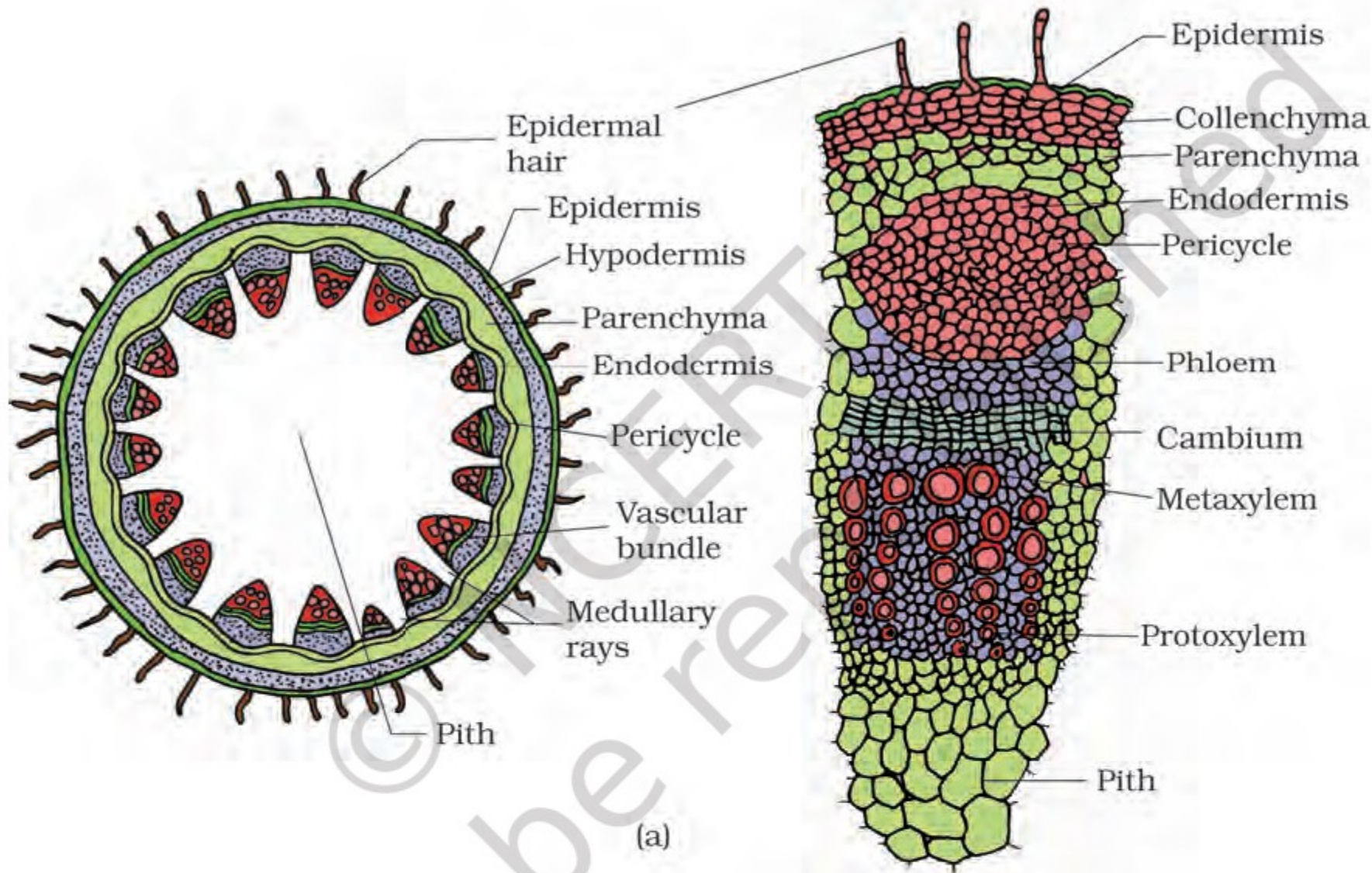


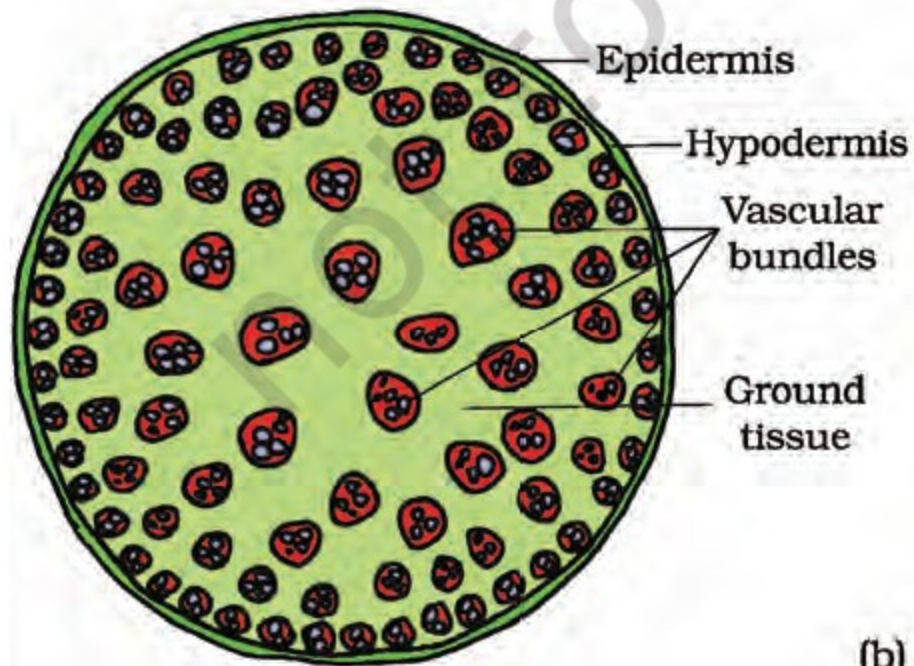




