★ VEGETATIVE REPRODUCTION: FRAGMENTATION.
★ ASEXUAL REPRODUCTION: ZOOSPORE (COMMON)
MOTILE (FLAGELLATED), ENDOGENOUS FORMED IN ZOOSPORANGIUM.

Thalloid (ROOT, STEM, LEAF) ABSENT, AUTOTROPH, CHLOROPHYL, AQUATIC (FRESH H_2O, MARINE H_2O) WOOD, SOIL, MOIST STONE

★ AIGAE + FUNGUS: LICHEN ON SLOTH BEAR
★ FRUIT, FLOWER, SEED, EMBRYO, VASCULAR TISSUE: ABSENT

★ SIZE, FORM: HIGHLY VARIABLE EG: VOLVOX (COLONIAL) AND ULOTHRIX, SPIROGYRA (FILAMENTOUS) AND SOME MARINE AIGAE ARE MASSIVE/BIG (KELPS) → BROWN AIGAE

★ HAIF OF CO_2: FIX: PHOTOSYNTHESIS, INCREASE O_2 CONTENT, PRODUCER, SYNTHESIS FOOD UPON AQUATIC ANIMAL DEPEND.

★ PORPHYRA (RED), LAMINARIA & SARGASSUM (BROWN AIGAE) AMONG 70 MARINE SPECIES, USED (FOOD)

★ CHLORELLA (PROTISTA), SPACE FOOD, PROTEIN UNICELLULAR

★ SOME GA → PYRENOID PRESENT IN CHLOROPLAST
→ CENTRE: PROTEIN
→ PERIPHERY: STARCH.

HYDROCOLLOID

SUBSTANCE: H_2O ABSORBING CAPACITY.
AIGIN: BA AND CARRAGEEN: RA
AGAR-AGAR: RA (GRACILARIA, GELIDIUM), USED TO GROW MICROBE IN LAB, PREPARATION OF ICE CREAM, JELLIES

OOGAMOUS

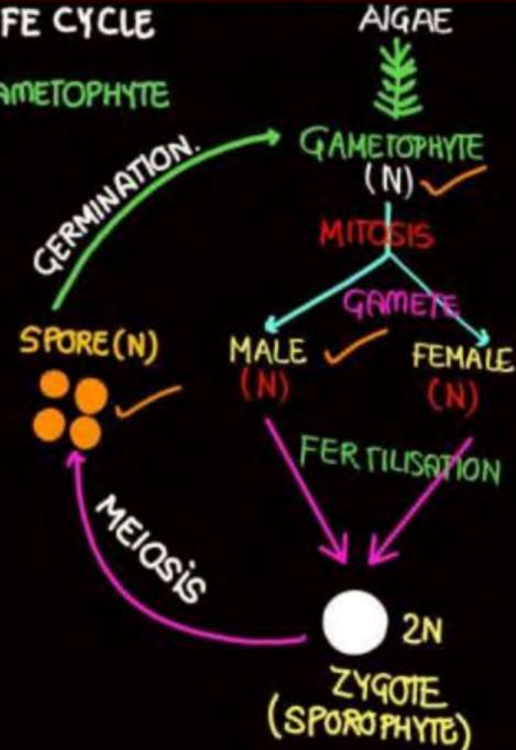
MALE GAMETE: USUALLY MOTILE, SMALL
FEMALE GAMETE: NON MOTILE, LARGE
eg VOLVOX (GA), FUCUS (BA), RED AIGAE → MALE GAMETE (NON MOTILE)

SEXUAL REPRODUCTION

ISOGAMOUS: FUSING GAMETE MORPHOLOGICALLY SIMILAR (FLAGELLATED, ULOTHRIX) NON FLAGELLATED, SPIROGYRA), GA
ANISOGAMOUS: MORPHOLOGICALLY DISIMILAR. EUDORINA, GA

LIFE CYCLE

MAIN BODY: GAMETOPHYTE
HAPLONTIC LIFE CYCLE, HAPLOID ALGAE



CHLOROPHYCEAE	PHAEOPHYCEAE	RHODOPHYCEAE

CHLOROPHYCEAE

* GREEN ALGAE(GA), Chl a,b Carotene, xanthophyll.
* CELL WALL: RIGID(HARD), DOUBLE LAYER, OUTER(PECTIN), INNER (CELLULOSE)
* PYRENOIDS PRESENT
* VEGETATIVE: FRAGMENTATION
* ASEXUAL: ZOOSPORE
* SEXUAL: ISOGAMOUS, ANISOGAMOUS, OOGAMOUS.
* CHLOROPLAST: DISC, PLATE, RETICULATE, CUP, SPIRAL/ RIBBON SHAPE
* UNICELLULAR: CHLAMYDOMONAS
* COLONIAL: VOLVOX
* FILAMENTOUS: ULOTHRIX, SPIROGYRA.
* STORED FOOD: STARCH & OIL DROPLETS (IN FEW)

PHAEOPHYCEAE

* BROWN ALGAE (OLIVE GREEN TO DIFFERENT SHADES OF BROWN COLOUR, DEPEND UPON XANTHOPHYLL.
* Chl a, c carotene, FUCOXANTHIN ↑
* MOSTLY MARINE, MULTICELLULAR,
* FOOD: LAMINARIN & MANNITOL (COMPLEX, CARBOHYDRATE).
* PROTOPLASM: NUCLEUS, PLASTID, VACUOLE PRESENT
* BODY: SIMPLE BRANCHED, FILAMENTOUS ECTOCARPUS OR PROFUSELY (BUSHY) BRANCHED MASSIVE/GIANT ⟶ KELPS, 100m (LAMINARIA)
* BODY: ① HOLDFAST: ATTACHMENT ② STIPE: FOOD CONDUCTION ③ FROND/LEAF LIKE. PHOTO-SYNTHESIS
* VEGETATIVE: FRAGMENTATION & ASEXUAL: ZOOSPORE PEAR/PYRIFORM SHAPE, FLAGELLA UNEQUAL, AT LATERAL END.
* SEXUAL: ISOGAMOUS, ANISOGAMOUS, OOGAMOUS. PEAR/PYRIFORM SHAPE: GAMETES, FLAGELLA AT LATERAL END.
* FERTILISATION: H_2O (EXTERNAL) & OOGONIUM (INTERNAL) (OOGAMOUS TYPE)

RHODOPHYCEAE

* RED ALGAE (Chl a, d, phycoerythrin), MOSTLY MARINE, MULTICELLULAR,
* VEGETATIVE: FRAGMENTATION. AND ASEXUAL: NON MOTILE SPORE
* SEXUAL: ONLY OOGAMOUS (MALE, FEMALE GAMETE: NON MOTILE)
* MORE: WARMER REGION (HIGH TEMP).
* WELL LIGHTER REGION & BOTTOM OF SEA.
* FOOD: FLORIDEAN STARCH. (SIMILAR TO GLYCOGEN & AMYLOPECTIN)
* COMPLEX POST FERTILISATION STRUCTURE FORMED

eg: GRACILARIA, GELIDIUM, POLYSIPHONIA, PORPYRA.

LIVERWORTS 'G' 'S'

⇒ GAMETOPHYTE + SPOROPHYTE

'G'	'S'
★ (GREEN, PROSTRATE)	(ERECT)
★ HAPLOID FORMED GAMETE (MITOSIS)	★ DIPLOID FORMED SPORE (MEIOSIS)
★ PHOTOSYNTHETIC	★ NON-PHOTOSYNT.
★ INDEPENDENT, FREE LIVING, DOMINANT/MAIN BODY.	★ DEPENDENT ON 'G'
★ MULTICELLULAR	★ MULTICELLULAR.
★ MALE & FEMALE SEX ORGAN (ANTHERIDIA & ARCHEGONIA (FLASKSHAPE).	★ ROOT, STEM, LEAF, XYLEM, PHLOEM, SEED, FRUIT ABSENT.
	★ RHIZOIDS: UNICELLULAR, UNBRANCHED.

★ MALE GAMETE TRANSFER INTO ARCHEGONIUM WITH HELP OF H_2O, DEPEND UPON H_2O FOR FERTILISATION (AMPHIBIAN OF PLANT KINGDOM)

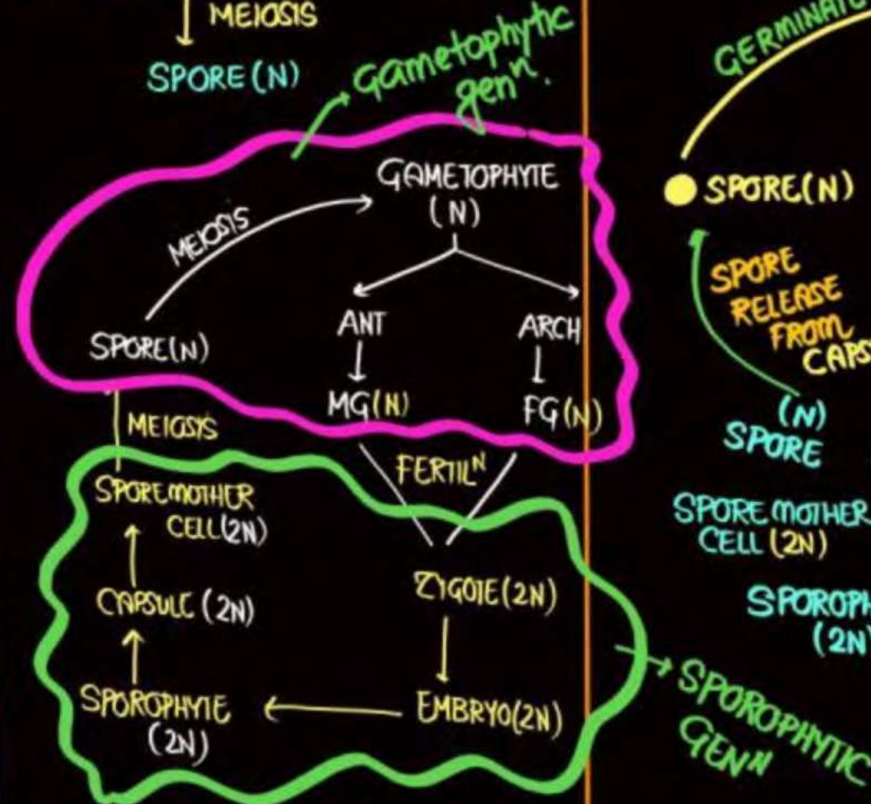
BRYOPHYTE

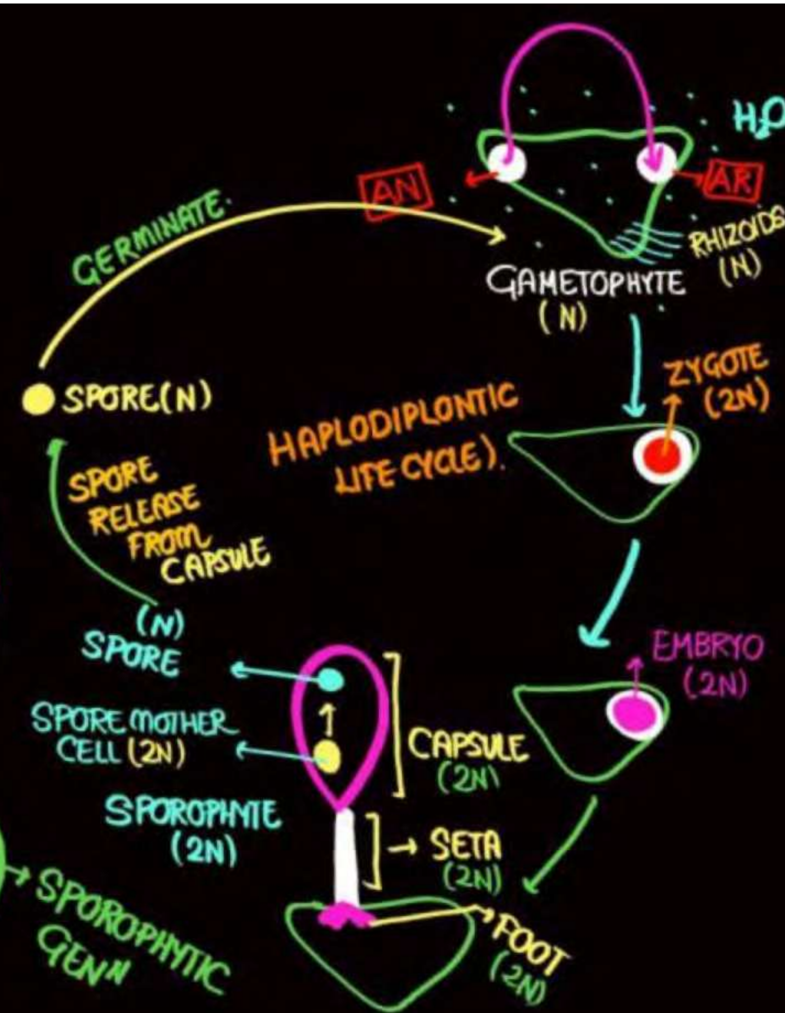
LIFE CYCLE.

★ SOME CELLS IN CAPSULE OF SPOROPHYTE PRESENT: SMC (2N)

↓ MEIOSIS

SPORE (N)





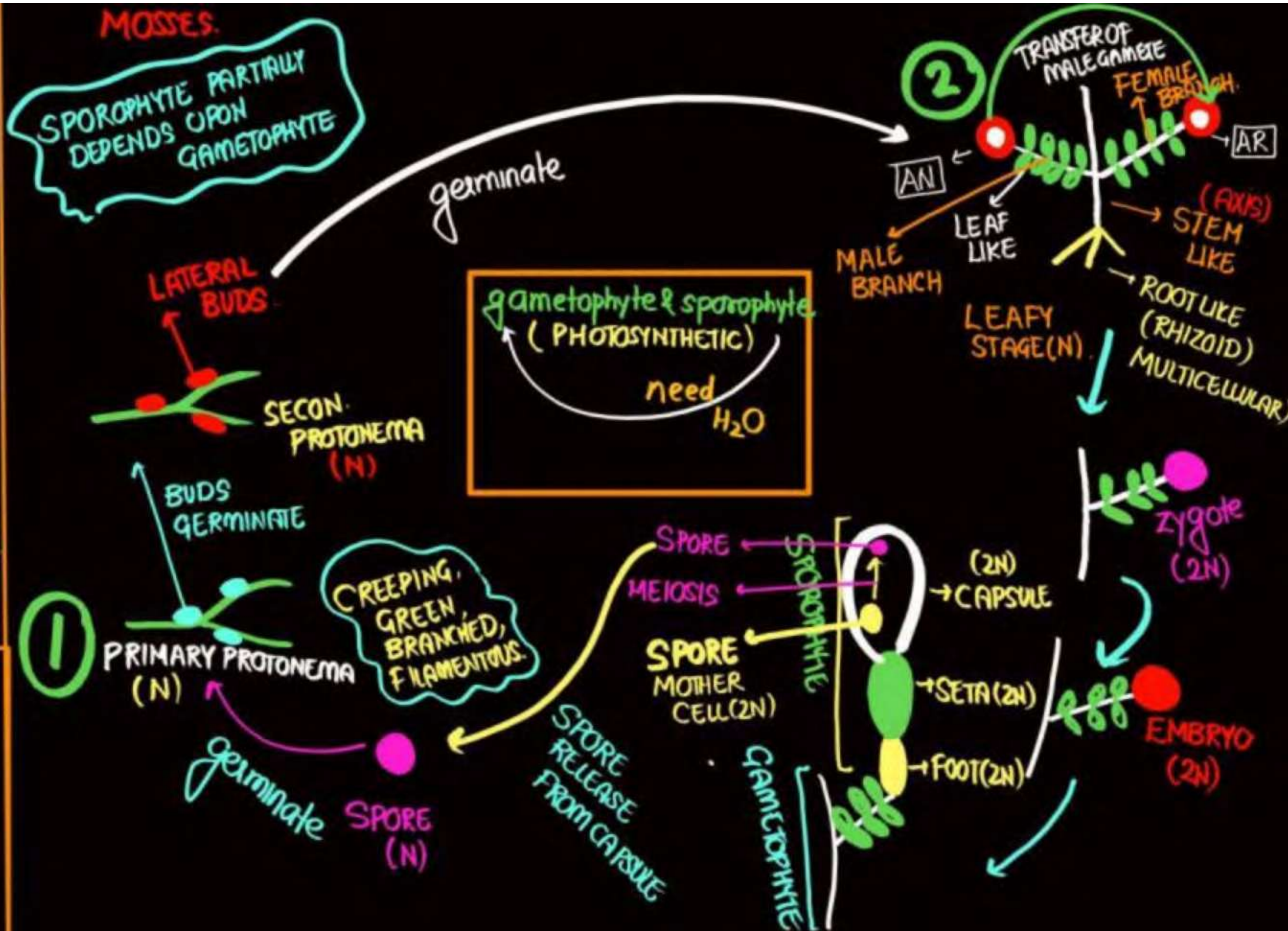
★ ASEX REP^N BY FRAGMENTATION OR GEMMA.

★ BRYOPHYTE BODY MORE DIFFERENTIATED THAN ALGAE.

MOSSES.

★ GAMETOPHYTE CONSIST OF TWO STAGES ① PROTONEMA ② LEAFY STAGE.

★ SEX ORGAN PRESENT AT APEX OF LEAFY SHOOT



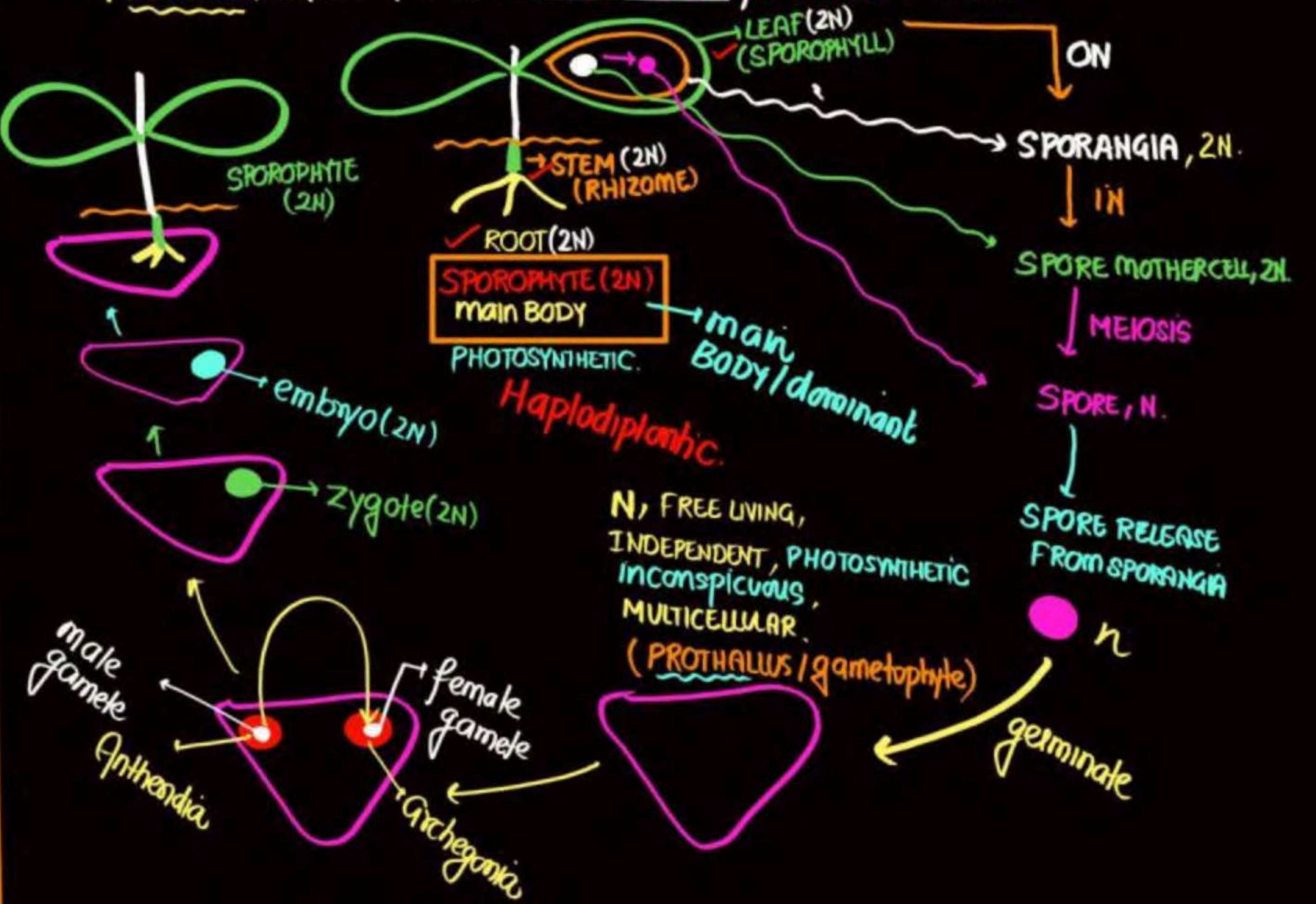
★ 1st Time: ROOT, STEM, LEAF, XYLEM PHOLEM APPEAR.

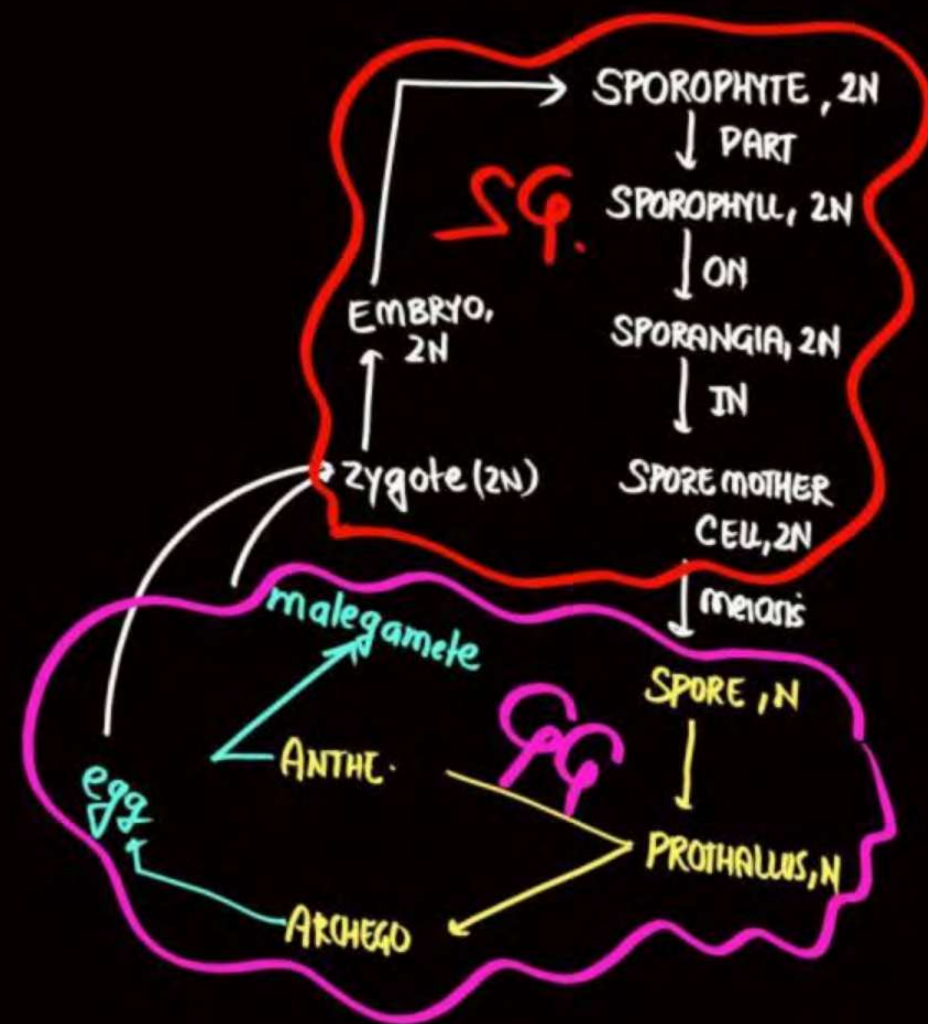
LEAF

- small (microphyll)
  - eg Selaginella
  - equisetum
- large (megaphyll/ Macrophyll)
  - eg: Ferns

★ sporophyll aggregate to form strobilus/CONE

PTERIDOPHYTE (LIFE CYCLE OF HOMOSPOROS PTERIDOPHYTE (MOSTLY).