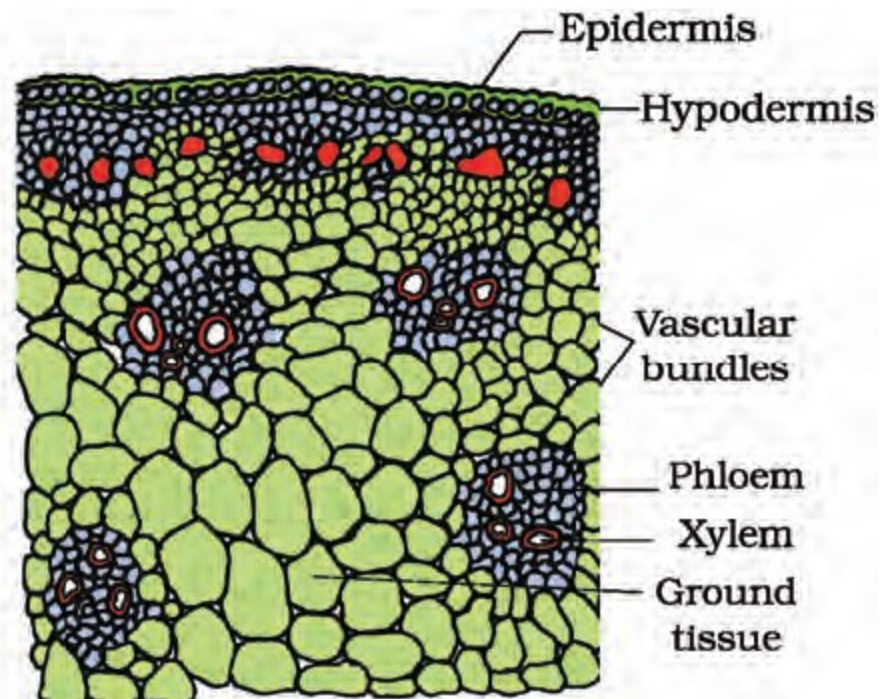


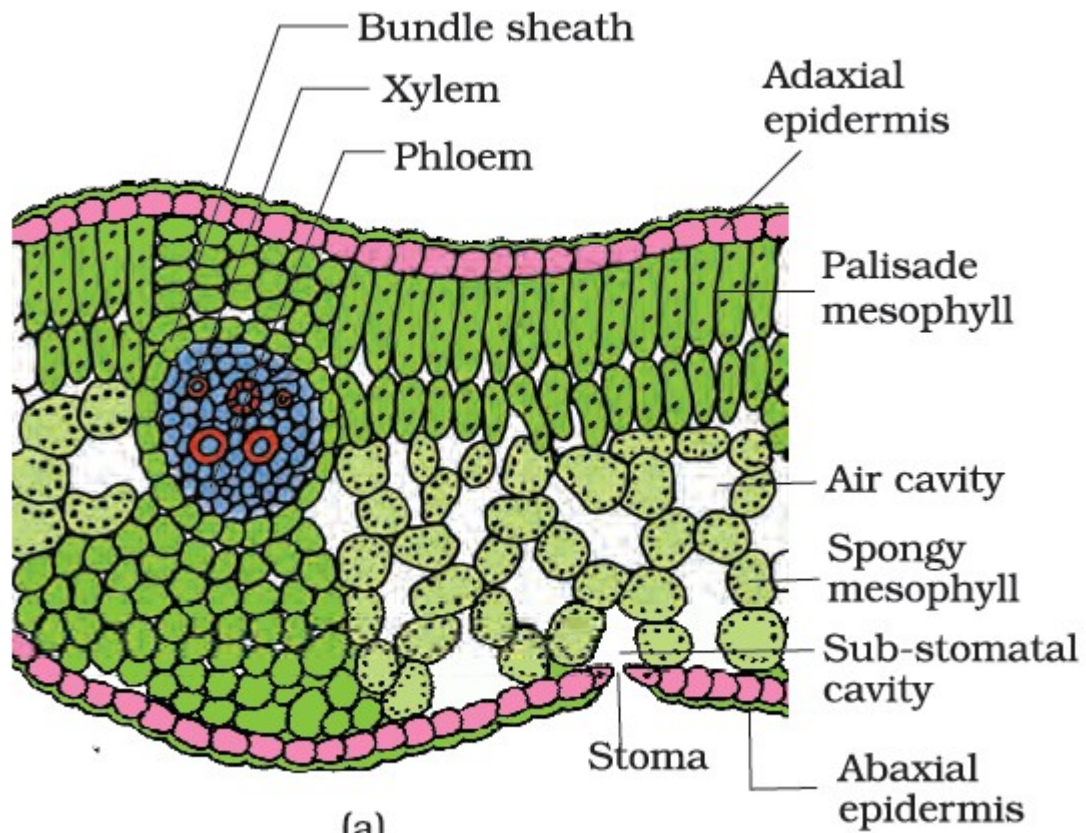


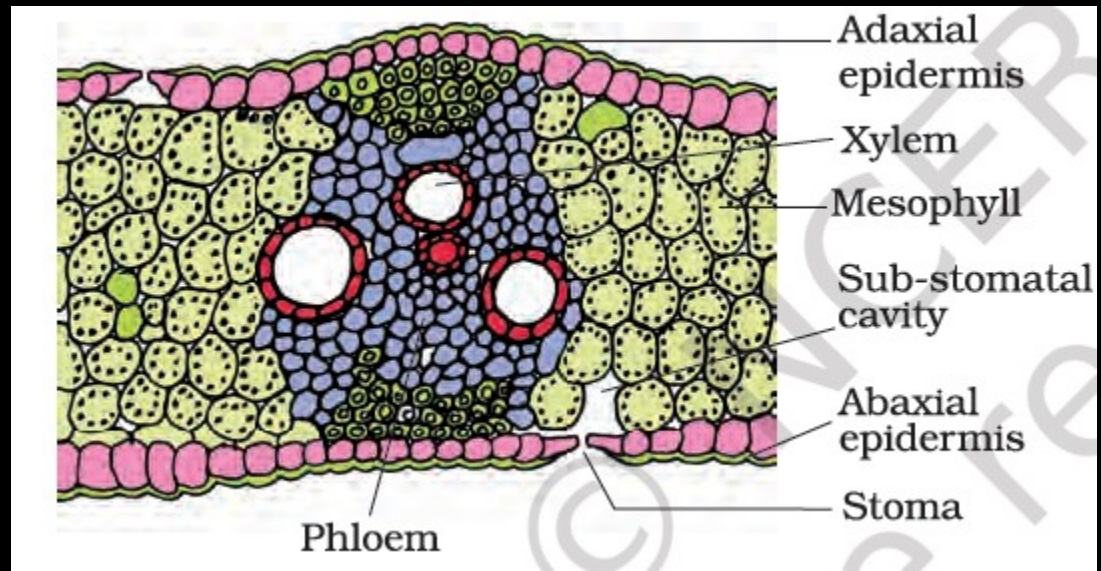