SPOROPHYTE, 2N
PART
SPOROPHYLL, 2N
ON
SPORANGIA, 2N
IN
SPORE MOTHER CELL, 2N
meiosis
SPORE, N
PROTHALLUS, N
ANTHE.
ARCHEGO
malegamete
egg
zygote (2N)
EMBRYO, 2N
SG.
GG

Angiosperm.

FERTILISATION

Gymnosperm

OVULE (NAKED)

→ seed (NOT COVERED BY FRUIT)

GYMNOSPERM.

⇒ medium size TREE, (cycas)
SHRUB, (EPHEDRA)
TALLTREE (PINUS)

⇒ Tallest: Red wood TREE (SEQUOIA).

⇒ PINUS ROOT + FUNGUS: SYMBIOTIC RELATION (MYCORRHIZA).

⇒ CYCAS: COROLLOID ROOT, NEGATIVELY GEOTROPHIC (BLUE GREEN ALGAE, ANABAENA, N_2 FIXT^n).

⇒ CYCAS: STEM: UNBRANCHED
PINUS: STEM: BRANCHED & CEDRUS

⇒ ROOT USUALLY: TAPROOT (formed from (RADICLE)

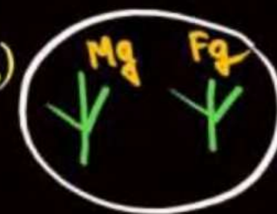
⇒ SIMPLE & COMPOUND LEAF (PINNATE LEAF).

★ All Hetrosporous.

★ main Body: sporophyte, 2N. (dominant).

★ gametophyte: NOT FREE LIVING, NOT INDEPENDENT.

★ mostly dioecious (cycas)



diff TREE

BUT PINUS MONOECIOUS

same TREE.

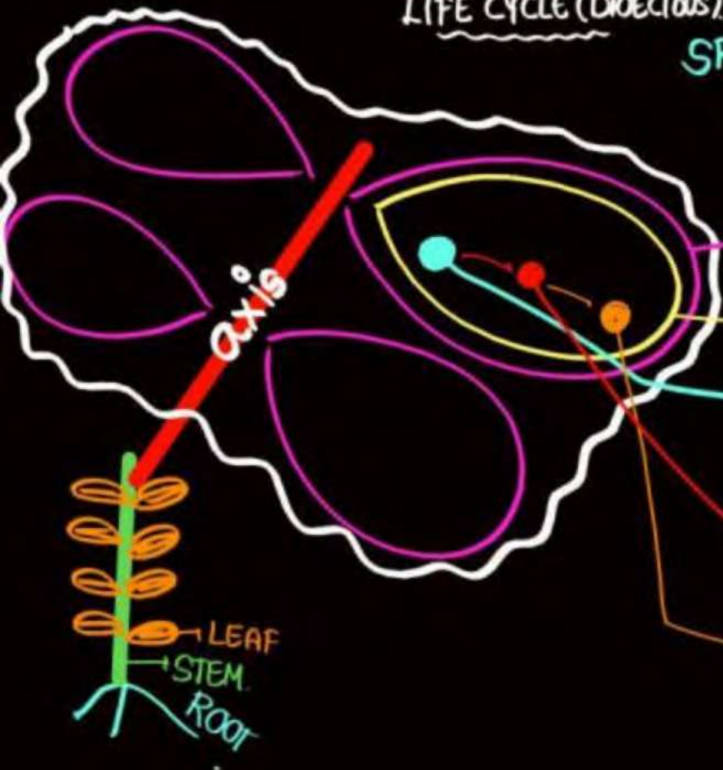
⇒ seed (1st Time)

⇒ FRUIT absent

⇒ Vascular Tissue ✓

	A	B	P	G	A.
Gam	M.B	M.B	Indep.	Dep	Dep
Sporo		Dep^n	M.B Inde	M.B Inde	M.B Inde

LIFE CYCLE (DIOECIOUS)

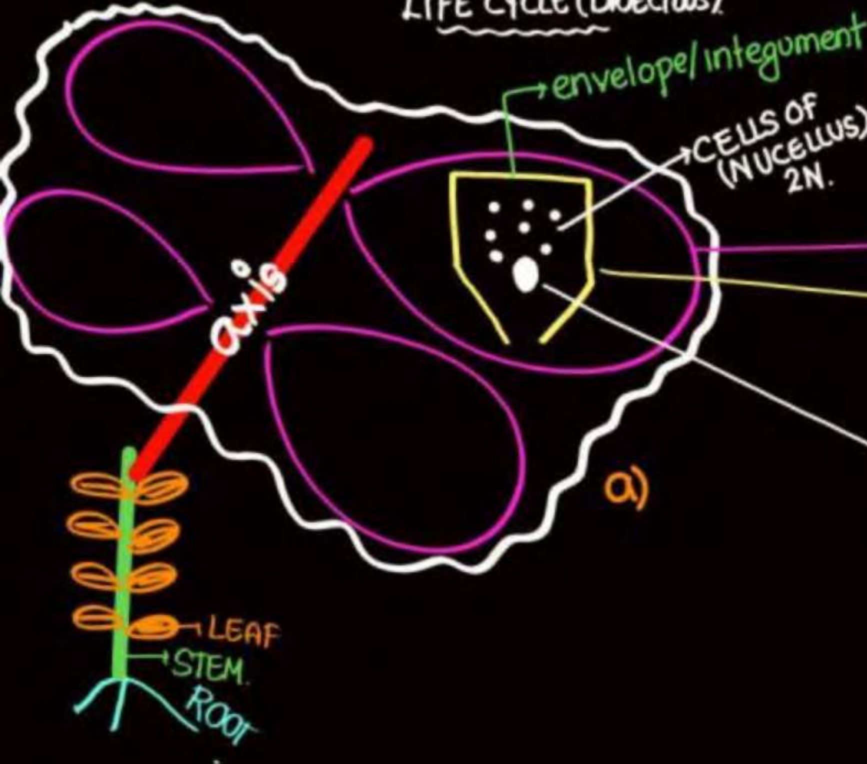


MALE TREE
(SPOROPHYTE)

SPOROPHYTE, 2N (MALE TREE).
↓
MALE CONE/MICROSPORANGIATE/STROBILUS. 2N.
↓ aggregation
MICROSPOROPHYLL, 2N
↓ ON
MICROSPORANGIA, 2N.
↓ IN
MICROSPORE MOTHER CELL, 2N
↓ MEIOSIS
MICROSPORE, N
↓
MALE GAMETOPHYTE
(POLLEN GRAIN), N.

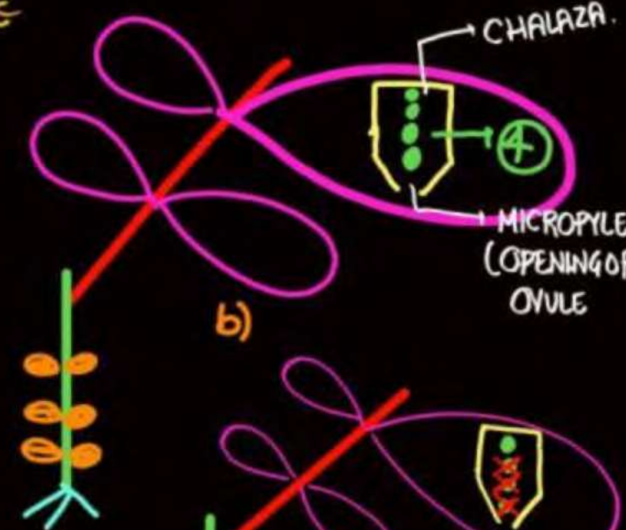
Release from microsporangia

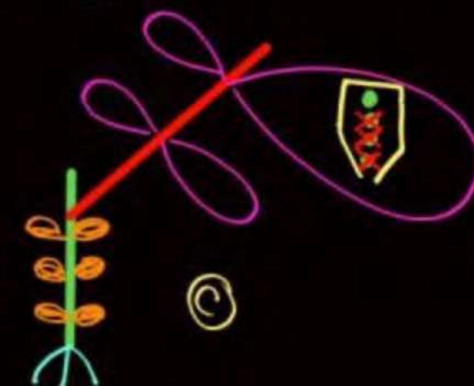
LIFE CYCLE (DIOECIOUS)

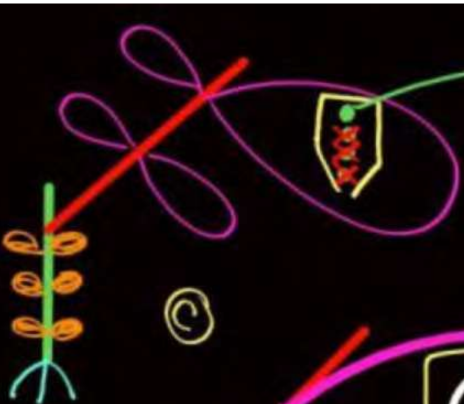


FEMALE TREE
(SPOROPHYTE)

Female TREE, SPOROPHYTE, 2N.
↓
FEMALE CONE/MACROSPORANGIATE
↓
aggregation of
Megasporophyll, 2N.
↓ ON
MEGASPORANGIA/OVULE (2N)
↓ IN
ONE OF CELL OF NUCELLUS increase in size called MEGASPORE MOTHER CELL (2N)
↓ MEIOSIS
4 MEGASPORE, N
↓ 3 ARE DEGENERATED
one is functional at chalaza end.





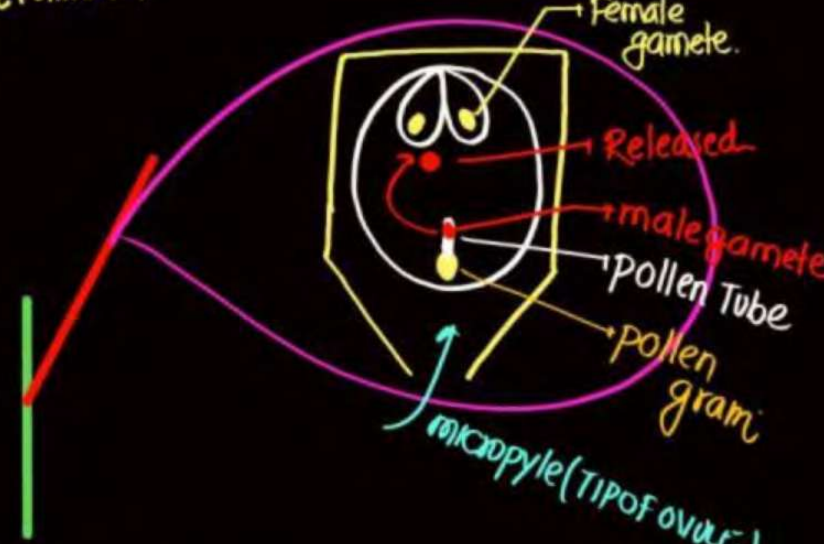


©

FUNCTIONAL MEGASPORE (N)
↓ FORM
FEMALE GAMETOPHYTE
IN
ARCHEGONIA → endosperm (n) (FORMED BEFORE FERTILISN.)
↓
egg/female gamete

d)

* pollen grain having pollen Tube which carry male gamete enter into female gametophyte through opening of ovule (micropyle)



* pollen Tube Release male gamete near mouth of archegonia → fertilisation (male gamete fertilise egg) → zygote → embryo (seed) →
↓
NEW PLANT (SPOROPHYTE)

ARTIFICAL C

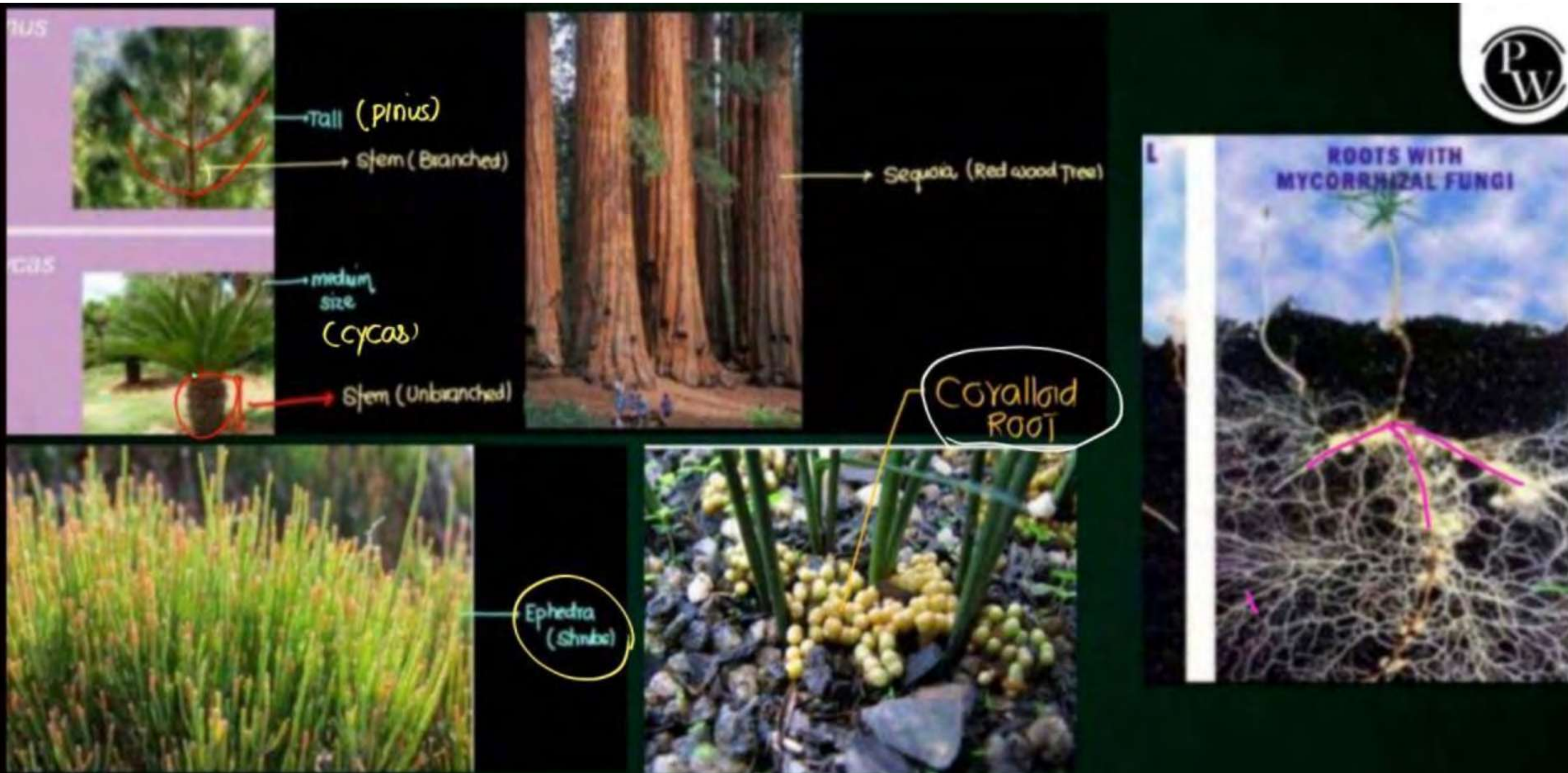
* ARISTOTLE, LINNAEUS.
* ONE OR FEW CRITERIA (MORPHOLOGICAL CHARACTER /EXTERNAL)

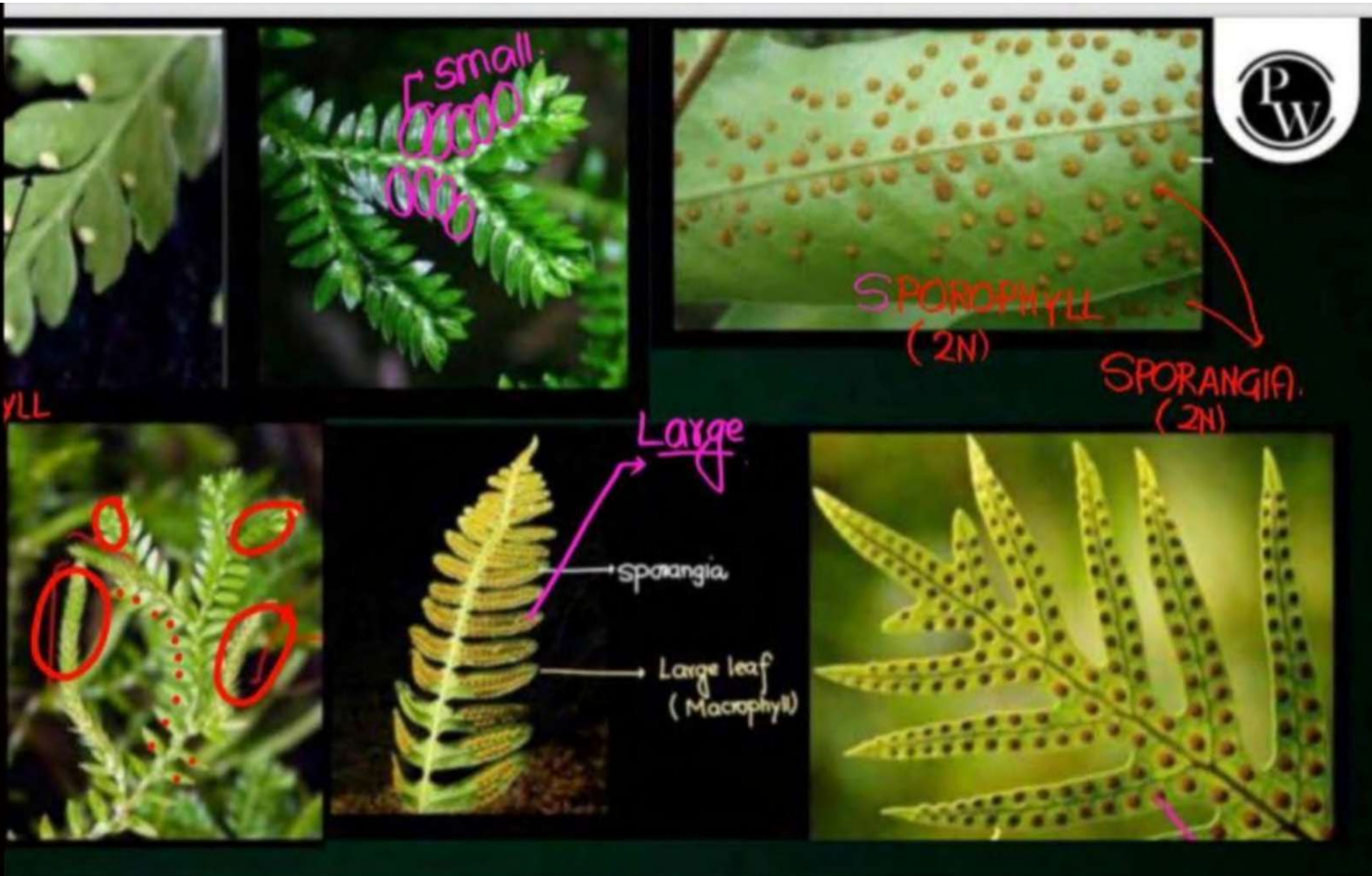
number, colour, shape, HABIT OF LEAVES (VEGETATIVE CHARACTER)

* LINNAEUS : CRITERIA (ANDROECIUM STRUCTURE)

DRAWBACK

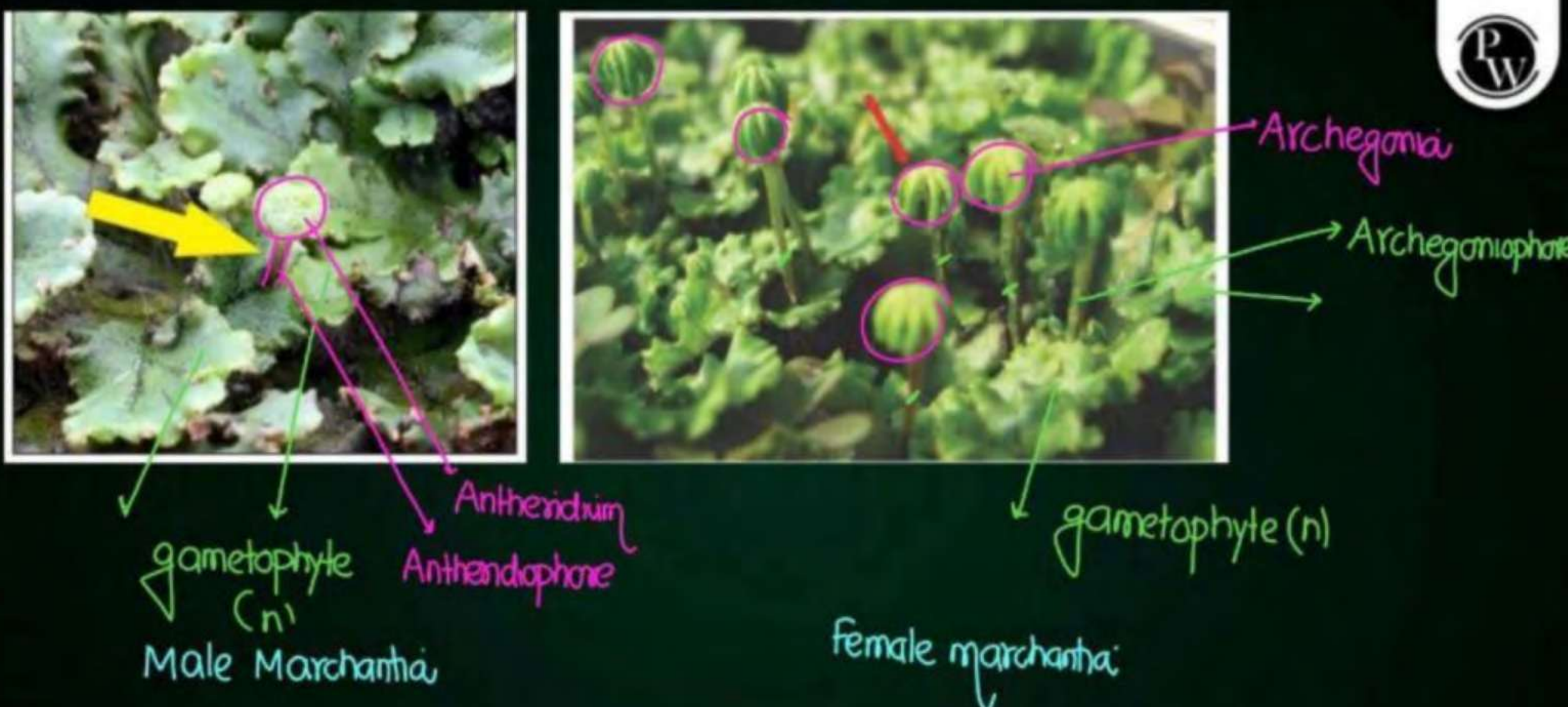
* equal importance to vegetative & Reproductive character. BUT Rep. character is more Conservative Because least affected By environment.
* They seperated closely Related species on Basis of few character.


Tall (pinus)
Stem (Branched)
medium size
(cycas)
Stem (Unbranched)
Sequoia (Red wood Tree)
Coralloid Root
Ephedra (Shrubs)
ROOTS WITH MYCORRHIZAL FUNGI


small
SPOROPHYLL
(2N)
SPORANGIA.
(2N)
Large
Sporangia
Large leaf
(Macrophyll)



SPOROPHYTE
(2N)
CAPSULE
Liverworts (Bryophyte)
GAMETOPHYTE
(N)
stem like
LEAF LIKE
dorsal: gemma cup
ventral: Rhizoids
gemma cup
gemmae
PORELLA
(LIVERWORT)



Archegonia
Archegoniophore
Antheridium
gametophyte (n)
Antheridiophore
Male Marchantia
gametophyte (n)
female marchantia

TABLE 3.1 Divisions of Algae and their Main Characteristics

Classes	Common Name	Major Pigments	Stored Food	Cell Wall	Flagellar Number and Position of Insertions	Habitat
Chlorophyceae	Green algae	Chlorophyll *a*, *b*	Starch	Cellulose	2-8, equal, apical	Fresh water, brackish water, salt water (MARINE)
Phaeophyceae	Brown algae	Chlorophyll *a*, *c*, fucoxanthin	Mannitol, laminarin	Cellulose and algin Cellulose cell wall covered By algin	2, unequal, lateral	Fresh water (rare) brackish water, salt water
Rhodophyceae	Red algae	Chlorophyll *a*, *d*, phycoerythrin	Floridean starch	Cellulose, pectin and poly sulphate esters	Absent	Fresh water (some), brackish water, salt water (most)

MAIN PIGMENT

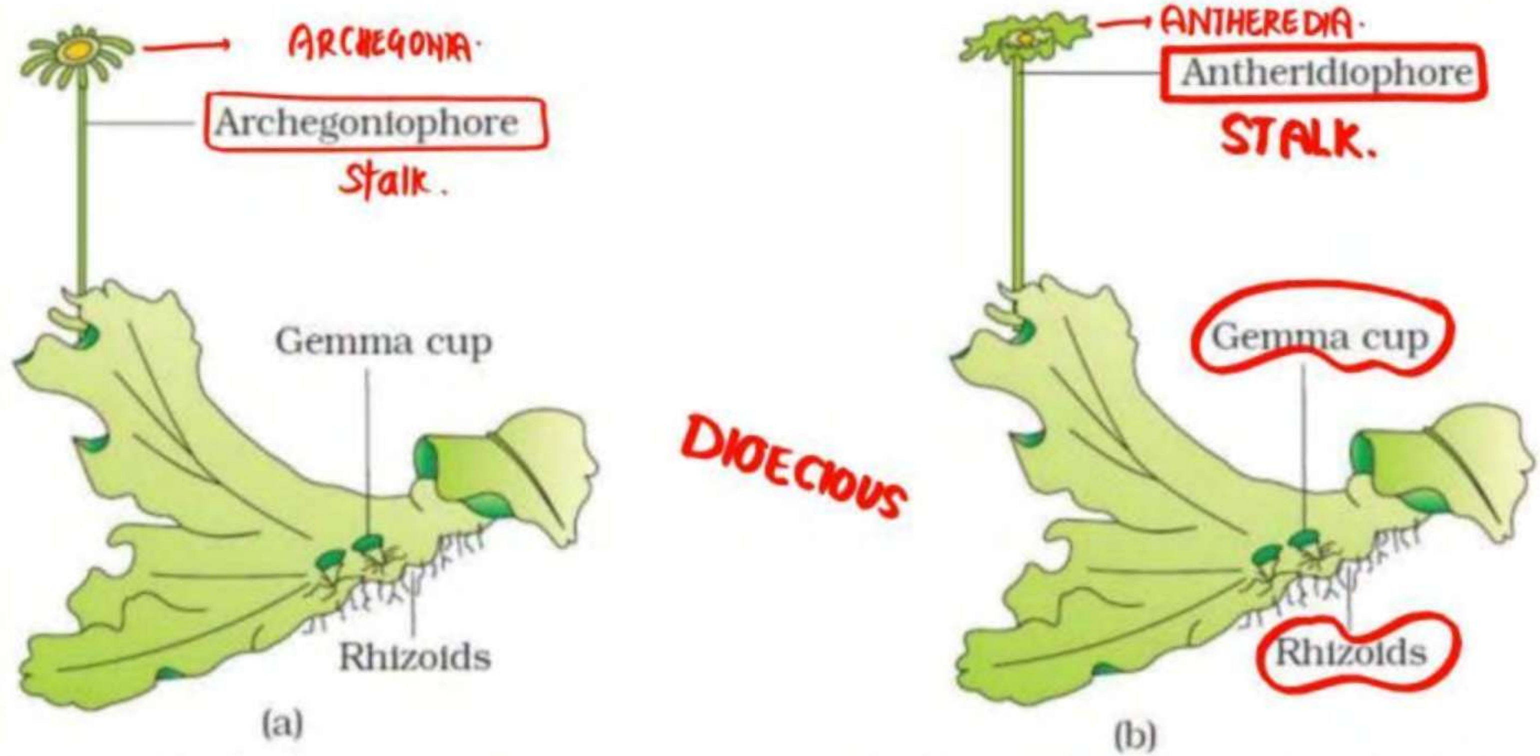


Figure 3.2 Bryophytes: A liverwort – *Marchantia* (a) Female thallus (b) Male thallus Mosses – (c) *Funaria*, gametophyte and sporophyte (d) *Sphagnum* gametophyte

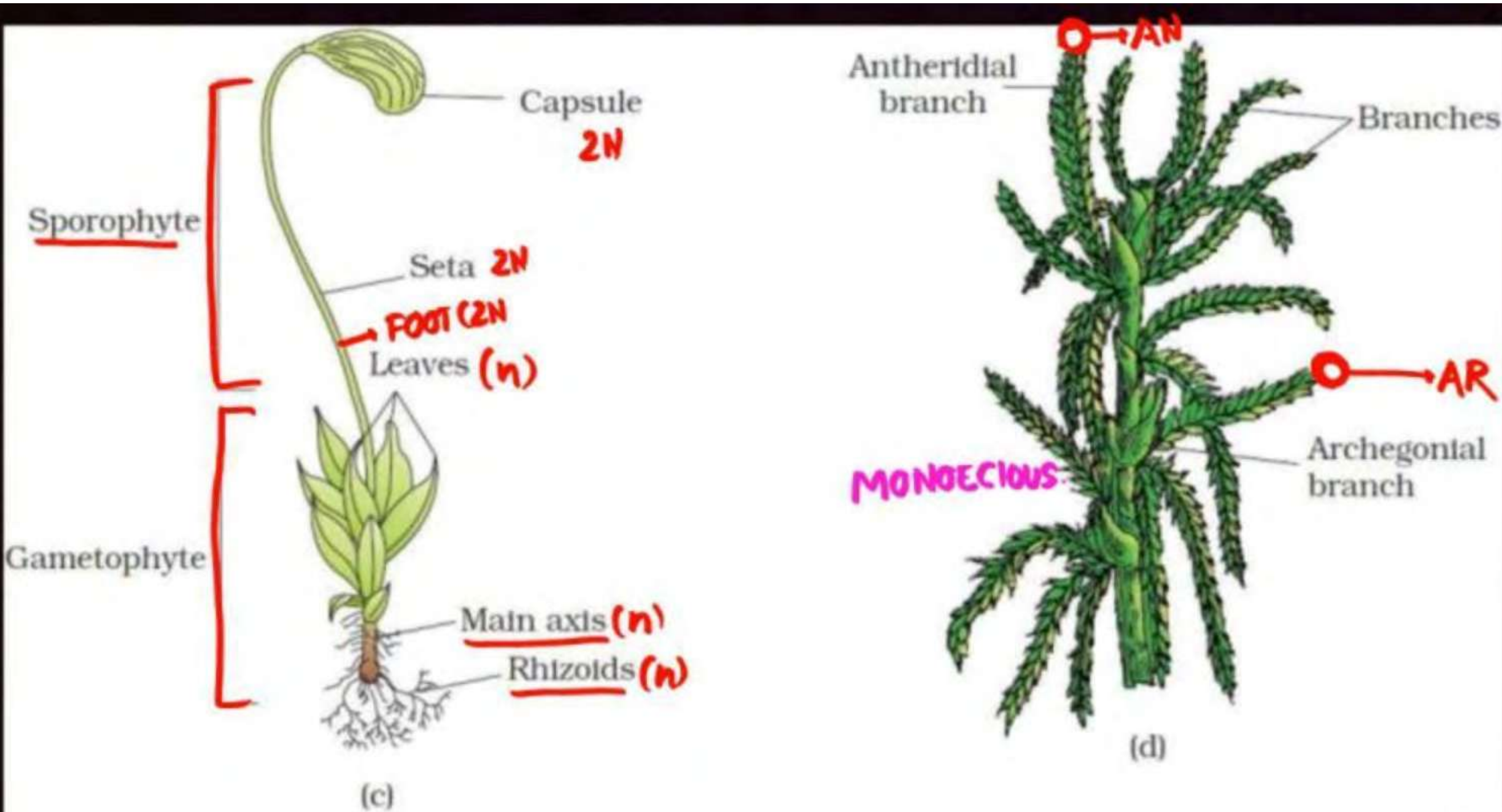
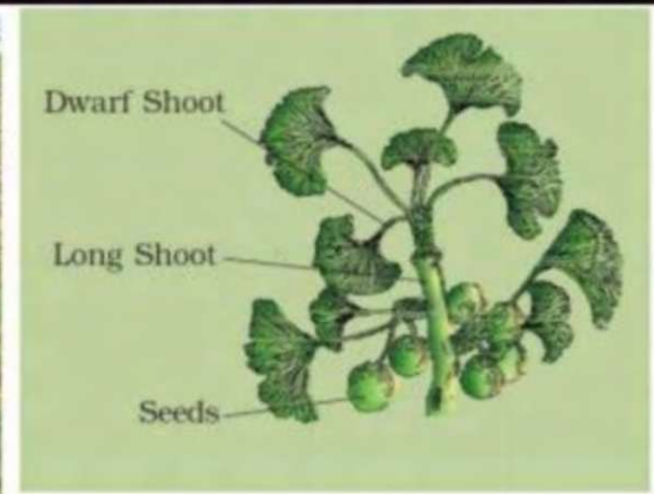


Figure 3.2 Bryophytes: A liverwort – *Marchantia* (a) Female thallus (b) Male thallus Mosses – (c) *Funaria*, gametophyte and sporophyte (d) *Sphagnum* gametophyte

Figure 3.3 Pteridophytes : (a) *Selaginella* (b) *Equisetum* (c) Fern (d) *Salvinia*

(a)

(b)



(c)

Figure 3.4 Gymnosperms: (a) *Cycas* (b) *Pinus* (c) *Ginkgo*

EXPERIMENT

①

VERIGATED LEAF → GREEN ✓ ; → NON GREEN X

LIGHT → (STARCH TEST). CHLOROPHYL

GREEN PART	NON GREEN PART
⇒ Iodine solⁿ	⇒ Iodine solⁿ
⇒ BLUISH BLACK	X
⇒ STARCH ✓	X
glucose ↓ PHOTOSYNTHESIS PRESENT	NO GLUCOSE ↓ NO PHOTOSY.

$\boxed{\text{ROLE OF GREEN PART (CHLOROPHYLL)}}$ ✓ *

② *

	I_2 SOLⁿ.	BLUISH BLACK	PHOTOSY
REGION: EXPOSED (LIGHT ✓)	✓	✓ starch ✓	✓
REGION: COVERED WITH BLACK PAPER (LIGHT X)	✓	X. starch X	X

$\boxed{\text{ROLE OF LIGHT}}$ ✓ *

③ MOLL HALF LEAF EXP.

ROLE OF CO_2

→ Cotton (KOH solution) ↓ absorb CO_2

	OUTSIDE THE TEST TOBE	INSIDE TOBE
⇒ LIGHT:	✓	✓
⇒ CO_2:	✓	X
⇒ STARCH TEST:	BLUISH BLACK. PHOTO ✓	X X

④ PRIESTLEY EXP.

O_2 discovered

CANDLE & MOUSE ⟿ UTILISED O_2 → RELEASE CO_2 → CANDLE EXTINGUISHED ; → MOUSE DEATH.

PLANT PURIFY AIR

CANDLE & MOUSE RELEASE CO_2 ⟿ CO_2 TAKEN BY MINT → CO_2 ⟶ O_2 → CANDLE DO NOT EXTINGUISHED ; → MOUSE SURVIVE

⑤ Ingenhousz

⇒ Exp : aquatic plant (Hydrilla)

		LIGHT	GAS(O_2)	PHOTOSYNTH.
 $\rightarrow H_2O$, (H)	$\xrightarrow[\text{LIGHT}]{\text{BRIGHT}}$	✓	✓	✓
 $\rightarrow H_2O$, (H)	$\xrightarrow[\text{DARK}]{}$	X	X	X

⑥ VON SACH :

AS PLANT GROW ⟶ glucose accumulation increase

glucose synthesis ⇝ green part (chlorophyll)

glucose $\xrightarrow{\text{stored}}$ starch

green pigment Chlorophyll ⇝ present in CHLOROPLAST

NOTE : By 19th century.

$$CO_2 + H_2O \xrightarrow[\text{CHLOROPHYL}]{\text{LIGHT}} (CH_2O)$$

Carbohydrate (glucose).

⑦ Van NIEL.

PURPLE SULPHUR, GREEN SULPHUR ⟶ PHOTOSYNTHETIC BACTERIA

$$CO_2 + 2H_2A \xrightarrow[(O_2 \text{ NOT RELEASED})]{\text{NON-OXYGENIC}} \boxed{(CH_2O)} + 2A + H_2O$$

Reduction

$2H_2A$ ↓ Release H atom (Oxidisable Compound) BINDS WITH CO_2

$2H_2S$

(CH_2O): Carbohydrate synthesis / glucase

2A: 2S

PLANTS

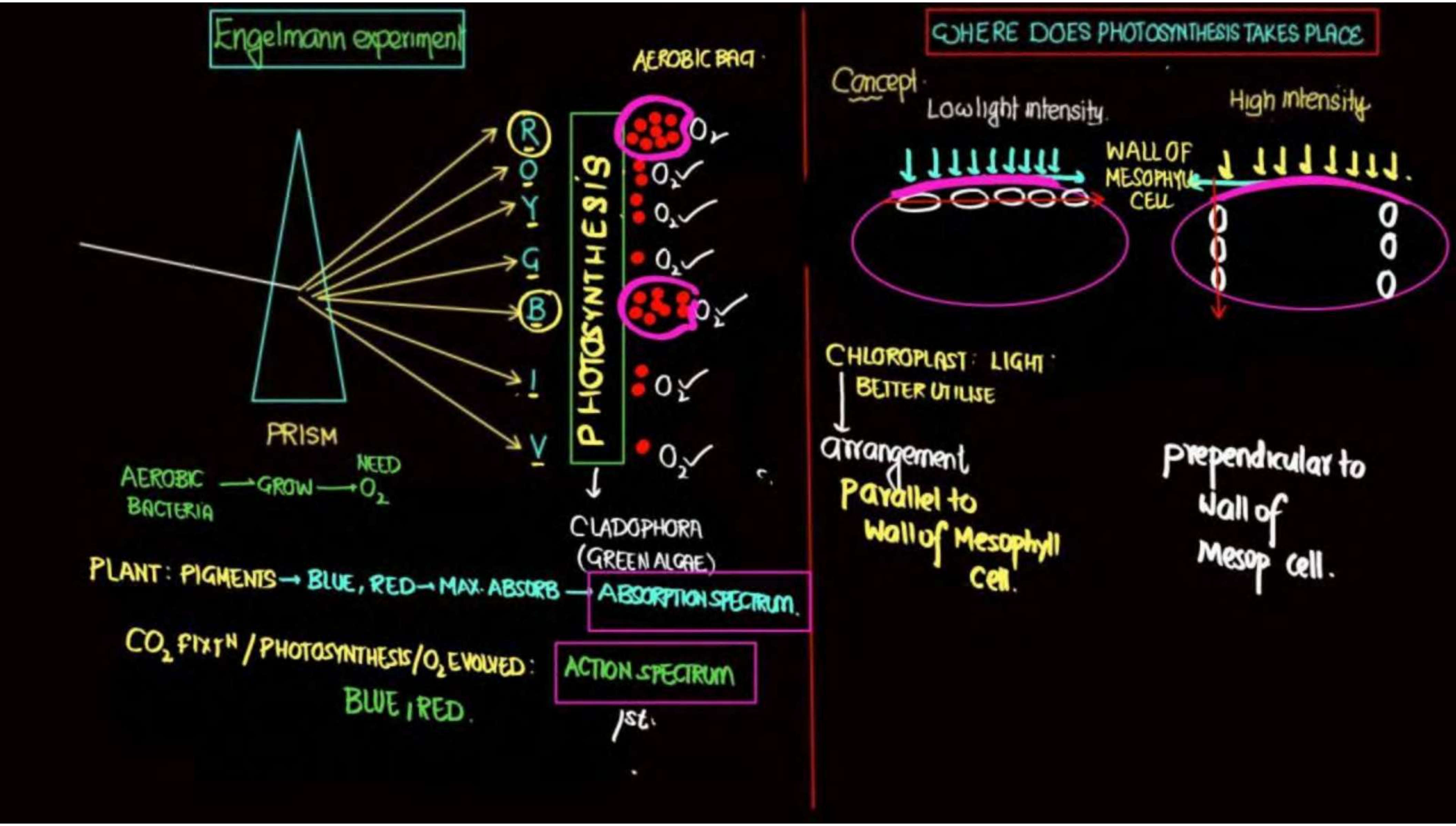
BUT DIDN'T PROOF.

⇒ $H_2O \longrightarrow \frac{1}{2}O_2$

⇒ O_2 COMES FROM H_2O NOT CO_2.

⑧ RUBAN, KAMAN

$$CO_2^{16} + H_2O^{18} \longrightarrow O_2^{18}$$



Engelmann experiment
AEROBIC BAG
R
O
Y
G
B
I
V
PHOTOSYNTHESIS
O_2 ✓
O_2 ✓
O_2 ✓
O_2 ✓
O_2 ✓
O_2 ✓
O_2 ✓
PRISM
AEROBIC BACTERIA → GROW → NEED O_2
CLADOPHORA (GREEN ALGAE)
PLANT: PIGMENTS → BLUE, RED → MAX. ABSORB → ABSORPTION SPECTRUM.
CO_2 FIXT^N / PHOTOSYNTHESIS / O_2 EVOLVED: ACTION SPECTRUM
BLUE, RED.
1st.
WHERE DOES PHOTOSYNTHESIS TAKES PLACE
Concept.
Low light intensity.
High intensity
WALL OF MESOPHYLL CELL
CHLOROPLAST: LIGHT
BETTER UTILISE
arrangement
Parallel to Wall of Mesophyll Cell.
Prependicular to Wall of Mesop cell.

HOW MANY TYPES OF PIGMENT

PAPER CHROMATOGRAPHY
↓
PIGMENTS OF LEAF COMES ON PAPER.

Chlorophyll a /main/UNIVERSAL → BLUISH GREEN

Chlorophyll b : YELLOWISH GREEN / OLIVE GREEN.

Carotene : YELLOW/YELLOW TO ORANGE
+
Xanthophyll → YELLOW
↓
Carotenoids

ABSORPTION SPECTRUM.

ACTION SPECTRUM:

If we compare absorption spectrum of Chl a with action spectrum.
so it overlap at some Region BUT NOT OVERLAP COMPLETELY.

DURING PHOTOSYNTHESIS LIGHT ALSO ABSORB BY

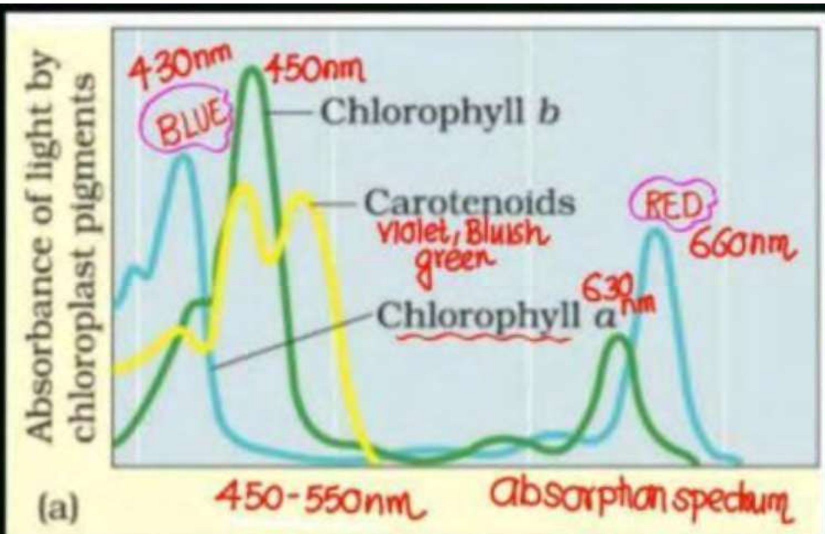
Chl b, Carotenoid → accessory pigments.
↓
also participate in PHOTOSYNTHESIS (INDIRECTLY)

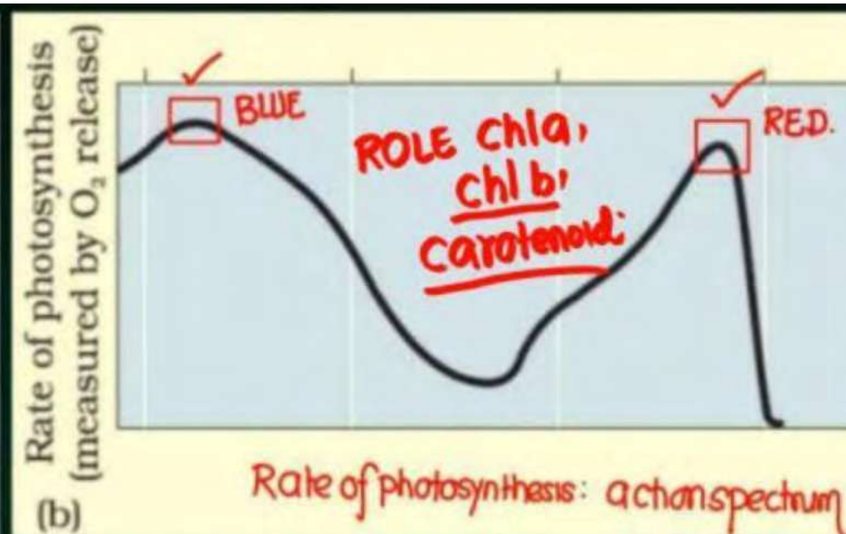
?