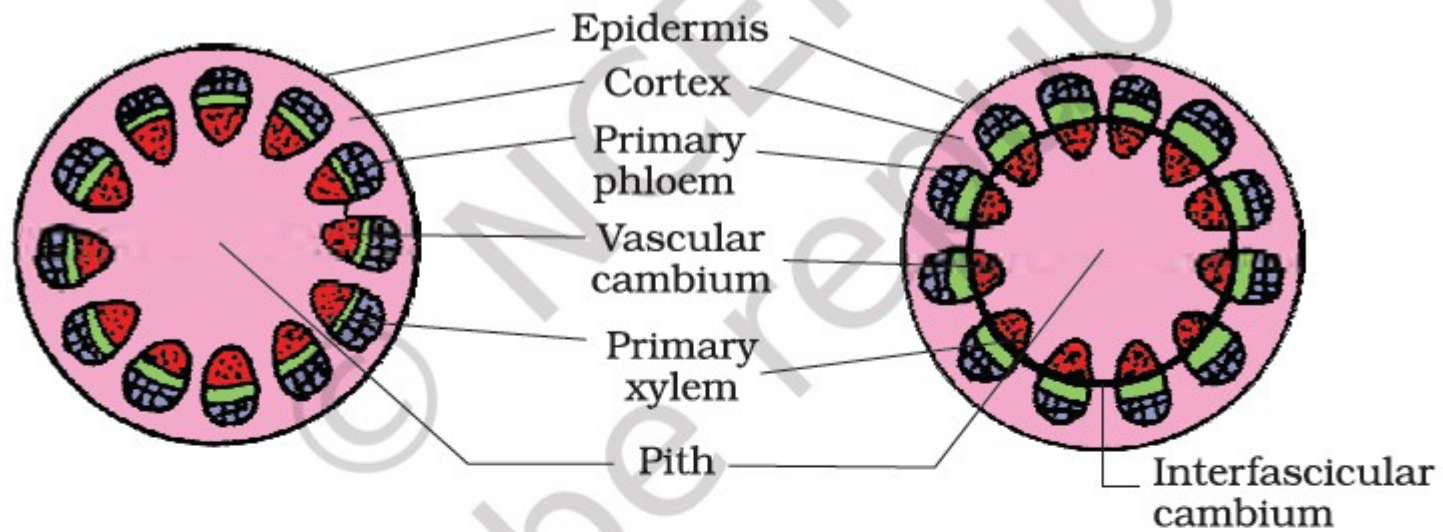


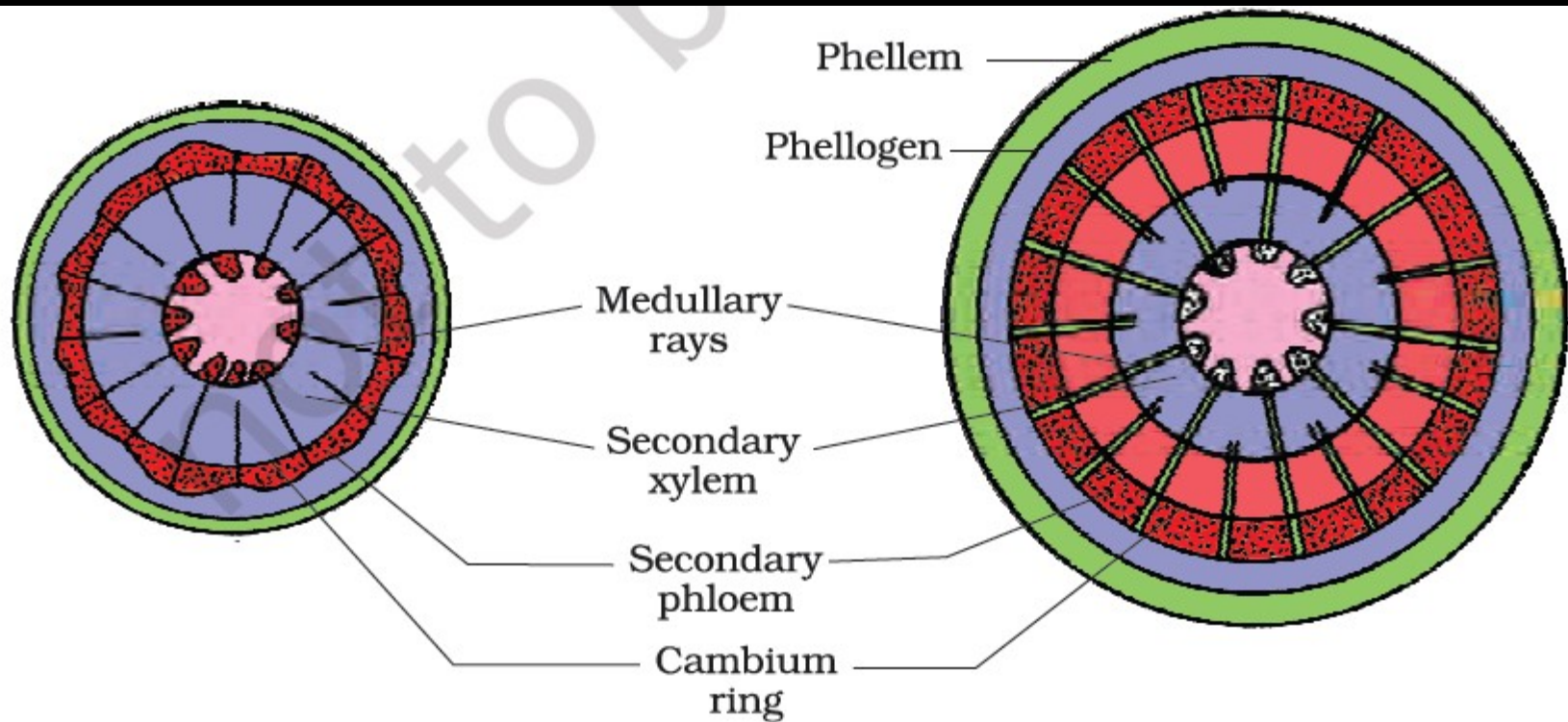
(b)