Chl a (main pigment) (DIRECTLY PARTICIPATE)

?

WAIT





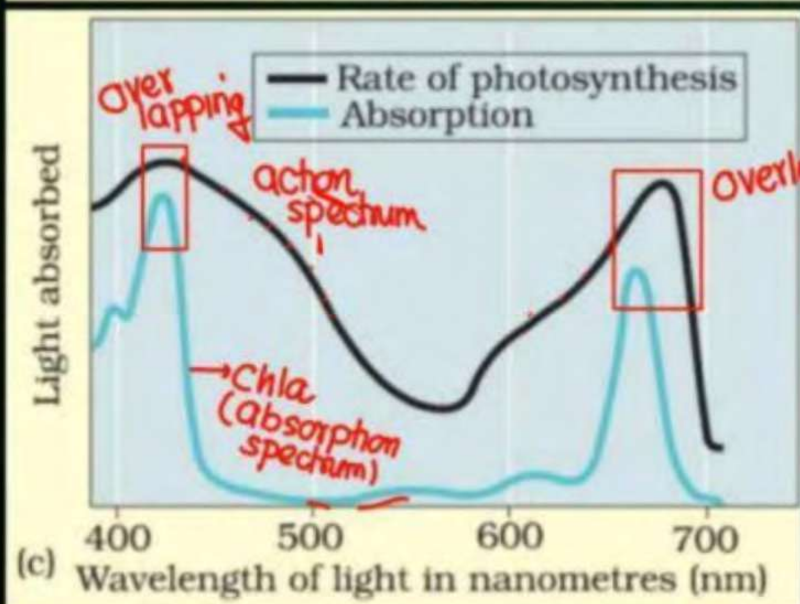


Figure 11.3a Graph showing the absorption spectrum of chlorophyll *a*, *b* and the carotenoids

Figure 11.3b Graph showing action spectrum of photosynthesis

Figure 11.3c Graph showing action spectrum of photosynthesis superimposed on absorption spectrum of chlorophyll *a*

LIGHT

Chla Chl b carotenoid

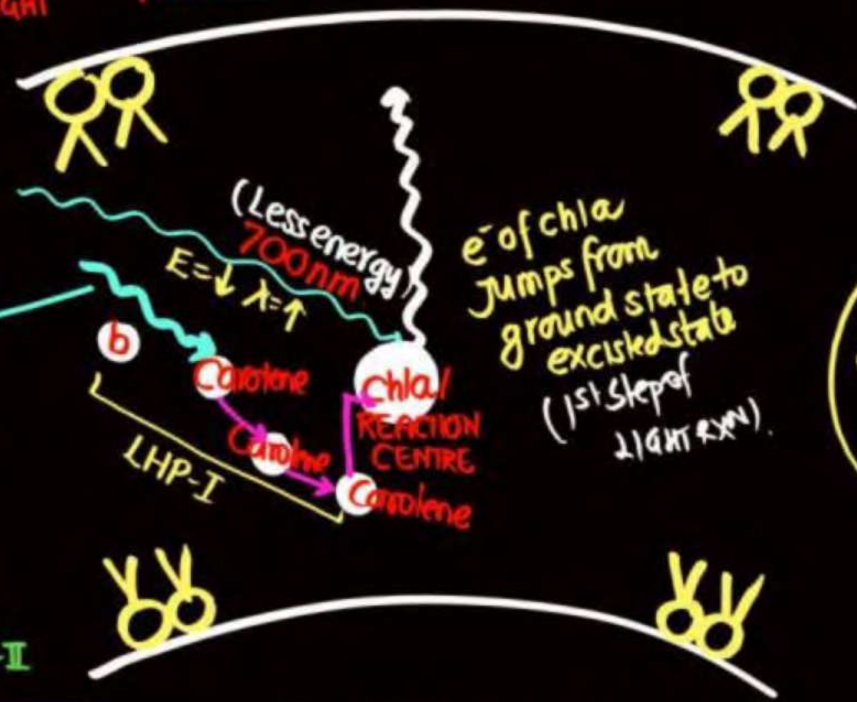
Chloroplast
↓
Rate of photosy.
(CO_2 Fixt^n)
or
O_2 evolution
↓
Check.
(action) spectrum

grana
↓
Thylakoid
↓
membrane
↓
$\boxed{\text{PIGMENTS}}$

PHOTOSYSTEM-I/PS-I

PHOTO → LIGHT

SYSTEM → PIGMENTS



450nm
550nm
580nm

2nd discovered.

$\boxed{\text{PS-II}}$

- RC/chla (680nm)
- LHC-II
  - LHP-II
  - PROTEIN

e^- of chla jumps from ground state to excited state (1st step of LIGHT RXN).

NOW CHL a gets sufficient energy.

PS-I 1st discovered

- Reaction centre/ chla /single molecule.
  $E = \frac{hc}{\lambda}$ (700nm↑)
- LIGHT HARVESTING COMPLEX (LHC-I)
  - LIGHT HARVESTING PIGMENT (LHP-I)
  - PROTEIN

energy TRANSFER.

$\boxed{\begin{array}{l}\text{Chlb}\\ \text{Carotene}\\ \text{Xanthophyll}\end{array}}$ → access. pigment/ antenna molecule

Shorter wavelength
LIGHT ABSORB
ENERGY HIGH.

LIGHT RX^{N}

ADP + ip $\xrightarrow{\text{LIGHT}}$ ATP

$\boxed{\text{PHOTO PHOSPHORYLATION.}}$

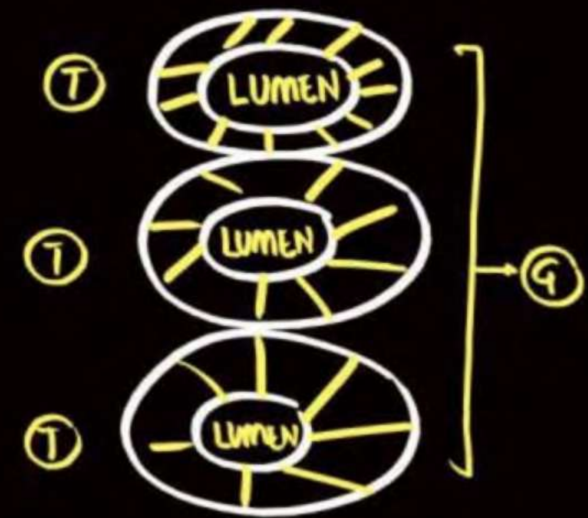
NON-CYCLIC

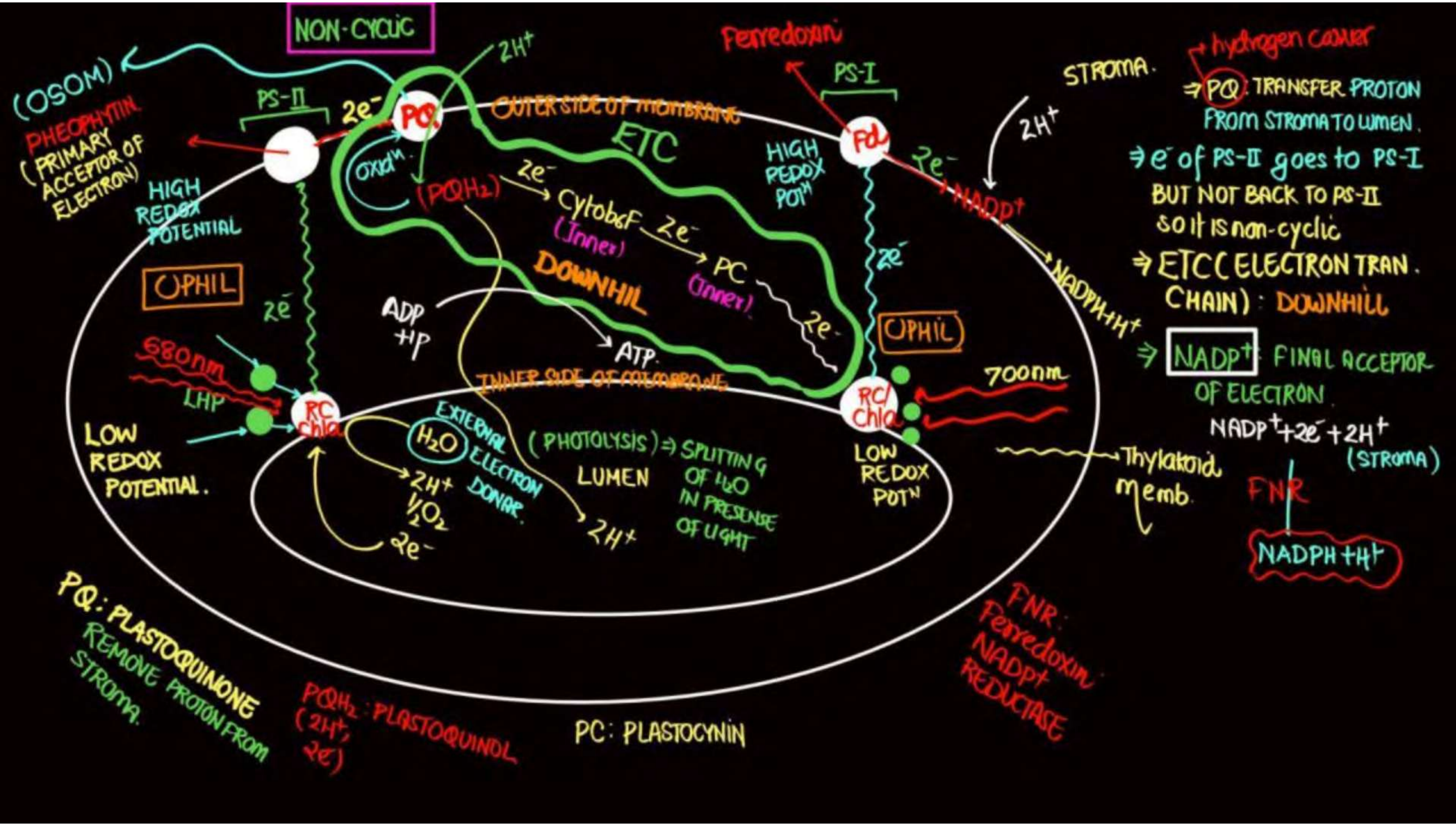
(grana)

↓

Thylakoid

CYCLIC



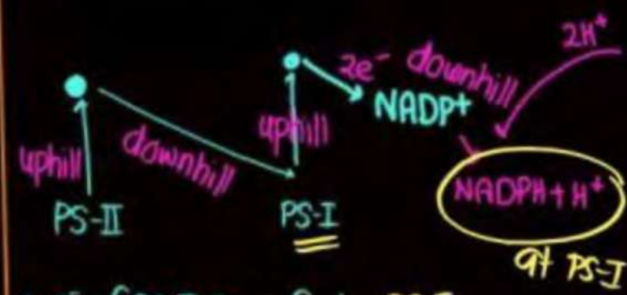


NON-CYCLIC
(OSOM)
PHEOPHYTIN
(PRIMARY ACCEPTOR OF ELECTRON)
PS-II
2e⁻
PQ
2H⁺
OUTER SIDE OF MEMBRANE
ETC
Ferredoxin
PS-I
Fd
HIGH REDOX POTⁿ
2e⁻
NADP⁺
STROMA.
2H⁺
hydrogen carrier
⇒ PQ: TRANSFER PROTON FROM STROMA TO LUMEN.
⇒ e⁻ of PS-II goes to PS-I BUT NOT BACK TO PS-II so it is non-cyclic
⇒ ETC (ELECTRON TRAN. CHAIN): DOWNHILL
⇒ NADP⁺: FINAL ACCEPTOR OF ELECTRON.
NADP⁺ + 2e⁻ + 2H⁺ (STROMA)
FNR
NADPH + H⁺
HIGH REDOX POTENTIAL
oxidⁿ
(PQH₂)
2e⁻
Cytob6F (Inner)
2e⁻
PC (Inner)
DOWNHIL
2e⁻
2e⁻
NADPH+H⁺
UPHIL
UPHIL
2e⁻
ADP +P
ATP
INNER SIDE OF MEMBRANE
680nm
LHP
700nm
RC Chla
RC/Chla
LOW REDOX POTENTIAL.
H₂O
EXTERNAL ELECTRON DONAR.
2H⁺
½O₂
2e⁻
(PHOTOLYSIS) ⇒ SPLITTING OF H₂O IN PRESENSE OF LIGHT
LUMEN
2H⁺
LOW REDOX POTⁿ
Thylakoid memb.
PQ: PLASTOQUINONE
REMOVE PROTON FROM STROMA.
PQH₂: PLASTOQUINOL (2H⁺, 2e⁻)
PC: PLASTOCYNIN
FNR: Ferredoxin NADP⁺ REDUCTASE

Non-cyclic

- SITE : GRANA
- Flow of e^- : PS-II to PS-I
- primary acceptor : PHEOPHYTIN
- External e^- donor : H_2O
- H_2O splitting : LUMEN
- PQ Remove $2H^+$ from stroma, TRANSFER TO LUMEN
- O_2 evolution. (H_2O splitting) at PS-II (Photolysis).

PQ

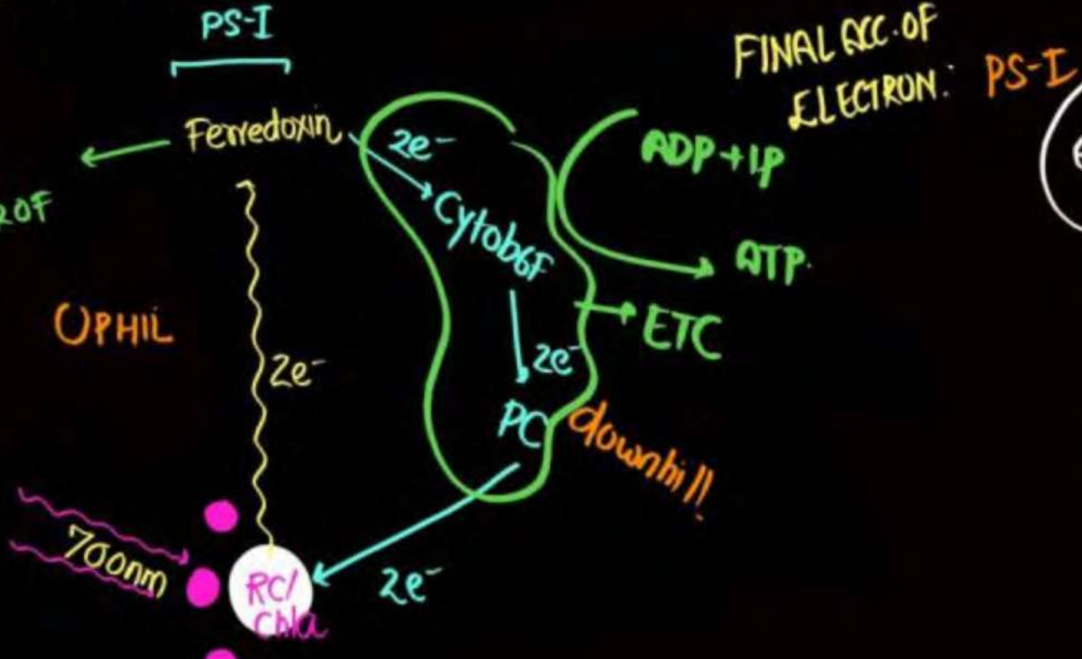


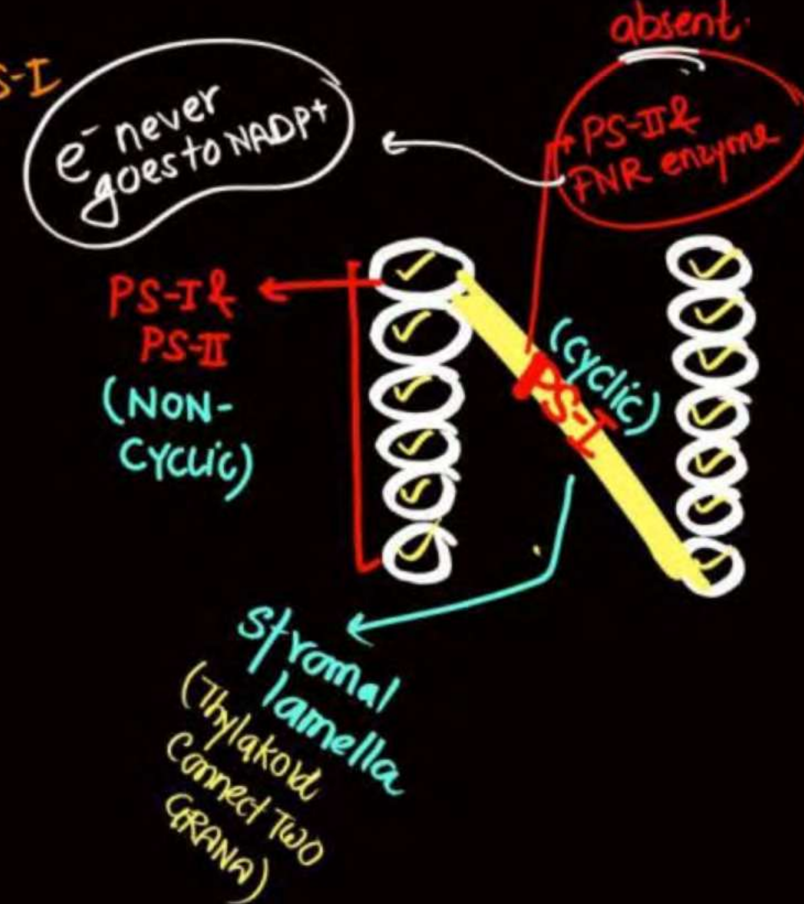
- e^- of PS-II Transfer to PS-I
- Cytob6F, PC : Inn. side of membrane.
- $NADP^+$ Reductase enzyme (FNR), PQ, Phaeophytin, $NADP^+$: OS OThyl. membrane.

- Final acceptor of e^- : $NADP^+$

CYCLIC PHOTOPHOSPHORYLATION

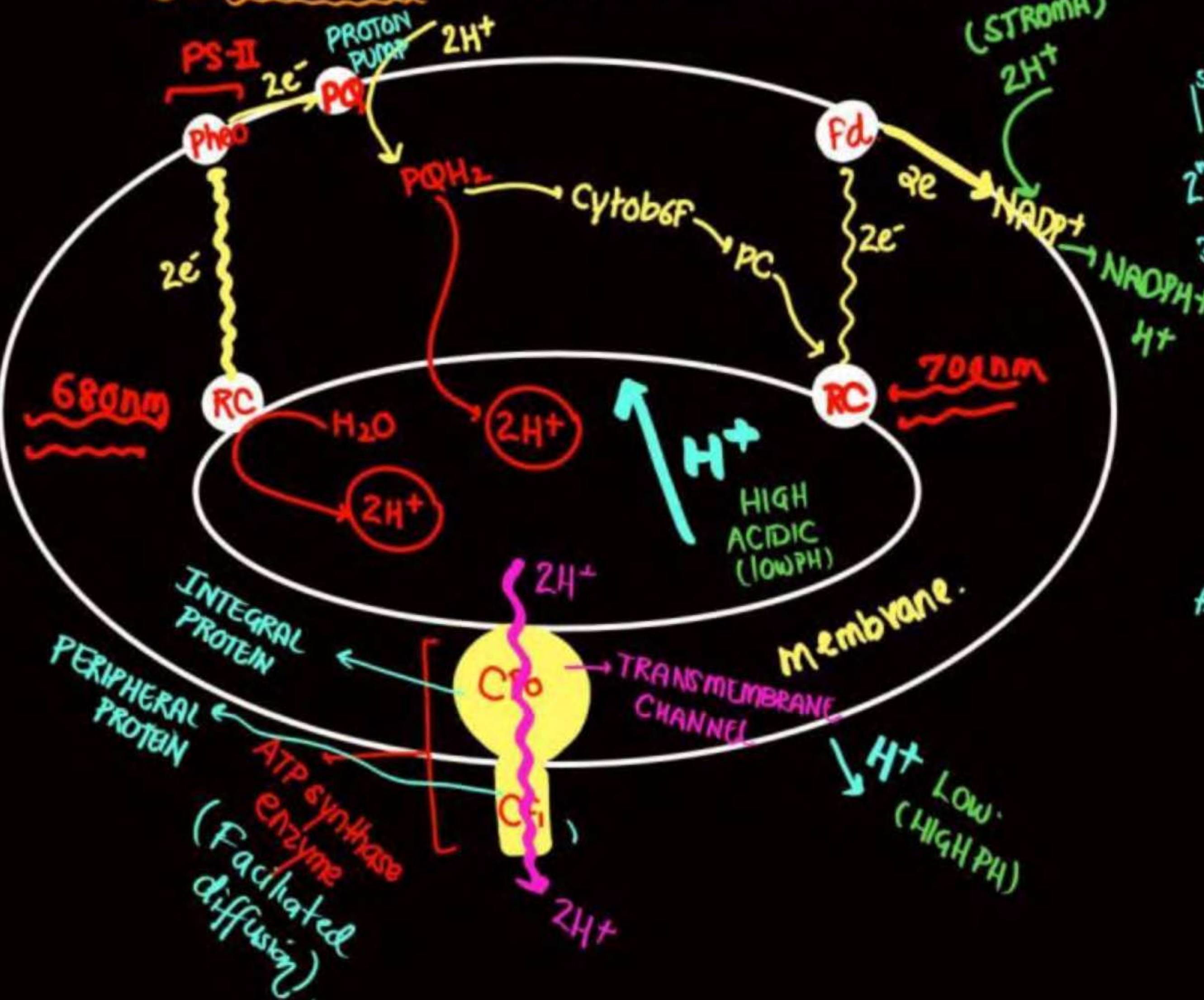
* SITE: STROMAL LAMELLA.
* ONLY PS-I PRESENT





	NON-CYCLIC	CYCLIC
SITE	GRANA	STROMAL LAMELLA.
PHOTOSYSTEM	PS-II & PS-I	PS-I
External e^- donar (H_2O)	PRESENT	ABSENT (mov. of e^- is cyclic)
FINAL Electron acceptor	$NADP^+$	PS-I
PHOTOLYSIS / O_2 evol^n	✓ ✓	X X.
$NADPH + H^+$	yes.	NO
ATP synthesis	yes (ETC)	yes (ETC)
primary acceptor of e^-	Pheophytin	ferredoxin
Z- scheme	yes	NO
Ferredoxin. NADP Reductase (FNR)	PRESENT	ABSENT

CHEMIOSMOTIC HYPOTHESIS (ATP FORMN) → Peter MITCHELL.



PROTON ACCUMULATION IN LUMEN INCREASE COMPARE TO STROMA.

1st ★ $H_2O \xrightarrow{\text{PHOTOLYSIS}} 2H^+$

2nd ★ PQ TRANSFER PROTON FROM STROMA TO LUMEN.

3rd ★ NADP+ REMOVE PROTON FROM STROMA

PROTON GRADIENT FORMED ACROSS MEMBRANE

↓

NOW NEED TO BREAK PROTON GRADIENT (LUMEN TO STROMA)

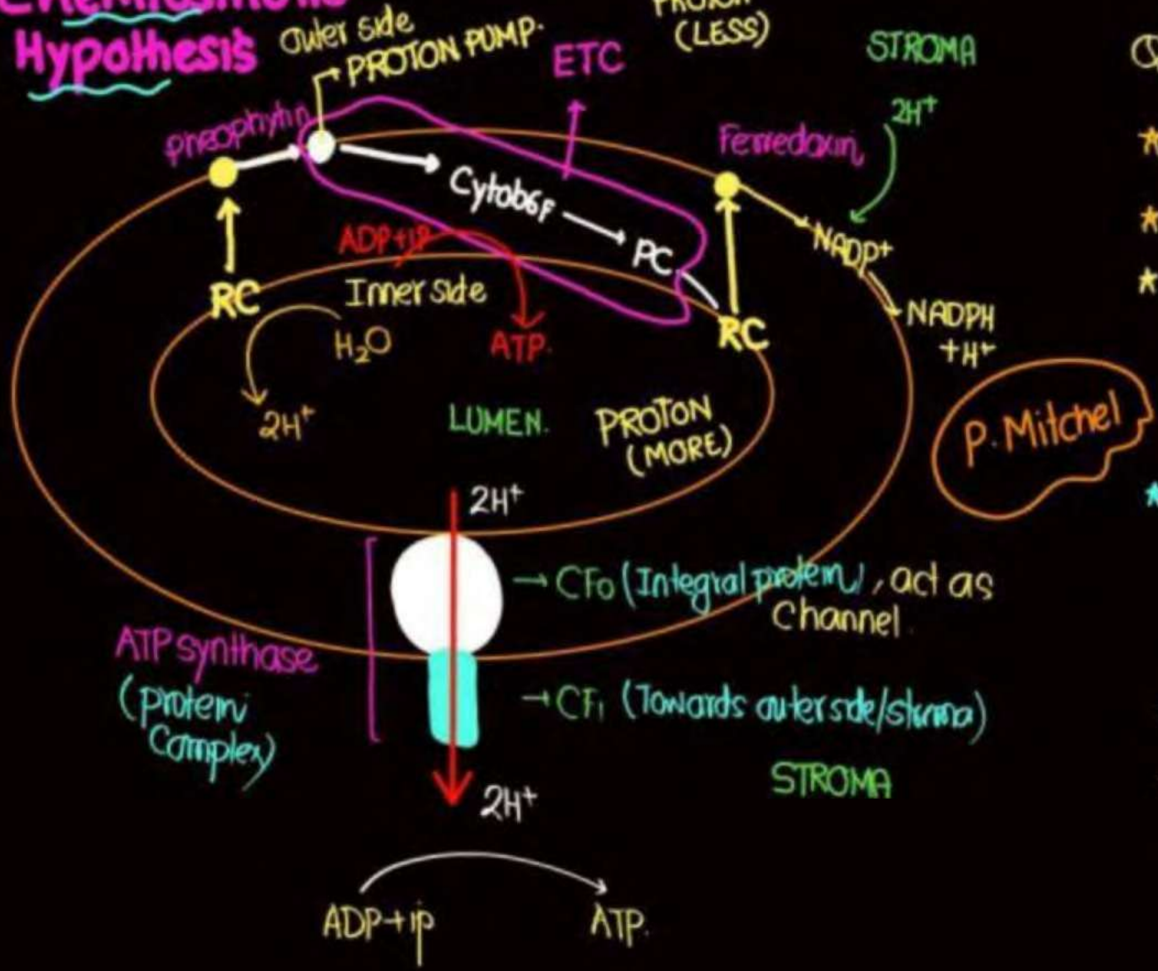
HIGH TO LOW (DOWNHILL)

(ALONG CONN: PASSIVE TRANSPORT

★ AS PROTON MOVE THROUGH ATP synthase (from stroma to LUMEN) there is conformational change in CF1 part

$ADP + iP \xrightarrow{2H^+} ATP \text{ synthesis}$

Chemiosmotic Hypothesis



Reason

Q Proton accumulation increase in Lumen of Thylakoid compare to stroma

★ $H_2O \xrightarrow{\text{PHOTOLYSIS}} 2H^+$

★ PQ Transfer H^+ from stroma into LUMEN.

★ H^+ of stroma Bind with $NADP^+$ to form $NADPH + H^+$ so H^+ conⁿ decrease in Stroma.

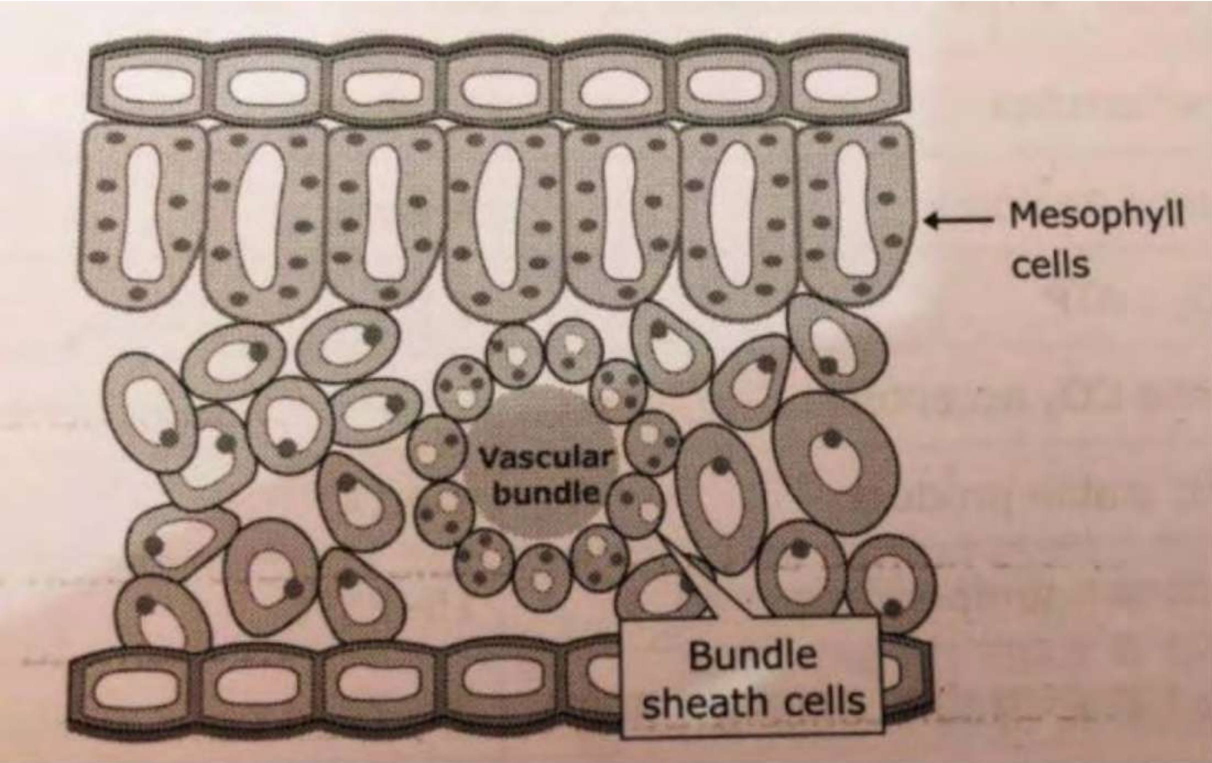
PROTON GRADIENT FORMED ACROSS THYLAKOID MEMBRANE

★ LUMEN: PH: LOW, H^+ more & STROMA: PH: HIGH: H^+ less.

YOU HAVE TO BREAK PROTON GRADIENT so proton moves from LUMEN TO STROMA. (HIGH TO LOW conⁿ, PASSIVE TRANSPORT

★ CF: Coupling factor

★ As proton pass through this complex, there is conformational change in CF₁ (catalytic site) & energy of proton utilised in synthesis of ATP from ADP & ip. (Photophosphorylation)


Mesophyll cells
Vascular bundle
Bundle sheath cells

PRODUCT OF LIGHT RX^n

O_2, ATP, NADPH FORMED. ⟶ 18ATP, 12NADPH.

DARK RX^N.

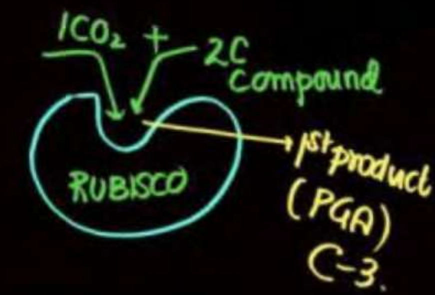
CALVIN-CYCLE/C-3.cycle : FOODSYNTHESIS (glucose)

6 TURN OF C-3 cycle

$6CO_2$ ($Fixt^n$) $\xrightarrow[\text{18ATP, 12NADPH CONSUMED.}]{\text{DARK } RX^N}$ One mole of glucose.

$1CO_2$ ($Fixt^n$) $\xrightarrow[\text{3ATP, 2NADPH CONSUMED.}]{\text{DARK } RX^N}$

(1 TURN OF C-3cycle) CALVIN CYCLE (FOOD SYNTHESIS)



Earlier it was Believed

CO_2 + ~~PRIMARY ACCEPTOR~~ of CO_2 ~~2C compound~~ $\xrightarrow{\text{RUBISCO}}$ $\boxed{\text{3-PHOSPHOGLYCERIC ACID (C-3)}}$ ← FIRST PRODUCT

1C

WRONG

(RIBULOSE 1,5 BISPHOSPHATE RUBP

CO_2 + 5C ketose sugar $\xrightarrow{\text{RUBISCO}}$ $\boxed{\text{2 molecule 3-PHOSPHOGLYCERIC (C-3)} \quad 3C + 3C \rightarrow 6C}$

RIGHT CONCEPT 1C 5C PRIMARY acceptor.

RUBISCO ENZYME

- most abundant enzyme in earth.
- carboxylase activity
- oxygenase activity
- BIFUNCTIONAL ENZYME

GOOD BOY.

$\underbrace{RUBP + CO_2}_{RUBISCO} \xrightarrow[\text{of RUBP}]{\text{Carboxylation}}$ C-3 cycle start (CO_2 FIXT^N).

$CO_2 \uparrow$

$O_2 \downarrow$

O_2 con $\uparrow$

CO_2 con $\downarrow$

around RUBISCO

$\underbrace{RUBP + O_2}_{RUBISCO} \xrightarrow[\text{RUBP}]{\text{oxygenation of}}$ NO FIXT^N OF CO_2.

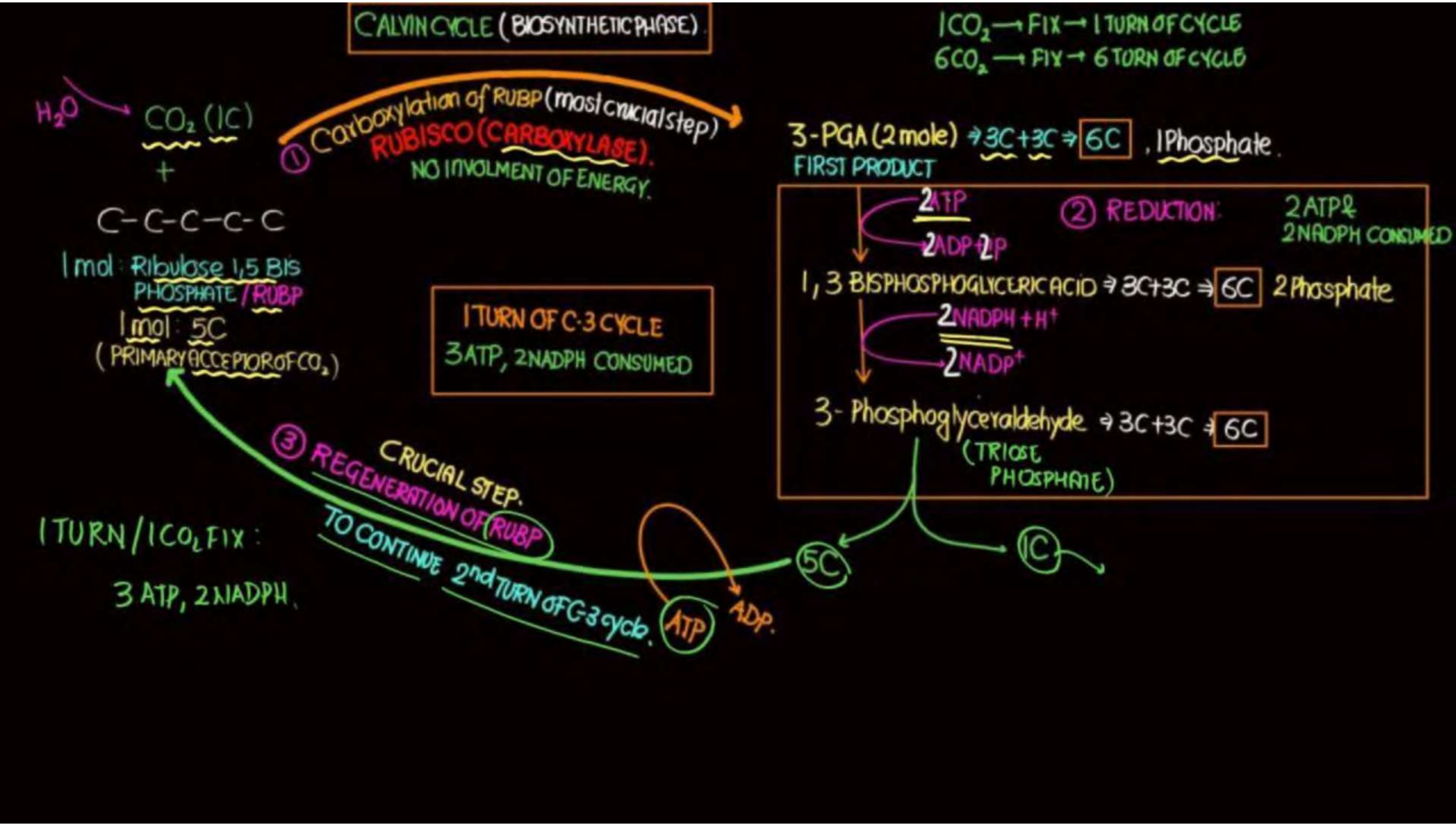
NO GLUCOSE

Carbon loss.

PHOTORESPIRATION

BAD BOY

Ribulose 1,5 BISPHOSPHATE
CARBOXYLASE
OXYGENASE


CALVIN CYCLE (BIOSYNTHETIC PHASE)
1CO2 → FIX → 1 TURN OF CYCLE
6CO2 → FIX → 6 TURN OF CYCLE
H2O
CO2 (1C)
+
C-C-C-C-C
1 mol: Ribulose 1,5 Bis PHOSPHATE / RUBP
1 mol: 5C
(PRIMARY ACCEPTOR OF CO2)
① Carboxylation of RUBP (most crucial step)
RUBISCO (CARBOXYLASE).
NO INVOLMENT OF ENERGY.
3-PGA (2 mole) ⇒ 3C + 3C ⇒ 6C, 1 Phosphate.
FIRST PRODUCT
2ATP
2ADP + 2P
② REDUCTION:
2ATP & 2NADPH CONSUMED
1,3 BISPHOSPHOGLYCERIC ACID ⇒ 3C+3C ⇒ 6C 2 Phosphate
2NADPH + H+
2NADP+
3- Phosphoglyceraldehyde ⇒ 3C+3C ⇒ 6C
(TRIOSE PHOSPHATE)
1 TURN OF C-3 CYCLE
3ATP, 2NADPH CONSUMED
③ REGENERATION OF RUBP
CRUCIAL STEP.
TO CONTINUE 2nd TURN OF C-3 cycle.
ATP
ADP.
5C
1C
1 TURN / 1 CO2 FIX:
3 ATP, 2 NADPH.

CALCULATION

1 CO_2 FIX/1 TURN OF CYCLE : Red^n : 2 ATP, 2 NADPH

Reg^n : 1 ATP

3 ATP, 2 NADPH

6 CO_2/6 TURN OF C-3 CYCLE : Red^n : $6 \times 2 = 12$ ATP, $6 \times 2 = 12$ NADPH

Reg^n : $6 \times 1 = 6$ ATP

18 ATP, 12 NADPH.

1 TURN/1 CO_2 FIX $\longrightarrow$ 1C

6 TURN/6 CO_2 FIX $\longrightarrow$ 1C + 1C + 1C + 1C + 1C + 1C $\longrightarrow$ one molecule of glucose.

1st 2nd 3rd 4th 5th 6th

C-4 cycle/Hatch & slack pathway

FOOD SYNTHESIS (THROUGH CALVIN CYCLE)

* Earlier Believed 1st product during food synthesis: 3 PGA (C-3)
* BUT ONE DAY: SUGARCANE, MAIZE, 1st PRODUCT: OAA (C-4), OXALOACETIC ACID NOT 3-PGA
* We Found alternate pathway: C-4 cycle./C-4 plants
* Dry Tropical Region / High light intensity / High Temperature adapted, 30-40°C → PHOTOSYNTHESIS HIGH.
* C-4 plant: KRANZ ANATOMY (LEAF): SPECIAL TYPE OF ANATOMY.

German WORD → WREATH / ARRANGEMENT OF

arrangement of BUNDLE SHEATH CELL AROUND VASCULAR BUNDLE.

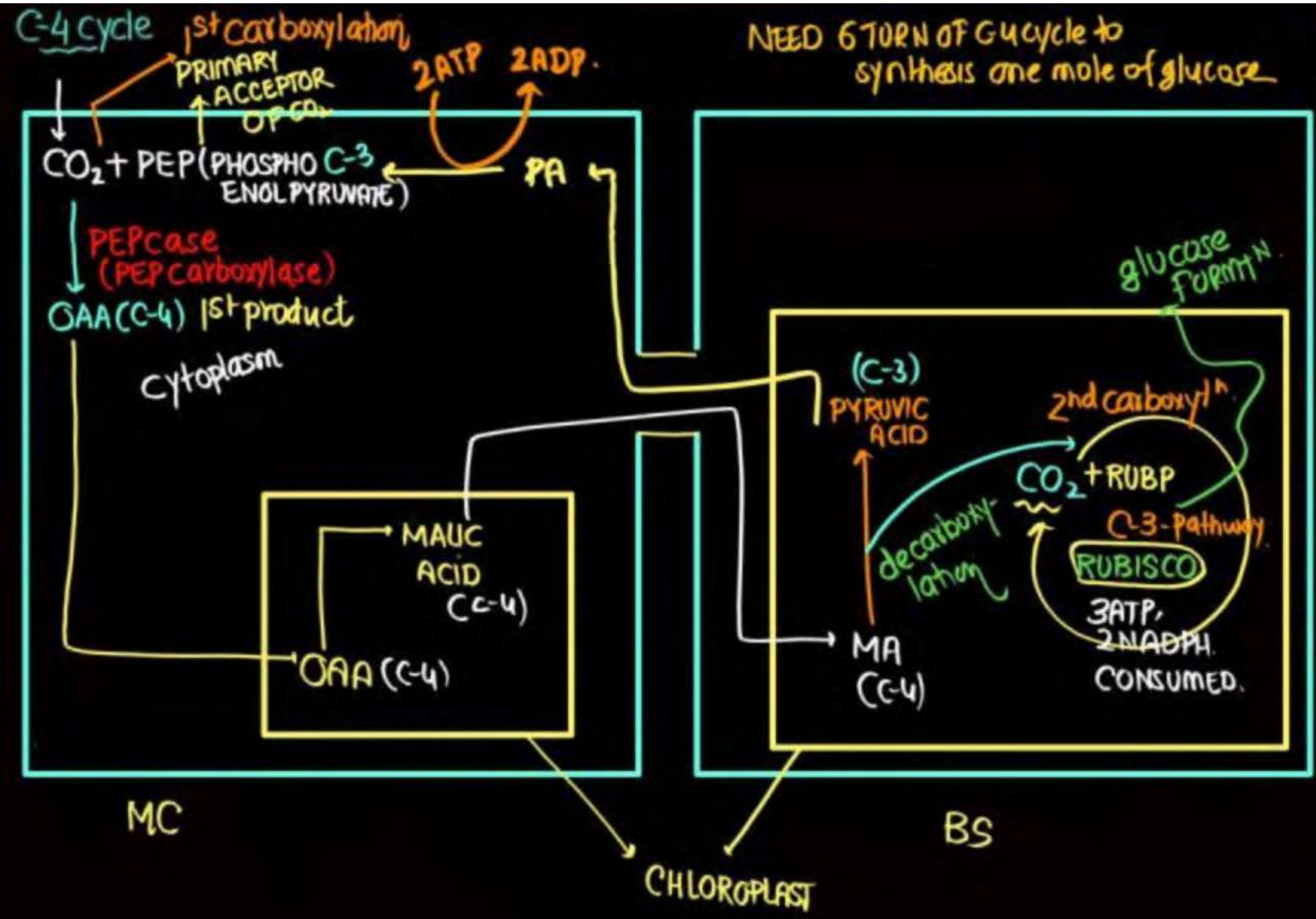
DIMORPHIC CHLOROPLAST

	Mesophyll cell	BUNDLE SHEATH CELL
Chloroplast (size, number)	small, less in number	LARGE IN NO. LARGE IN SIZE

NOTE: C-3 Chloroplast (Mesophyll cell) MONOMORPHIC

BUNDLE SHEATH CELL ⤳

- several layers around Vascular BUNDLE
- Intercellular space absent
- THICK CELL WALL (IMPERMEABLE TO GASE)



1 TURN OF C-4 cycle: MC & BS
($1CO_2$ FIXᵗⁿ) 2 ATP 3ATP, 2NADPH

5 ATP, 2NADPH.

1 TURN OF C-3 cycle: 3ATP, 2NADPH

	C-3 Plant	C-4 Plant
RUBISCO	Mesophyll cell	BUNDLE SHEATH
CARBOXYLATION	1st (Mesophyll Cell)	1st: MC 2nd: BS.
MAIN ENZYME	RUBISCO	PEPcase
1st product	3 PGA, C-3	OAA, C-4.
Primary acceptor	RUBP, C-5	PEP, C-3.
6 TURN/$6CO_2$ FIX	18ATP 12NADPH NEED	30ATP, 12NADPH NEED.