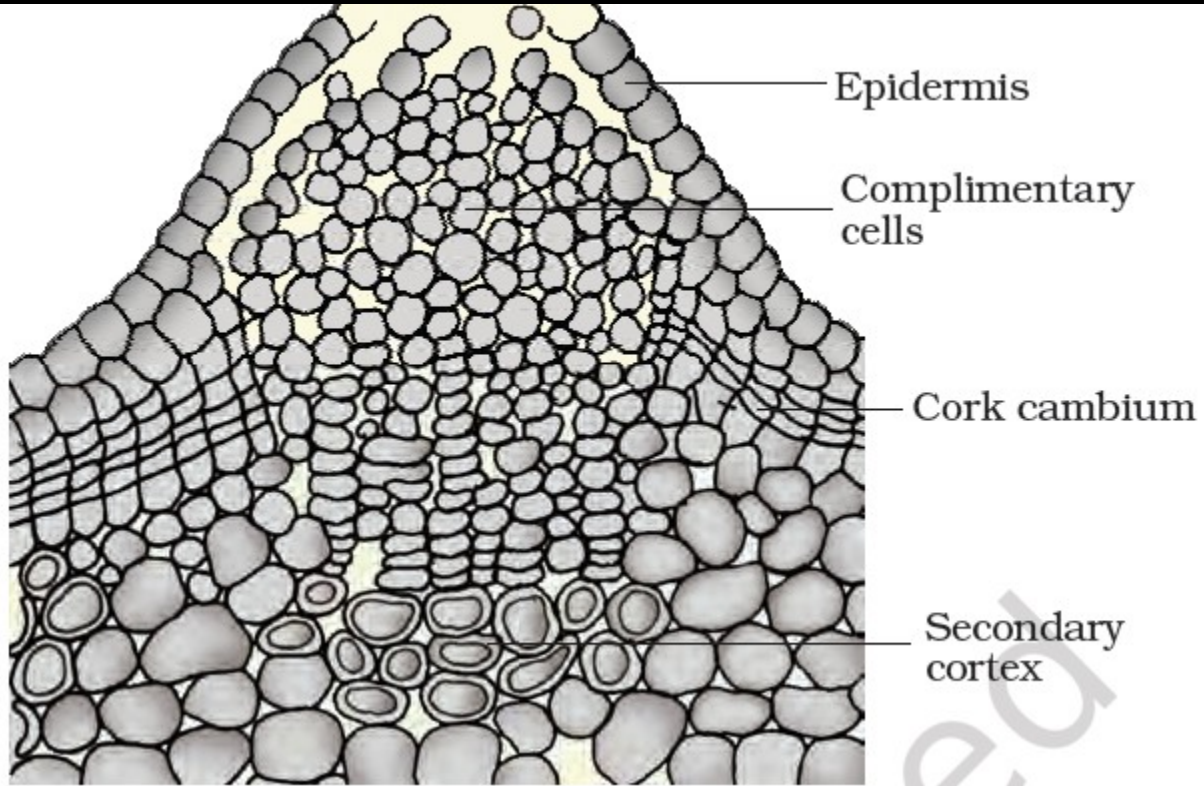


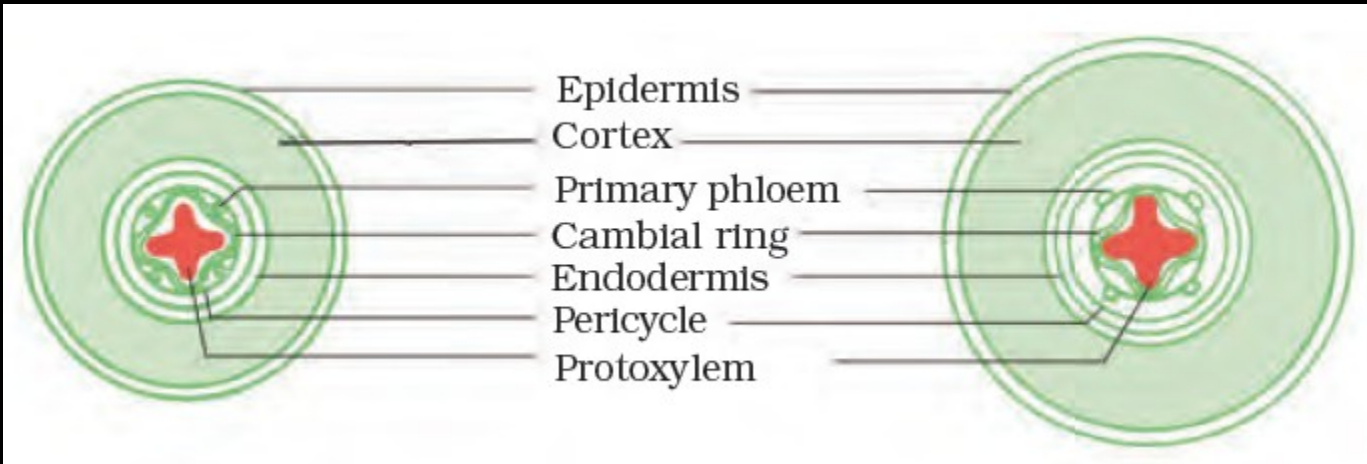


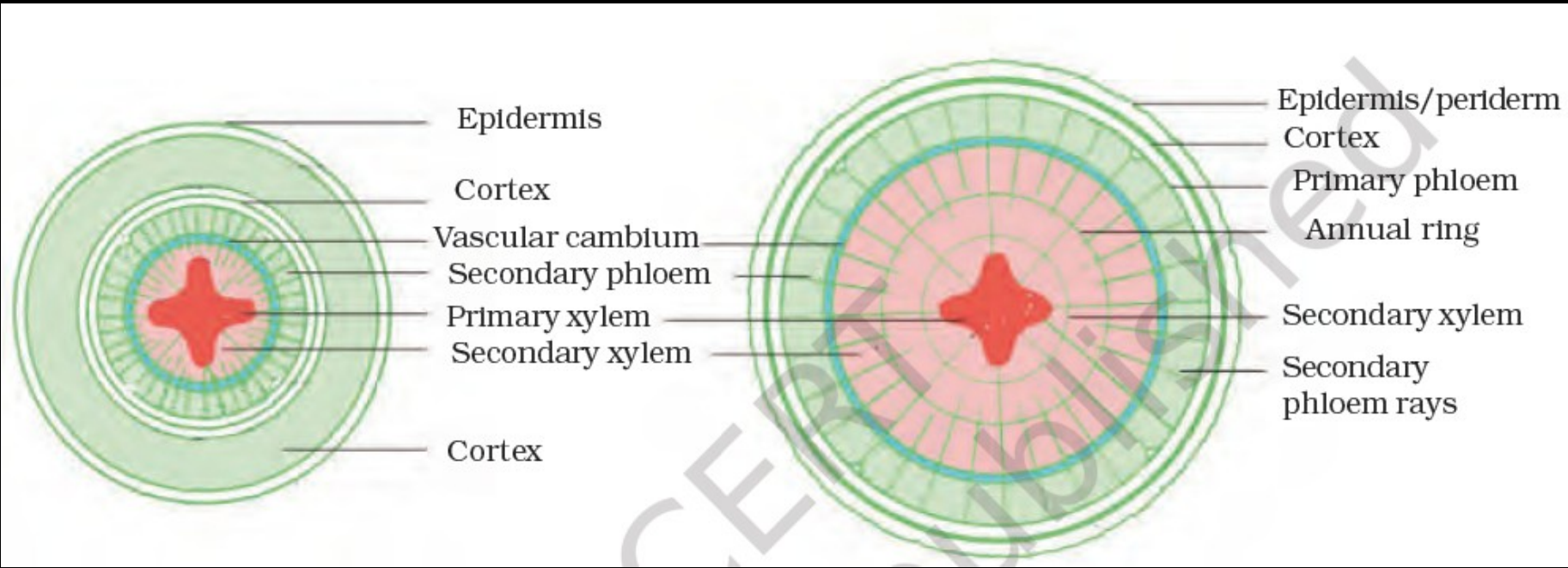












# Photoperiodism

Flowering is an annual rhythm controlled by exogenous (external) factors (many plants only flower at a particular time of the year). This response to the changing day-length (photo-period) is known as photoperiodism.

Plants can respond to changing day length in three different possible ways:



Note: while many plants recognise seasonal changes by changing photoperiod (day length), this is not always the sole determining factor. Many plants only flower when they are exposed to colder winter temperatures. This process is known as **vernalisation**.

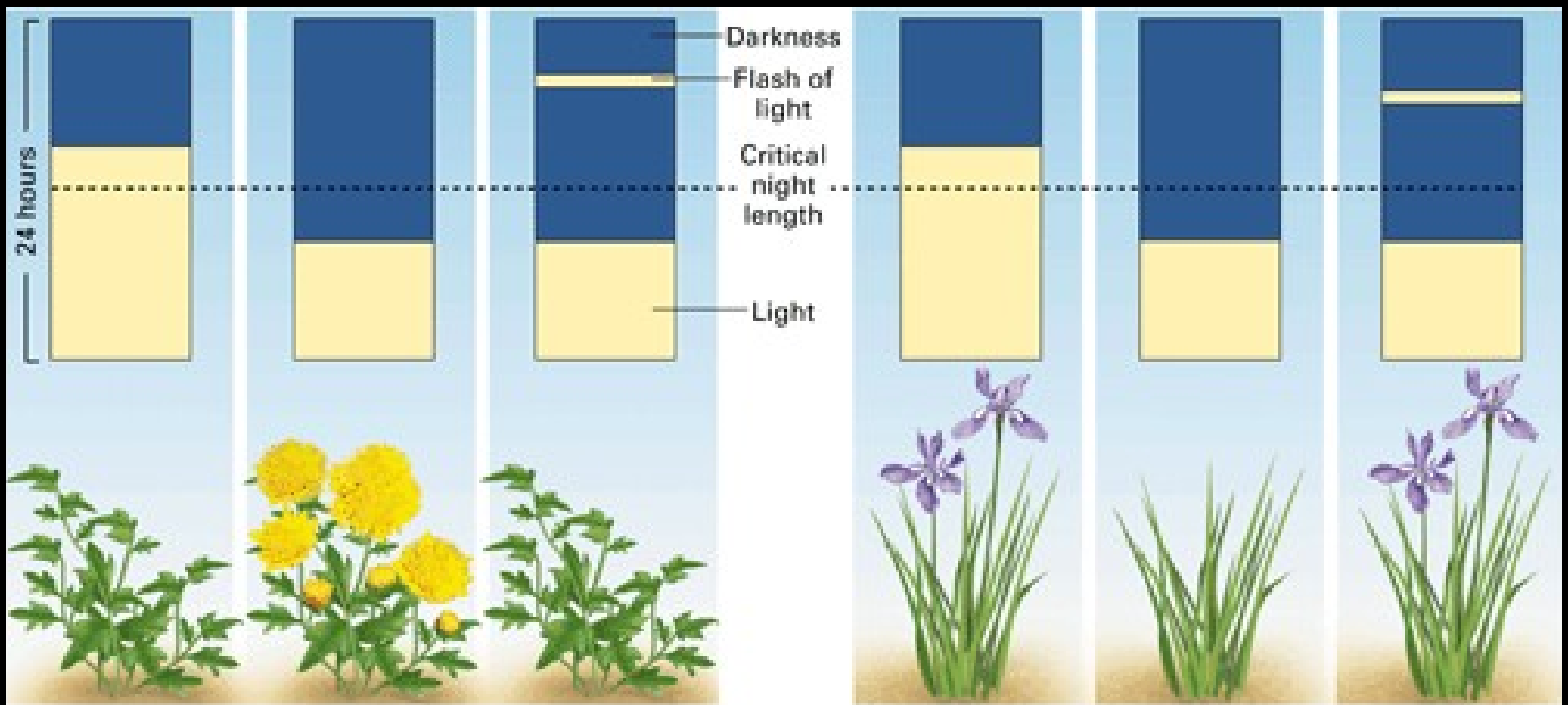
**Long Day Plants** flower when the photoperiod (day) exceeds a critical day length.

**Short Day Plants** flower when the photoperiod is less than the critical day length.

However, it has actually been discovered that it's the **night length**, not the day length that controls flowering.

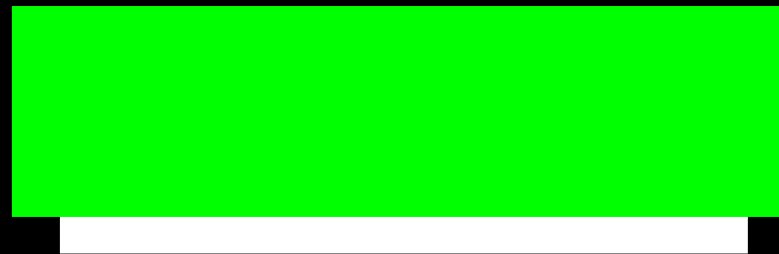
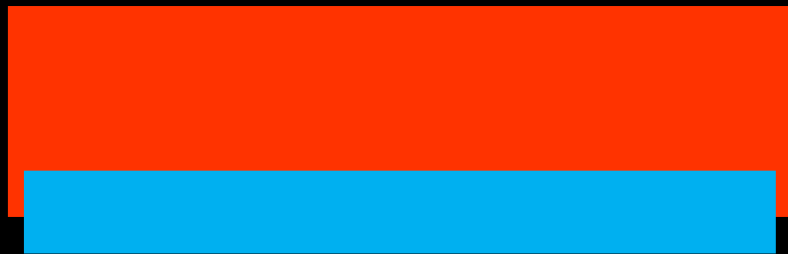
The period of uninterrupted darkness (critical night length) is what actually controls flowering. Therefore...