* Sorghum, sugarcane, maize (monocot)
  BUT also in DICOT : C-4 cycle
* Wheat, RICE : C-3 plant → C-3 cycle.
* C-3 plant : C-3 cycle ✓
* C-4 plant : C-3 pathway present.

All photosynthetic plant have C-3 pathway.

* C-3 pathway part of C-4 cycle. TRUE
* 6 TURN OF C-4 cycle need to FIX $6CO_2$ & FORM one molecule of glucose.

C-4 Better than C-3 plant

* PHOTORESPIRATION ABSENT IN C-4 PLANT / NO LOSS OF CO_2.
  HIGH YIELD/ PRODUCTIVITY PRESENT.
* C-4 : INTRACELLULAR CO_2 CONCENTRATING MECHANISM

$MA \rightarrow PA \rightarrow CO_2$

Con^n always HIGH AROUND RUBISCO SO IT ALWAYS BEHAVE AS CARBOXYLASE NOT OXYGENASE.

affinity of PEPcase > RUBISCO FOR CO_2.

Q. Total No. of ATP Require for formation of 2 Maltose through C-4 cycle.

1 MALTOSE : 2 GLUCOSE

2 MALTOSE : 4 GLUCOSE

1 GLUCOSE : 30 ATP, 12 NADPH NEED.

$= 4 \times 30$ 120 ATP

$= 4 \times 12 = 48$ NADPH.

PHOTORESPIRATION.

intake of O_2.

⇒ LIGHT PRESENSE (DAY TIME)

⇒ GREEN CELLS.

⇒ $O_2\uparrow$ $CO_2\downarrow$ RUBISCO → act as oxygenase

$$\underset{(5C)}{RUBP} + O_2 \xrightarrow[\text{oxygenase}]{\text{RUBISCO}} \underset{\text{(1mole 3C)}}{3PGA} + \underset{\text{(1mol) 2C}}{\text{Phosphoglycolate}}$$

→ NOT ENTER INTO C-3 cycle

Chloroplast
peroxisome
mitochondria

⇒ NO FIXn OF CO_2

⇒ CARBON LOSS

⇒ NO SUGAR SYNTHESIS

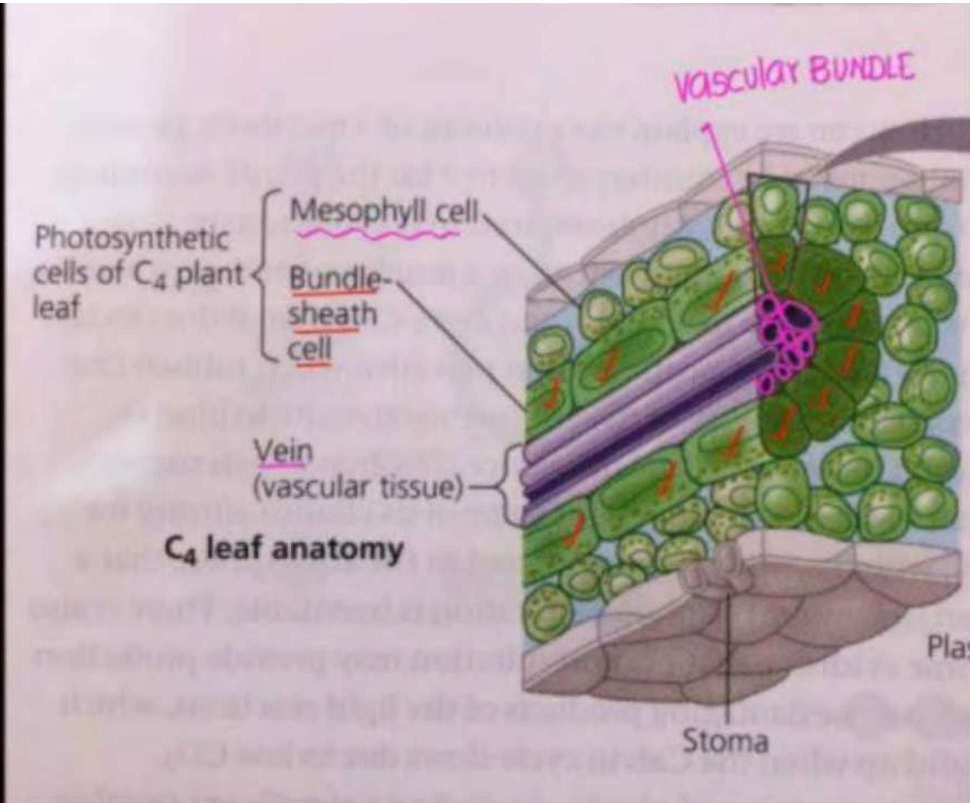
⇒ ATP, NADPH (ENERGY CONSUMED)

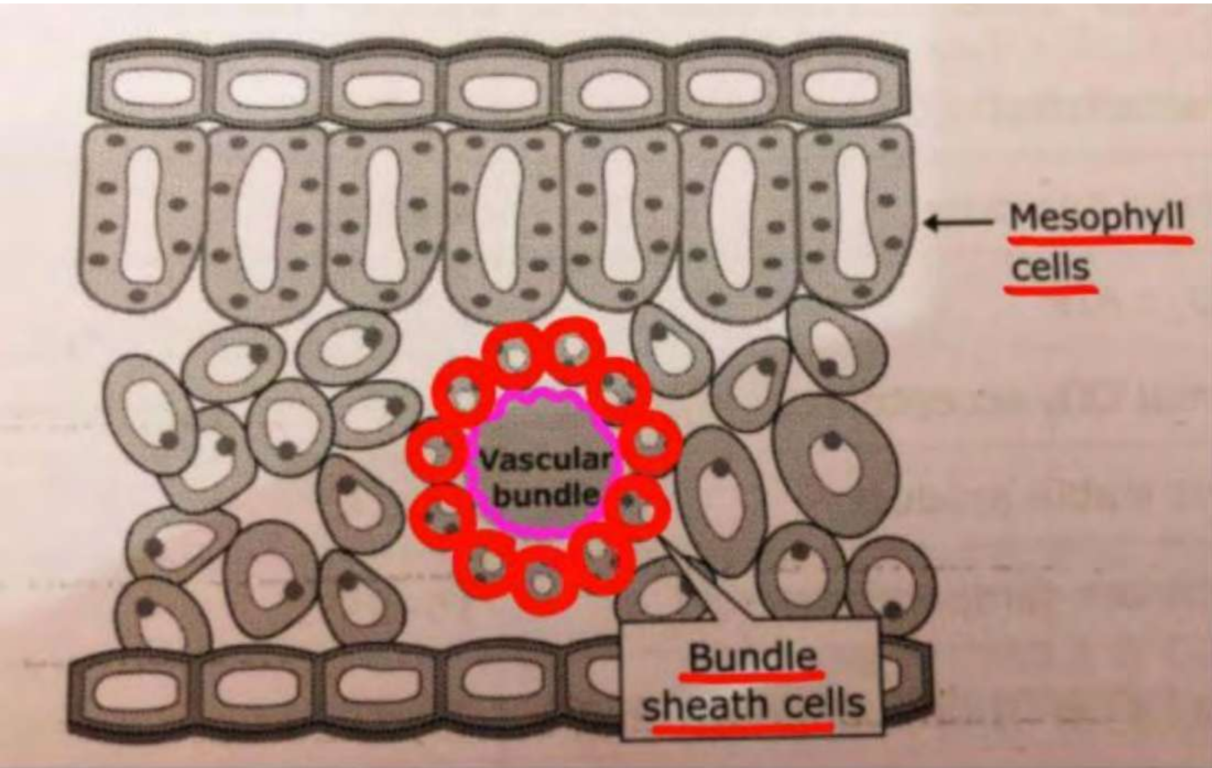
⇒ WASTEFUL PROCESS.

⇒ CO_2, NH_3 Released

HIGH TEMP/
HIGH LIGHT INTENSITY
$O_2\uparrow$ $CO_2\downarrow$

→ C-3 plant (PHOTORESPIRATION)


VASCULAR BUNDLE
Photosynthetic cells of C_4 plant leaf
Mesophyll cell
Bundle-sheath cell
Vein (vascular tissue)
C_4 leaf anatomy
Stoma


Mesophyll
cells
Vascular
bundle
Bundle
sheath cells

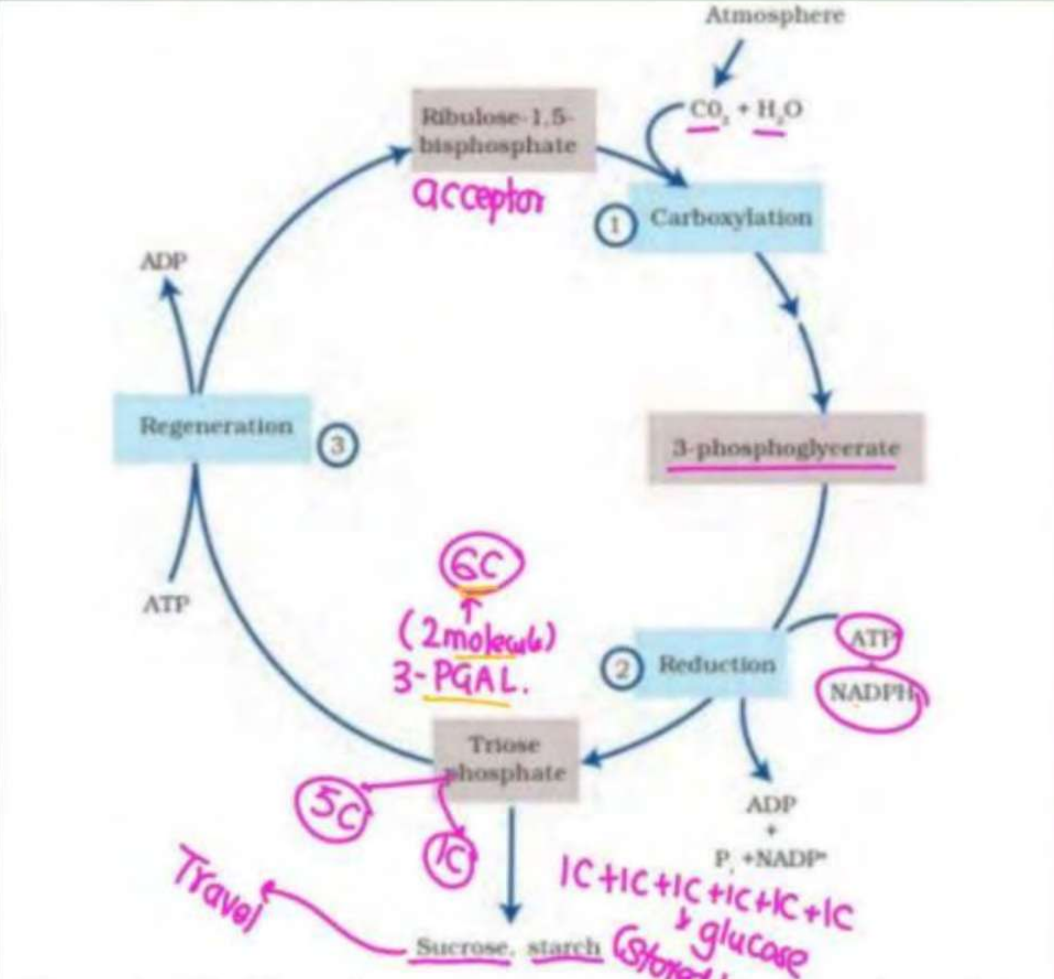


Figure 11.8 The Calvin cycle proceeds in three stages : (1) carboxylation, during which CO_2 combines with ribulose-1,5-bisphosphate; (2) reduction, during which carbohydrate is formed at the expense of the photochemically made ATP and NADPH; and (3) regeneration during which the CO_2 acceptor ribulose-1,5-bisphosphate is formed again so that the cycle continues

Red^n: glucose formed.

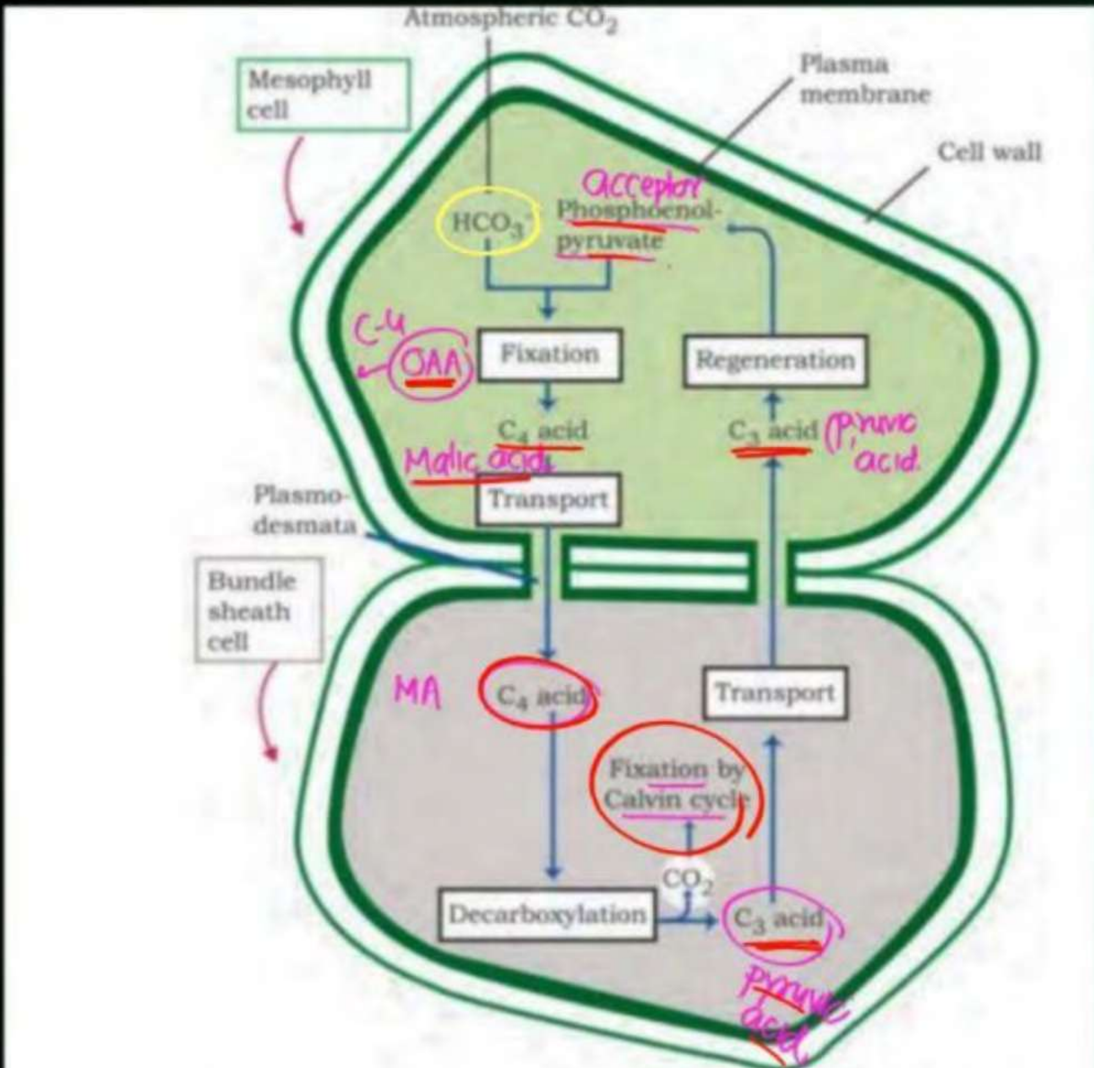


Figure 11.9 Diagrammatic representation of the Hatch and Slack Pathway

11.10 Factors affecting Photosynthesis

Rate↑ : yield↑
Rate↓ : yield↓

An understanding of the factors that affect photosynthesis is necessary. The rate of photosynthesis is very important in determining the yield of plants including crop plants. Photosynthesis is under the influence of several factors, both internal (plant) and external. The plant factors include (Internal Factor) the number, size, age and orientation of leaves, mesophyll cells and chloroplasts, internal CO_2 concentration and the amount of chlorophyll. The plant or internal factors are dependent on the genetic predisposition and the growth of the plant. ⇒ good : productivity High

number↑
Chloroplast↑
Photosynthesis↑

Photosyn↑

Leaf No↑ size↑] → Chloroplast Number↑ → Photosynthesis↑

↑age/Leaf old/mature : photosy↑

age : More : Leaf very old : Senescence Start (chlorophyll destruction) ⇒ death of Leaf

To get proper sunlight : Photosyn↑

genetic make up of Plant (DNA/chromosome)

The external factors would include the availability of sunlight, temperature, CO_2 concentration and water. As a plant photosynthesises, all these factors will simultaneously affect its rate. Hence, though several factors interact and simultaneously affect photosynthesis or CO_2 fixation, usually one factor is the major cause or is the one that limits the rate. Hence, at any point the rate will be determined by the factor available at sub-optimal levels.

Below expectation

Limiting

Rate of Rx^n.

↑

determine

↑

Limiting

चाय

Milk

पत्ती

अदरक

Sugar X

(minimum)

Water

CO_2

Chlorophyll

Cloudy day (Light) X

Rate of photosy : determine By Limiting factor : Light

You need optimal level

You do not need sub-optimal level

Bioyayayayayu

When several factors affect any [bio] chemical process, Blackman's (1905) **Law of Limiting Factors** comes into effect. This states the following:

If a chemical process is affected by more than one factor, then its rate will be determined by the factor which is nearest to its minimal value: it is the factor which directly affects the process if its quantity is changed.

light
Temp
CO_2
$\boxed{H_2O}$ X.
Chlorophyll

H_2O
sub-optimum level / Limiting.

If you supply $H_2O \longrightarrow$ Things will Be fine/ok

This too shall pass

For example, despite the presence of a green leaf and optimal light and CO_2 conditions, the plant may not photosynthesise if the temperature is very low. This leaf, if given the optimal temperature, will start photosynthesising.

Chlorophyll↑

11.10.1 Light

400-700nm (PAR: Photosynthetic active Radiation)
(Blue, Red)

We need to distinguish between light quality, light intensity and the duration of exposure to light, while discussing light as a factor that affects photosynthesis. There is a linear relationship between incident light and CO_2 fixation rates at low light intensities. At higher light intensities, gradually the rate does not show further increase as other factors become limiting (Figure 11.10). What is interesting to note is that light saturation occurs at 10 per cent of the full sunlight. Hence, except for plants in shade or in dense forests, light is rarely a limiting factor in nature. Increase in incident light beyond a point causes the breakdown of chlorophyll and a decrease in photosynthesis.

Rate of photosynthesis

H_2O, Chlorop, CO_2

(Photo-oxidation).
Maximum intensity of light
↓
Chlorophyll destruction

dark Region grow
(Sciophytes)

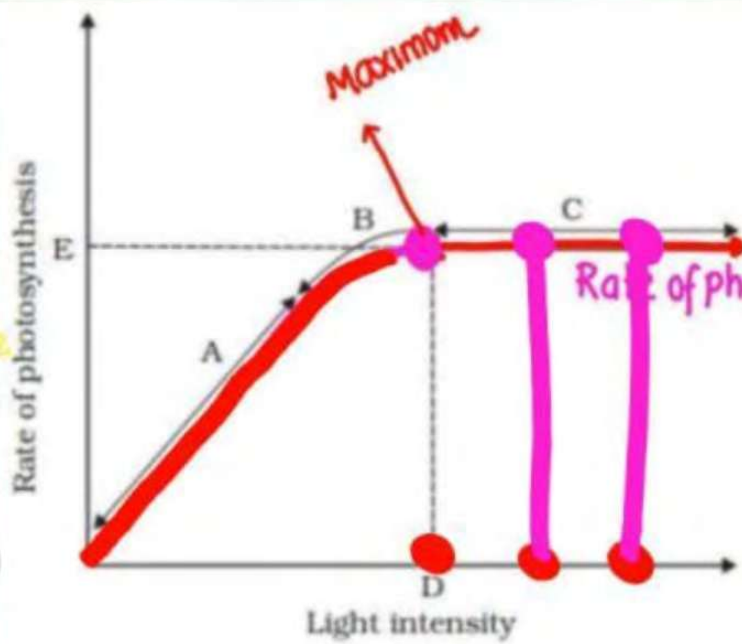


Figure 11.10 Graph of light intensity on the rate of photosynthesis

Rate of photosy : Constant

If you increase more intensity of Light, other Factors Become limiting.

11.10.2 Carbon dioxide Concentration

Carbon dioxide is the $\boxed{\text{major limiting factor}}$ for photosynthesis. The concentration of CO_2 is very low in the atmosphere (between 0.03 and 0.04 per cent). Increase in concentration upto 0.05 per cent can cause an increase in CO_2 fixation rates; beyond this the levels can become damaging over longer periods.

Rate of Photosyn ↑

CO_2 ↑ (more increase)
Other factors Become limiting.

The C_3 and C_4 plants respond differently to CO_2 concentrations. At low light conditions neither group responds to high CO_2 conditions. At high light intensities, both C_3 and C_4 plants show increase in the rates of photosynthesis. What is important to note is that the C_4 plants show saturation at about $\boxed{360\ \mu lL^{-1}}$ while C_3 responds to increased CO_2 concentration and saturation is seen only beyond $\boxed{450\ \mu lL^{-1}}$. Thus, current availability of CO_2 levels is limiting to the C_3 plants. Not for C-4 plant

	C-3	C-4
low light intensity, CO_2 High	NO (SAD)	NO (SAD)
Light intensity (High), CO_2 can High	Happy	Happy

C-4 : 360, Can Respond at low CO_2
C-3 : 450, Respond at High CO_2

The fact that C_3 plants respond to higher CO_2 concentration by showing increased rates of photosynthesis leading to higher productivity has been used for some greenhouse crops such as $\boxed{\text{tomatoes}}$ and $\boxed{\text{bell pepper}}$. They are allowed to grow in carbon dioxide enriched atmosphere that leads to higher yields.

grow in High CO_2 concⁿ
Rate of photosynthesis

No Need for C_4 plant
CO_2 not limiting.

Temp effect

dark > Light
Rxn Rxn
↓
enzymatic
Controlled.

11.10.3 Temperature

Temp↑ : enzyme inactive

C-3cycle/C-4cycle

The dark reactions being enzymatic are temperature controlled. Though the light reactions are also temperature sensitive they are affected to a much lesser extent. The C_4 plants respond to higher temperatures and show higher rate of photosynthesis while C_3 plants have a much lower temperature optimum. 30-40C.

The temperature optimum for photosynthesis of different plants also depends on the habitat that they are adapted to. Tropical plants have a higher temperature optimum than the plants adapted to temperate climates. C-4 30-40C.