- Long Day Plants are actually Short Night Plants
- Short Day Plants are actually Long Night Plants

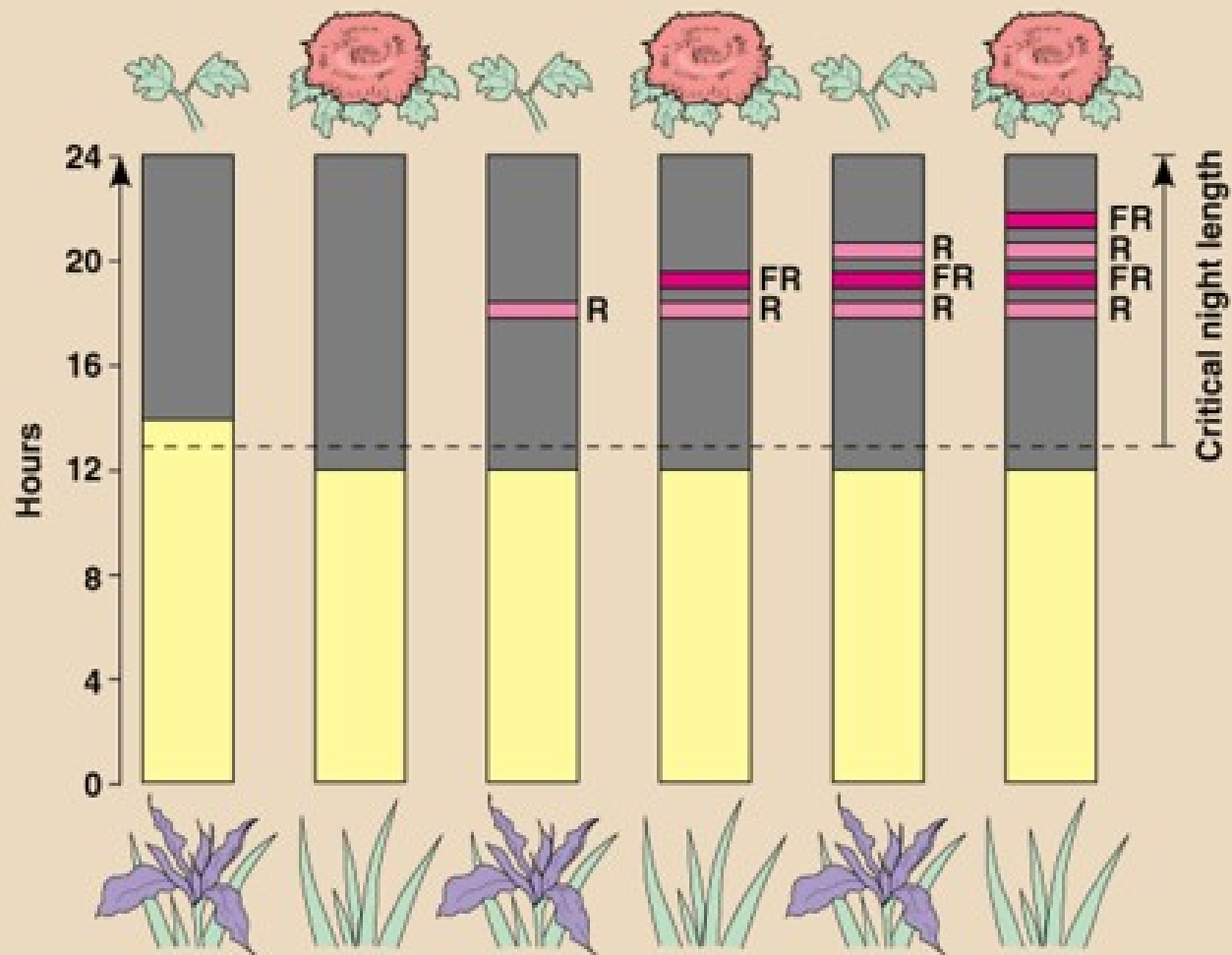


**a. Short-day (long-night) plants**

**b. Long-day (short-night) plants**



### Short-day (long-night) plant



### Long-day (short-night) plant