11.10.4 Water

Even though water is one of the reactants in the light reaction, the effect of water as a factor is more through its effect on the plant, rather than directly on photosynthesis. Water stress causes the stomata to close hence reducing the CO_2 availability. Besides, water stress also makes leaves wilt, thus, reducing the surface area of the leaves and their metabolic activity as well.

dry

Water: indirectly Control

$H_2O \downarrow$ (soil) ⇒ To minimise Transpiration → Stomata Closed → No avail of CO_2 → Rate of Photosynthesis decrease.

PLANT GROWTH REGULATOR/ PHYTOHORMONE / PLANT HORMONE

* Small
* Simple COMPOUND.
* DIVERSITY IN CHEMICAL COMPOSITION

GROWTH

PROMOTE → PROMOTORS : Cell div^{N}, cell elongation, flowering, seed germ^{n}, FRUITING,
TROPHIC GROWTH (SHOOT BEND TOWARDS LIGHT : PHOTOTROPHISM)
PATTERN FORMATION. (ROOT, STEM, LEAF FORMATION,
TO RELOCATE PARTICULAR CELL IN PARTICULAR LOCATION.

↓

PERFORM PARTICULAR FUNCTION.

eg : AUXIN
GIBBERELLIN
CYTOKININ

INHIBIT → INHIBITOR. eg ABSCISSIC ACID (ABA)

DORMANCY IN SEED

↓

NO GERMINATION

ABSCISSION

Falling of young leaf/flower

NOTE : ETHYLENE CAN FIT EITHER OF TWO CATEGORY.

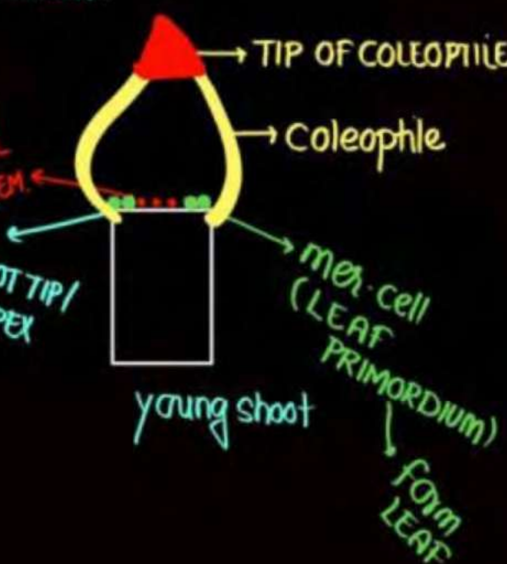
↓

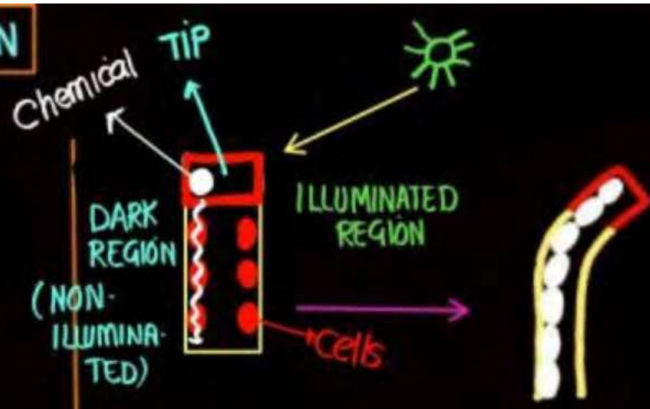
maximum activity (INHIBITORY).

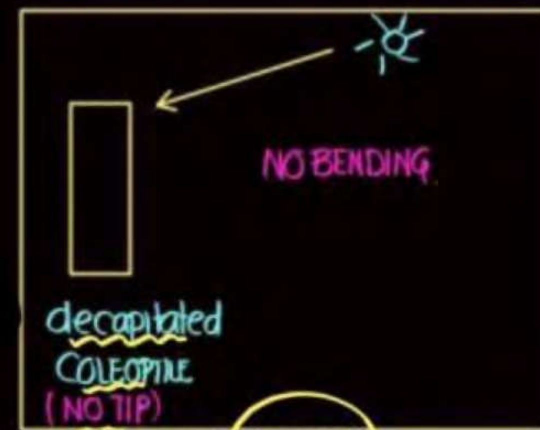
AUXIN

EXPERIMENT

CHARLES DARWIN & FRANCIS DARWIN
↓
CANARY GRASS / PHALARIS
↓
TAKEN COLEOPTILE ← PLUMULE → COVERING
(FORM SHOOT).







Coleoptile/ YOUNG SHOOT

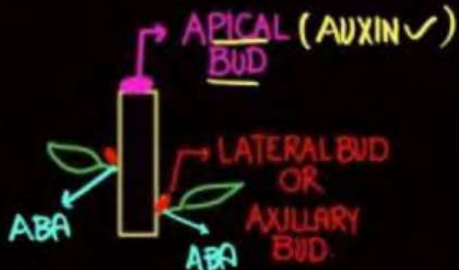
LIGHT (STIMULUS) → FALL ON TIP OF COLEOPTILE/SHOOT → SENSATION (CHEMICAL PRODUCED) [AUXIN] → THIS CHEMICAL ACCUMULATED IN DARK/SHADED REGION → CHEMICAL DIFFUSE FROM TIP TO BASE → available for cells in dark Region → cells show more growth Compare to cells of LIGHTED REGION
↓
BENDING OF SHOOT TOWARDS LIGHT (PHOTOTROPHISM)

F.W WENT: ISOLATE CHEMICAL (AUXIN)
discovery
OAT / AVENA SATIVA

HUMAN URINE: AUXIN ISOLATE.

ROLE OF AUXIN

① APICAL DOMINANCE



⇒ PRESENSE OF APICAL BUD (AUXIN) inhibit germination of Lateral BUD
↓
NO LATERAL BRANCH
↓
NO LEAVES / less in number

⇒ accumulation of ABA at lateral BUD. (INHIBITOR)

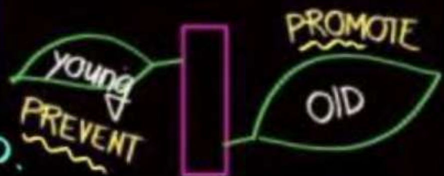
⇒ CYTOKININ SUPPLY INHIBIT AT LATERL BUD.

* If you Remove apical BUD
LATERL BUD → GERMINATE.
→ LATERAL BRANCH → MORE LEAVES.

TEA PRODUCTION, HEDGES MAKING
↓
APICAL BUD REMOVE OR AUXIN

② ABSCISSION (PREVENT)

Falling of leaves, flower, FRUIT ETC



③ FLOWERING IN PINEAPPLE

④ PARTHENOCARPY IN TOMATO.

⑤ PROMOTE GROWTH OF LATERAL ROOT ON STEM CUTTING

SHOOT TIP
ROOT TIP

⑥ NOTE: TYPES OF AUXIN

NATURAL	SYNTHETIC
* Isolate from plant	NAA (Napthalene acetic acid)
IAA (INDOLE-3-ACETIC ACID)	2,4-D (2,4 DICHLORO-PHENOXY ACETIC ACID)
IBA (INDOLE-3 BUTYRIC ACID)	

→ weedicide (weed free lawn) (Remove weed)
→ KILL DICOT
→ BUT NOT KILL MONOCOT.

⑦ XYLEM DIFFERENTIATION

HIGH AUXIN → XYLEM

⑧ CELL DIVISION (TISSUE CULTURE)

⑨ AGRICULTURE & HORTICULTURE
→ VEGETABLES
→ FLOWER
→ ORNAMENTAL

INDOLE DERIVATIVE

TRYTOPHAN
↓
AUXIN SYNTHESIS

GA

★ Japanese Farmer → RICE PLANT
Tall, Thin, yellow.

★ KUROSAWA: RICE PLANT → INFECTION → FUNGUS
GIBBERELA (BAKANE DISEASE / FOOLISH SEEDLING DISEASE).

FUNGUS → CHEMICAL ISOLATE → GIBBERELIN GA3.

GIBBERELIN → SYNTHETIC

COMMERCIAL LEVEL. ← GIBBERELIN

more than 100 GA: study

GA1, GA2, GA3 . . . .

GA1 → Bean plant

NATURAL.

ROLE

GRAPES, APPLE: shape, size increase

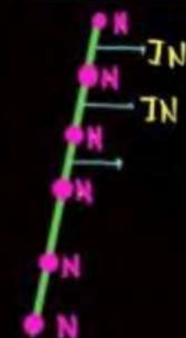
Stalk of fruit → Length (less)

INTERNODE SHORT

$\xrightarrow{GA}$

INTERNODE LONG.

LENGTH OF SUGARCANE



$\xrightarrow{GA}$

Length increase

INTERNODE ELONGATION

SUGAR PROD^N INCREASE

20 TONNES PER ACRE.

Gibberellin ⇒ ACIDIC

⇒ delay senescence (RIPENING PERIOD):
EXTEND THE PERIOD OF MARKETING.

⇒ Conifers (gymnosperm)
↓
early maturity
↓
early FERTILISATION
↓
early seed PRODN.

Note: Senescence: METABOLISM, PROTEIN SYNTHESIS / CHLOROPHYL SYNTHESIS INHIBIT → LEADS TO DEATH.

⇒ SEED GERMINATION
↓
enzymes synthesis
↓
α- amylase

ABA: INHIBIT SEED GERMINATION

GA & ABA: ANTAGONIST
GA → PROMOTE
ABA → PREVENT

⇒ MALTING PROCESS: SPEED UP

GA → BARLEY SEED
↓ SPEEDUP
α- amylase synthesis
↓
STARCH → MALTOSE
↓ MALTASE
GLUCOSE $\xrightarrow{\text{ZYMASE}}$ ETHANOL (BREWING INDUSTRY).

Starch + α-amylase → MALT

★ OVERCOME GENETIC DWARFISM
STEM ELONGATION / internode elongation (BOLTING).

⇒ PROMOTE BOLTING IN ROSETE PLANT (CABBAGE, BEET), JUST PRIOR TO FLOWERING
↓
INTERNODE SHORT

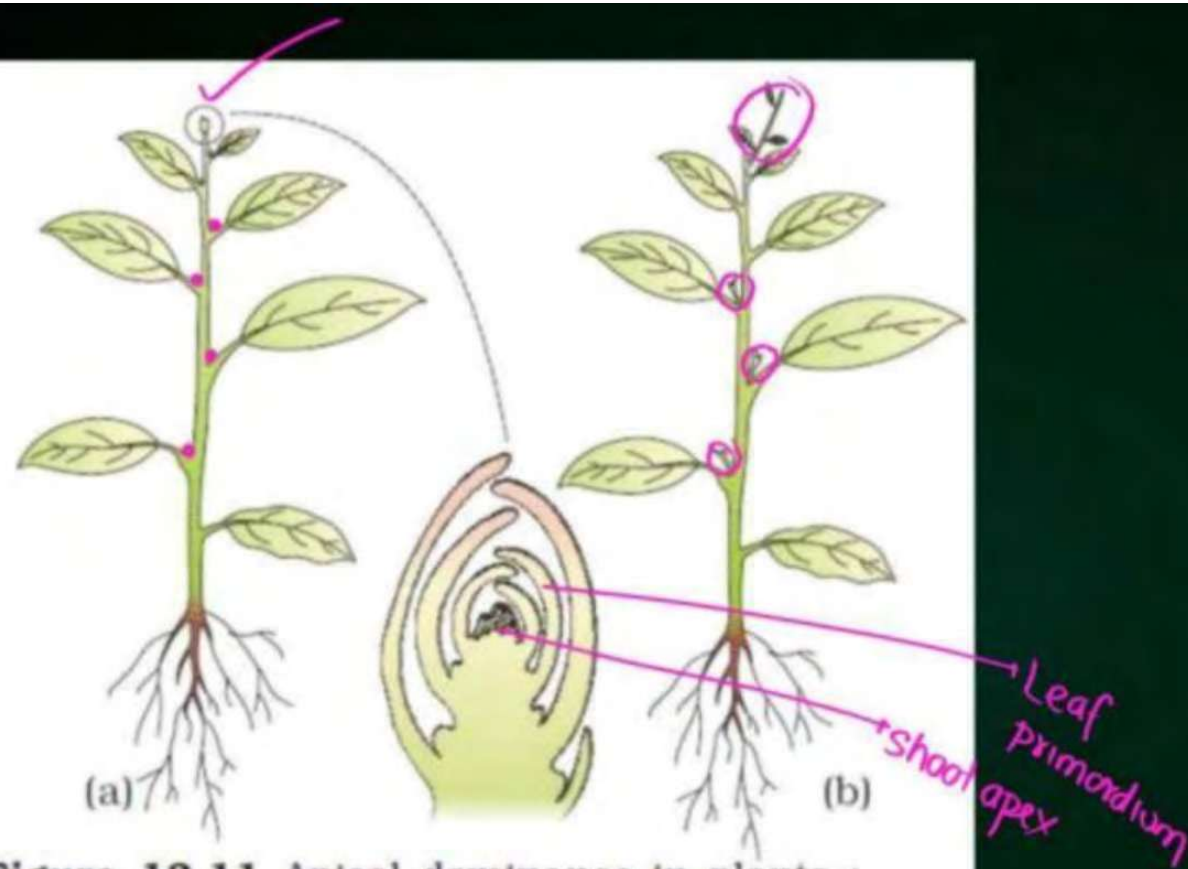


Figure 13.11 Apical dominance in plants :
(a) A plant with apical bud intact
(b) A plant with apical bud removed
Note the growth of lateral buds into branches after decapitation.

CYTOKININ / ADENINE (PURINE) derivative

SKOOG

AUXIN

COCONUT MILK / yeast / VASCULAR TISSUE

Role of cell division increase

cell (INTERNODE OF TOBACCO)

UNORGANISED MASS OF CELL (CALLUS)

MILLER

Herring fish sperm (DNA)

↓

add in TOBACCO CELL

↓

Cell division increase

KINETIN (SYNTHETIC CYTOKININ)

(N6 FURFURL AMINO PURINE)

MAIZE / CORN : ZEATIN (NATURAL CYTOKININ)

COCONUT

(BENZYLAMINOPURINE)

ROLE

★ INHIBIT APICAL DOMINANCE

↓

NUTRIENT SUPPLY INCREASE TOWARDS LATERAL BUD

↓

GERMIN^{N}

↓

LATERAL BRANCH → more LEAVES

PROMOTE ... INHIBIT

↑ ... ↑

AUXIN & CYTOKININ : ANTAGONIST

★ NUTRIENT SUPPLY INCREASE TOWARDS LEAF, CHLOROPLAST SYNTHESIS, METABOLISM : PROMOTE

SENESCENCE : DELAY

TISSUE CULTURE

NUTRIENT MEDIA

LEAF PART (cell)

DIVIDE →

mass of cell (callus)

CYTOKININ →

SHOOT FORMED

advent. SHOOT

AUXIN

ROOT FORMED

ORGANOGENESIS

TISSUE CULTURE

ROOT ←	AUXIN > CYTOKININ
SHOOT ←	AUXIN < CYTOKININ
CALLUS ←	AUXIN = CYTOKININ

↓

SYNERGIC EFFECT (Cell division PROMOTE)

ABA

GROWTH INHIBITOR.

INHIBIT : METABOLISM,
PROTEIN SYNTHESIS,
CHLOROPHYL SYNTHESIS,
SEED GERMINATION

PROMOTE : → ABSCISSION
→ SENESCENCE

STRESS CONDITION (HORMONE) : DROUGHT : H_2O LESS
↓
STOMATA : CLOSED
TRANSPIRATION : DECREASE

NOTE: Synthesis of PROTEIN
↓ HELP
SEED MATURATION

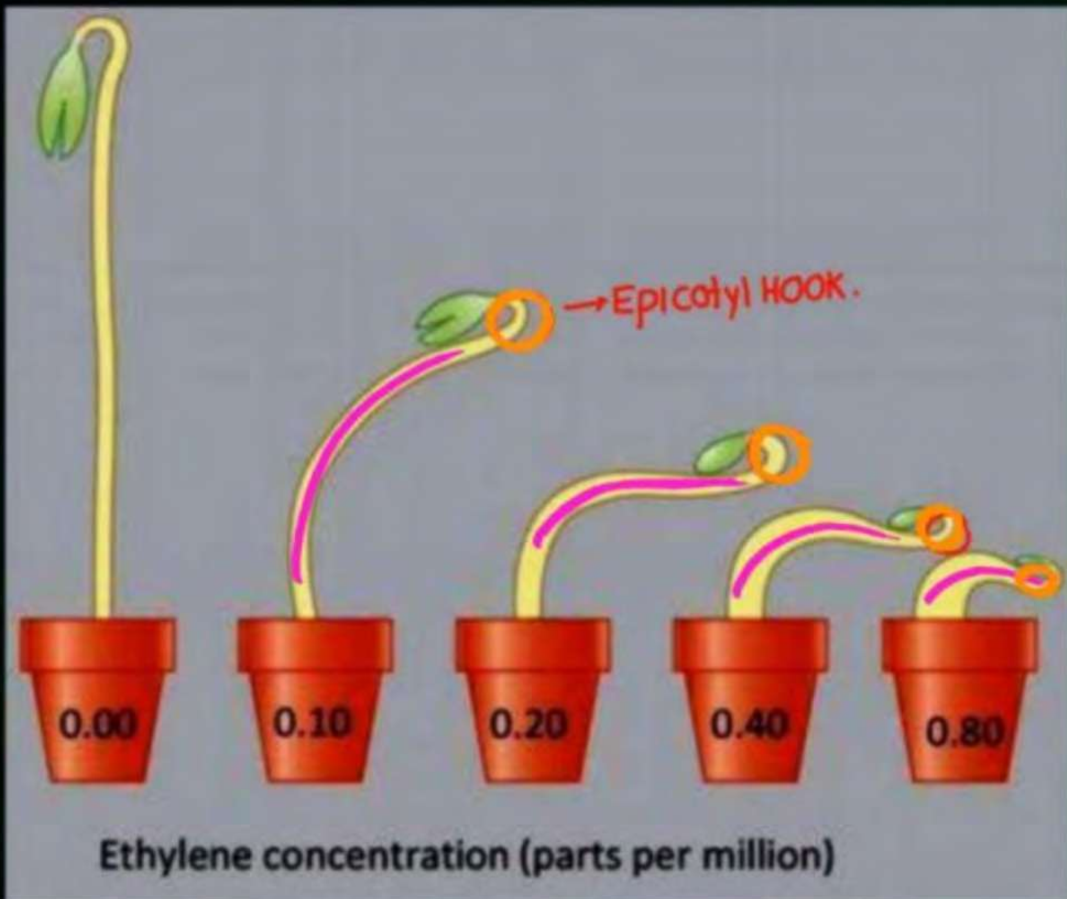
⇒ PROMOTE

Chemical same : Composition

- Inhibitor-β
- Abscission-II
- Dormin

→ isolated from diff source.

ABA



Ethylene

DICOT SEED IN SOIL

↓

SEEDLING

HORIZONTAL GROWTH.
SWELLING OF AXIS
TIP OF SHOOT → BED →

HOOK FORMn

TRIPLE RESPONSE.

ETHYLENE

FRUIT RIPENING HORMONE.

alREADY EXPLAINED ← TRIPLE RESPONSE

* Gaseous HORMONE, COUSIN

ORANGE $\xrightarrow{\text{gas}}$ UNRIPENED BANANA.
↓ RIPENING

RATE OF RESPIRATION:
INCREASE DURING RIPENING OF FRUIT

CLIMACTERIC RESPIRATION

* FLOWERING: PINE APPLE, MANGO.
* SENESCENCE, ABSCISSION: PROMOTE.

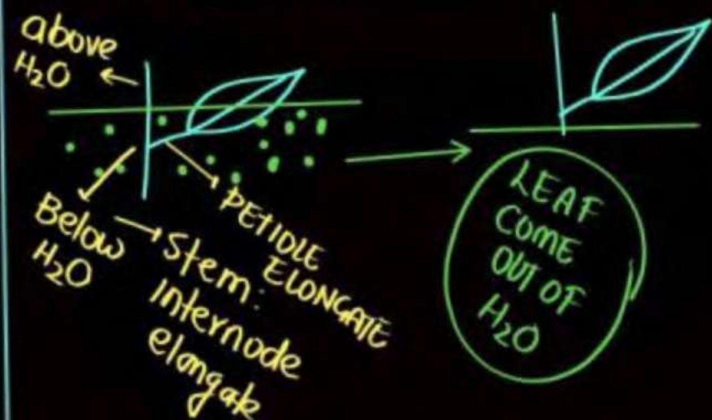
GA, CYTOKININ → INHIBIT → SENESCENCE
ABA, Ethylene → PROMOTE → SENESCENCE
ANTAGONIST

⇒ ROOT GROWTH/ROOT HAIR FORMN
ABSORPTION INCREASE.

⇒ SEED GERMINATION : PEA.

⇒ POTATO/TUBER : BUD DORMANCY BREAK.

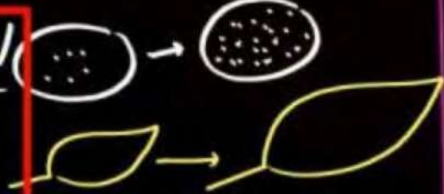
⇒ PETIOLE (RICE PLANT)



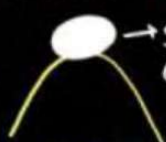
Ethepon (aqueous soln)
↓
SPRAY
↓
Ethepon $\xrightarrow{\text{metabolism}}$ **Ethylene**

GROWTH

★ INCREASE IN / NUMBER OF CELL / NUMBER OF INDIVIDUAL / SIZE OF ORGAN.



★ FUNDAMENTAL PROPERY → also shown BY NONLIVING



→ snow deposition ⟶ snow disappear.

Reversible

MOUNTAIN ⟶ size increase
↓
growth.

LIVING : IRREVERSIBLE

→ NEED ENERGY.
↓
FROM METABOLISM

wood (solid) ⟶ H_2O ⟶ wood swell ⟶ imbibition.
(NON-LIVING).

H_2O Remove ⟶ wood Regain its shape

Reversible

PLANT GROWTH

→ CONTINOUS / UnLimited / Indefinite

SHOOT
ROOT

→ MERISTEMATIC CELL ⟶ CONTINUOUS DIVIDE ⟶ LENGTH OF ROOT, STEM → INCREASE ⟶ PRIMARY GROWTH

OPEN TYPE OF GROWTH

(MC)
→ MERISTEMATIC CELL (DIVIDING CELL) $\xrightarrow{\text{divide}}$ Mer cell (NUMBER INCREASE) $\xrightarrow{\text{differentiation}}$ (stop division) permanent Tissue (parenchyma)

FORM
↓
ORGAN OF PLANT

LEAF (MESOPHYLL CELL) PARENCHYMATOUS TISSUE

GROWTH IS MEASURABLE

⇒ GROWTH ∝ PROTOPLASM INCREASE. (CONTENT OF NUCLEUS & CYTOPLASM INCREASE) → measurement difficult

SO WE MEASURE SOME DIFFERENT PARAMETER.

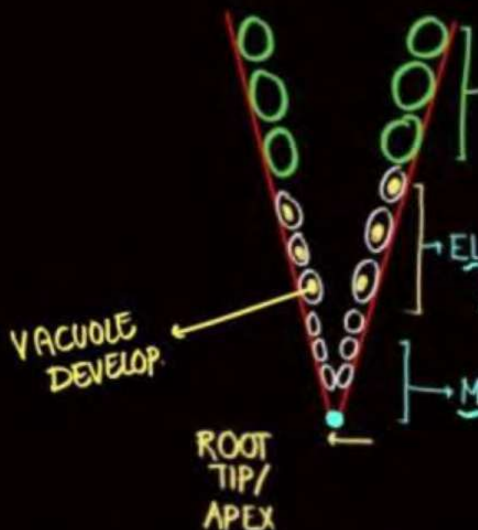
* Number : Maize : ROOT TIP → ONE CELL DIVIDE → 17500 Cell produce
  1 hour
* Size : (volume) → WATERMELON : Cell size increase 350,000 Times
* SURFACE AREA : Leaf (increase)

* LENGTH :
* FRESH WEIGHT : DRY WEIGHT + H_2O.

POLLEN GRAIN

Length of pollen tube ↑.

PHASE OF GROWTH

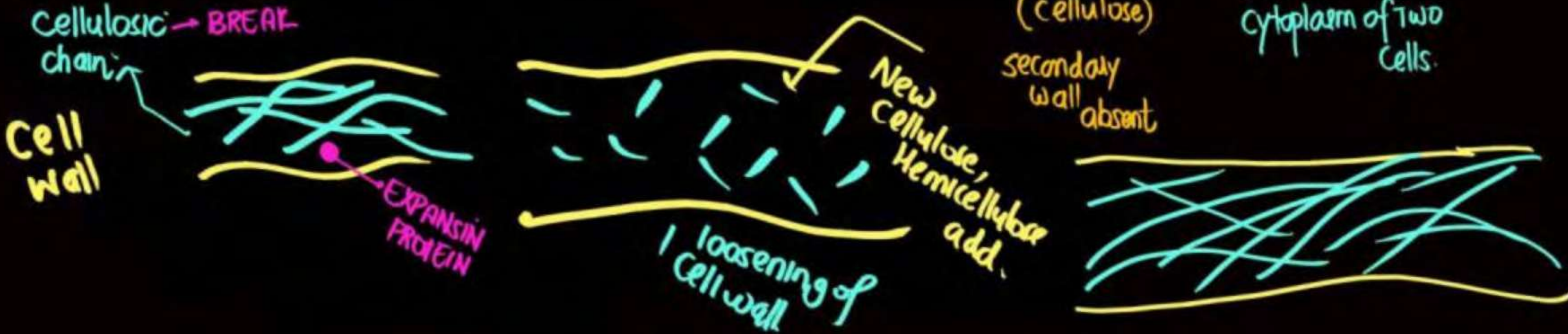


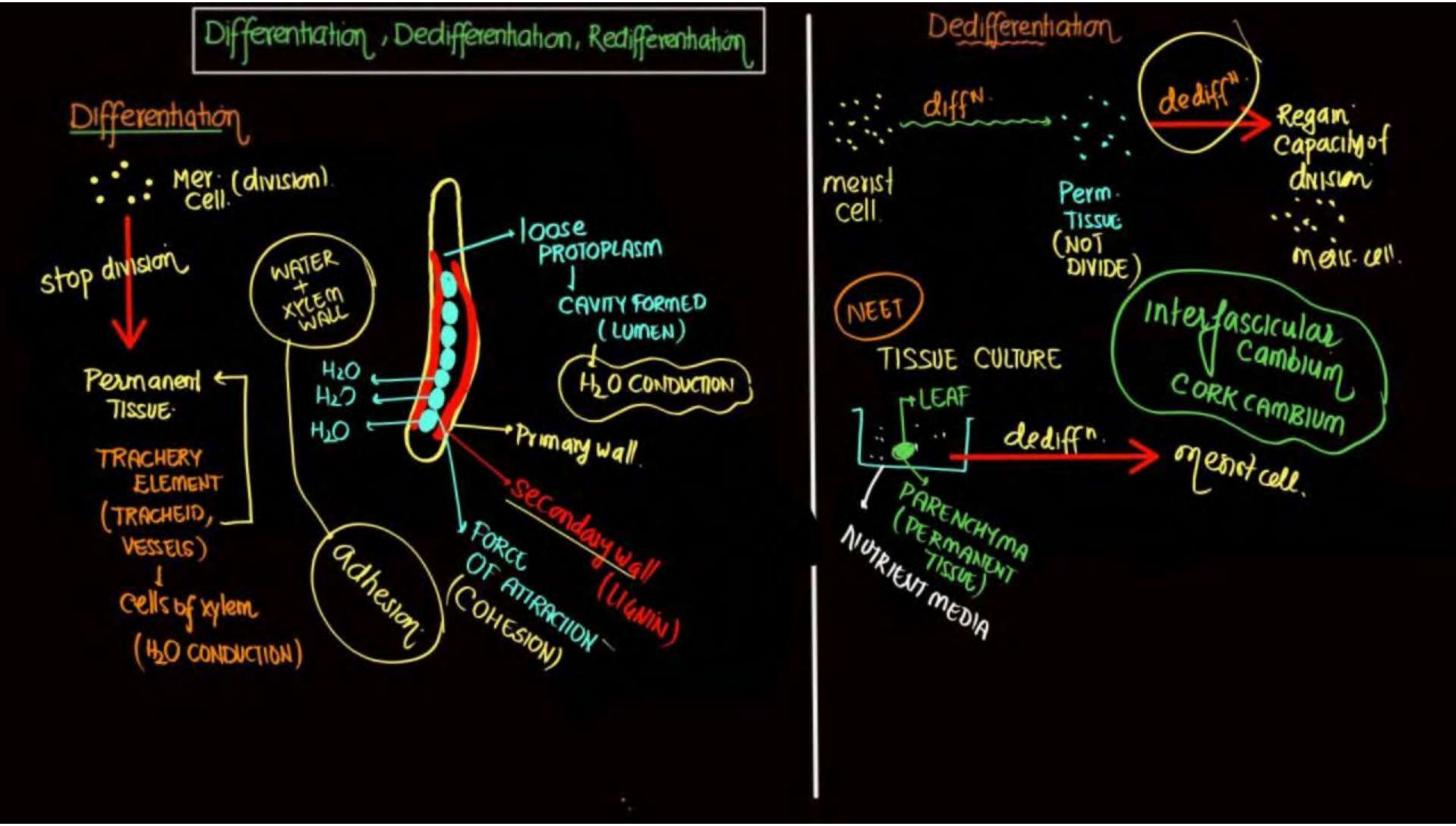
MATURATION ZONE → cell mature
- → THICKENING OF CELL WALL, secondary wall FORMED (THICK) (LIGNIN)
- → PROTOPLASM MODIFICATION.

TRACHEID → XYLEM.
PERMANENT TISSUE
- PW, SW (THICK) (LIGNIN)
- LOOSE PROTOPLASM → DEAD.

ELONGATION ZONE → ELONGATED, DEPOSITION OF WALL MATERIAL.

MERISTEMATIC ZONE: Cell → small, dense Cytoplasm, (Vacuole absent) NUCLEUS PRESENT → Cellwall: THIN (PRIMARY WALL PRESENT) (cellulose) secondary wall absent, abundant Plasmodesmeta → connect cytoplasm of two cells.





Differentiation, Dedifferentiation, Redifferentiation
Differentiation
Mer. Cell. (division)
stop division
Permanent TISSUE.
TRACHERY ELEMENT (TRACHEID, VESSELS)
Cells of xylem (H2O CONDUCTION)
WATER + XYLEM WALL
adhesion
H2O
H2O
H2O
loose PROTOPLASM
CAVITY FORMED (LUMEN)
H2O CONDUCTION
Primary wall
Secondary wall (LIGNIN)
FORCE OF ATTRACTION (COHESION)
Dedifferentiation
diffN.
merist cell
Perm. TISSUE (NOT DIVIDE)
dediffN.
Regain capacity of division
meris. cell.
NEET
TISSUE CULTURE
LEAF
dediffn.
merist cell.
PARENCHYMA (PERMANENT TISSUE)
NUTRIENT MEDIA
Interfascicular cambium
CORK CAMBIUM

Redifferentiation

mer. cell divN ✓

↓ differentiation

perm. Tissue. Cell NOT DIVIDING

↓ dediffN

cell Regain Capacity of divN.

mer. cell

↓ RediffN

per. Tissue.

eg: sec. xylem
sec. phloem
CORK.
secondary CORTEX

CONDITION FOR GROWTH

NUTRIENTS ✓

- Nitrogenous compound: synthesis protoplasm
- Carbohydrate: energy, cell wall synthesis
- MICRONUTRIENT & MACRONUTRIENT ✓

TEMPERATURE

- 25 - 30°C
- MORE TEMP: DENATURAION OF ENZYMES
- LOW TEMP: INACTIVATE ENZYME

LIGHT

- Chlorophyll synthesis
- Flowering

H_2O

- enter into cell ✓
  ↓
  cell swell (TURGIDITY) ✓
  ↓
  EXPANSION/ELONGATION IN CELL
- also provide medium for enzyme action ✓

Oxygen

- aerobic Resp^n ✓
- glucose Breakdown

Gravity

- Determine ROOT, SHOOT

13.1.4 Growth Rates

50 Bact $\xrightarrow{\text{20 minute}}$ 100 Bact (In Terms of number)

The increased growth per unit time is termed as growth rate. Thus, rate of growth can be expressed mathematically. An organism, or a part of the organism can produce more cells in a variety of ways.

Bacteria,

Leaf of plant

The growth rate shows an increase that may be $\boxed{\text{arithmetic}}$ or $\boxed{\text{geometrical}}$ (Figure 13.4).

Leaf $\xrightarrow[\text{6 day}]{\text{after}}$

SA: 5

SA: 10

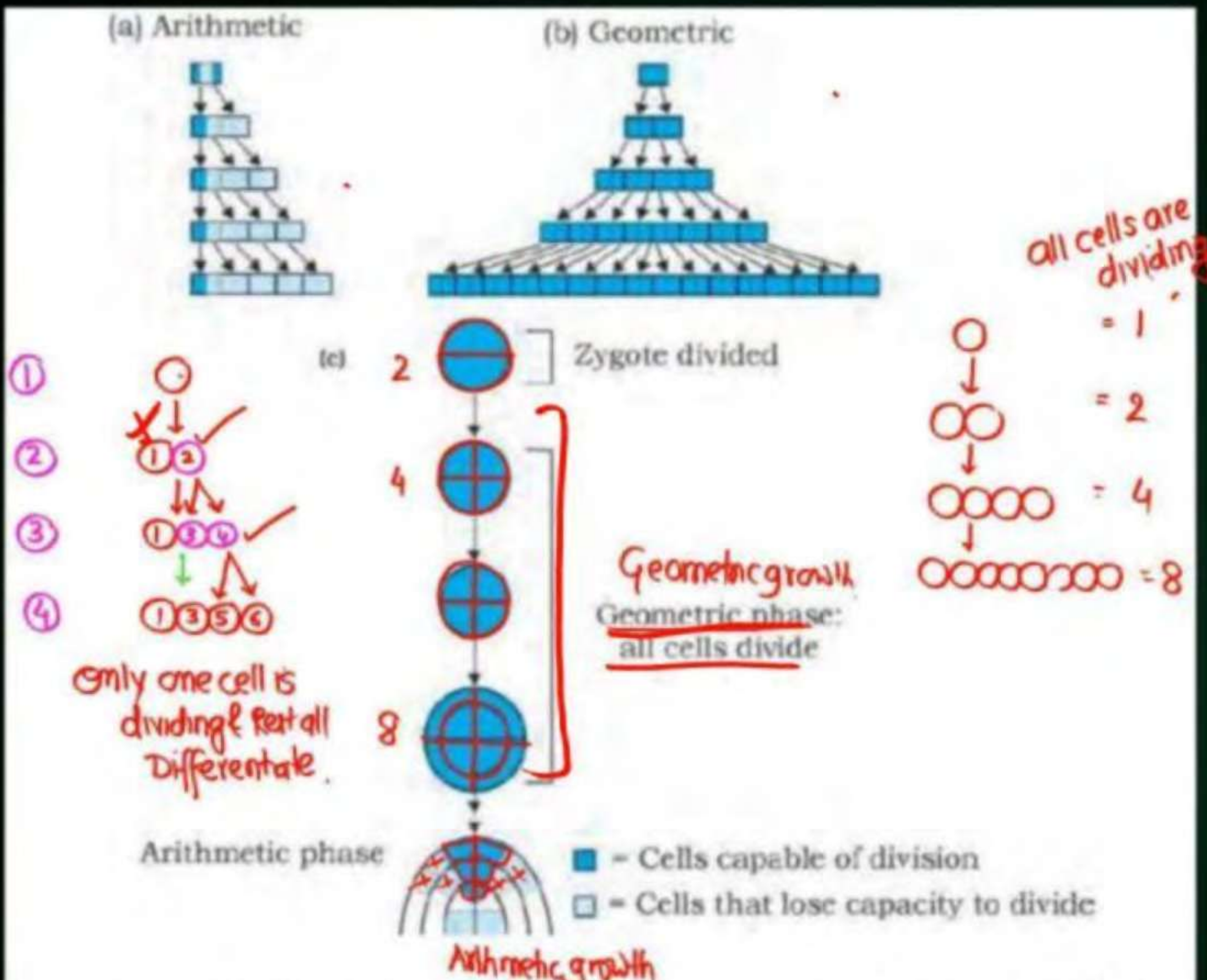


Figure 13.4 Diagrammatic representation of : (a) Arithmetic (b) Geometric growth and (c) Stages during embryo development showing geometric and arithematic phases

$\boxed{\text{Geomet growth > Arithmetic growth}}$

Initial : geometric growth
Later : arith. growth
→ dev. of zygote

In arithmetic growth, following mitotic cell division, only one daughter cell continues to divide while the other differentiates and matures. The simplest expression of arithmetic growth is exemplified by a root elongating at a constant rate. Look at Figure 13.5. On plotting the length of the organ against time, a linear curve is obtained. Mathematically, it is expressed as

Straight line
(Linear CURVE)

Initial

$$L_t = \boxed{L_0} + rt$$

L_t = length at time 't'

L_0 = length at time 'zero'

r = growth rate / elongation per unit time.

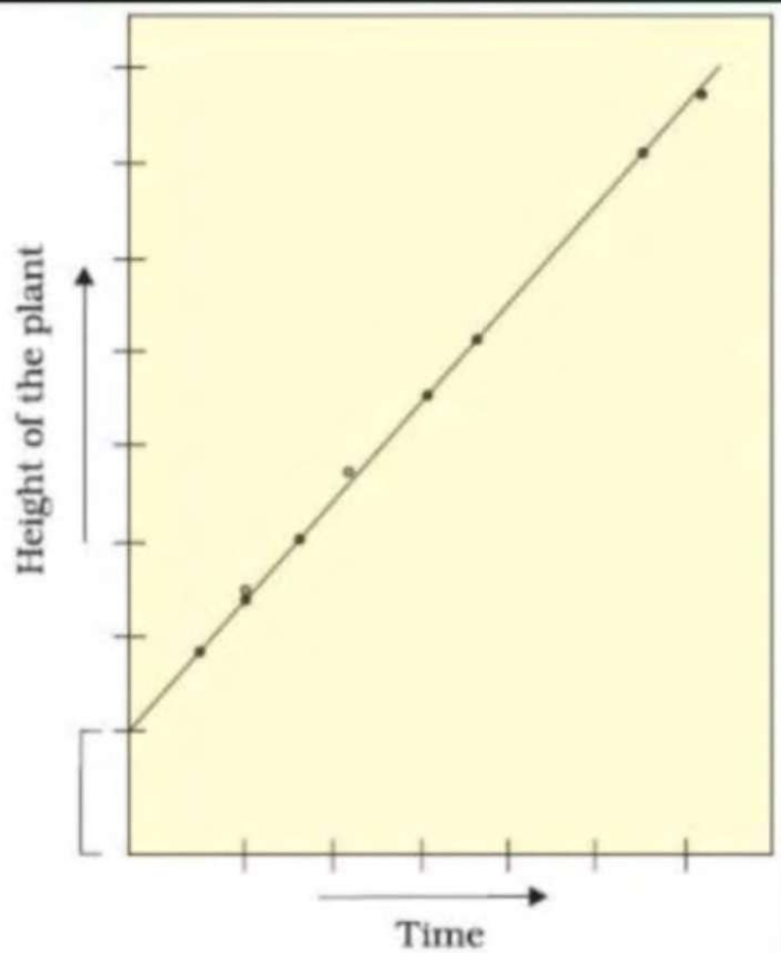
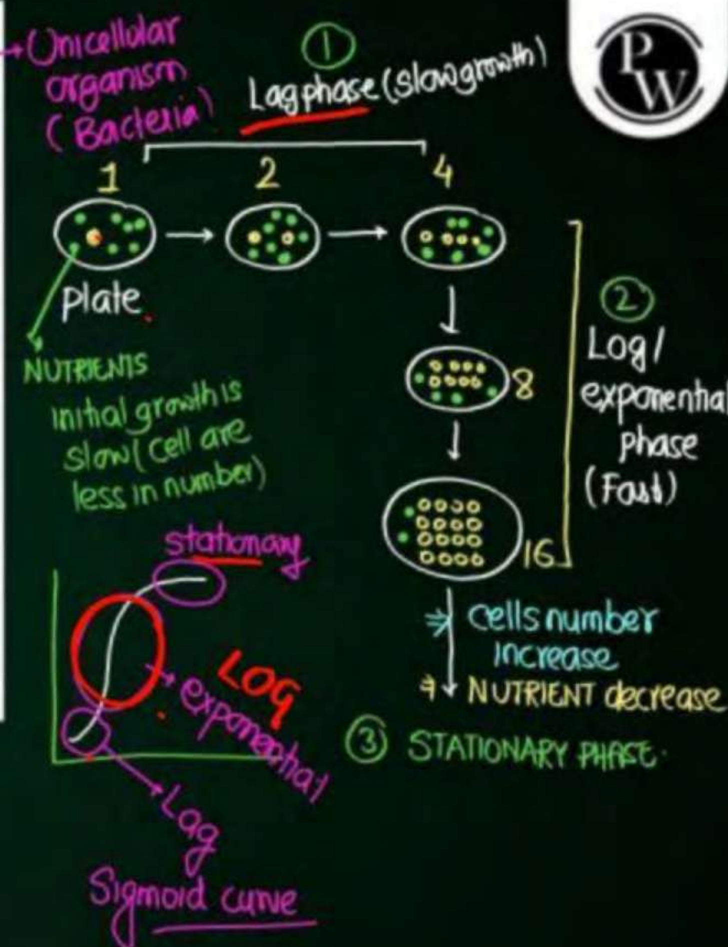


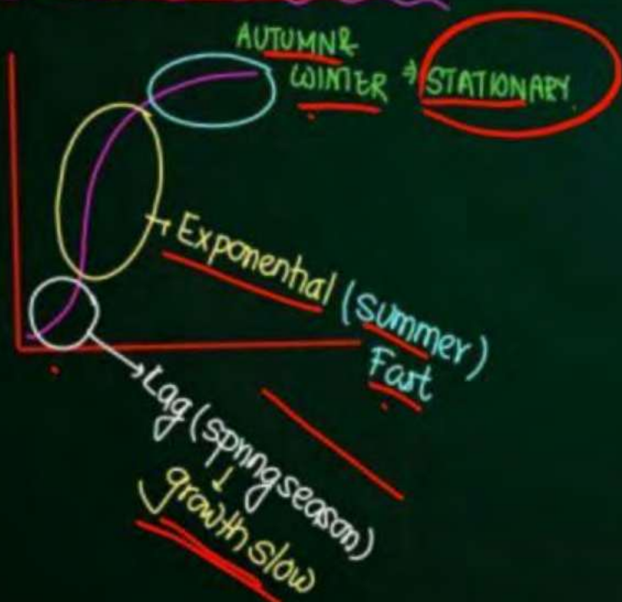
Figure 13.5 Constant linear growth, a plot of length L against time t

Let us now see what happens in geometrical growth. In most systems, the initial growth is slow (lag phase), and it increases rapidly thereafter – at an exponential rate (log or exponential phase). Here, both the progeny cells following mitotic cell division retain the ability to divide and continue to do so. However, with limited nutrient supply, the growth slows down leading to a stationary phase. If we plot the parameter of growth against time, we get a typical sigmoid or S-curve (Figure 13.6).



A sigmoid curve is a characteristic of living organism growing in a natural environment. It is typical for all cells, tissues and organs of a plant. *Can you think of more similar examples? What kind of a curve can you expect in a tree showing seasonal activities?* → Sigmoid curve

→ Bacteria



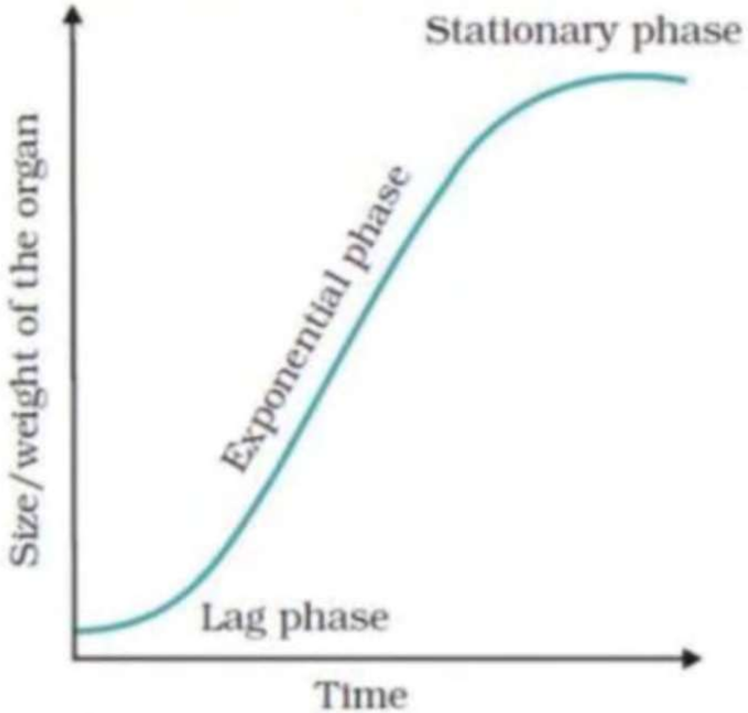


Figure 13.6 An idealised sigmoid growth curve typical of cells in culture, and many higher plants and plant organs

The exponential growth can be expressed as

$$W_1 = W_0 e^{rt}$$

W_1 = final size (weight, height, number etc.)

W_0 = initial size at the beginning of the period

r = growth rate

t = time of growth

e = base of natural logarithms

Here, r is the relative growth rate and is also the measure of the ability of the plant to produce new plant material, referred to as efficiency index. Hence, the final size of W_1 depends on the initial size, W_0.

FD : पैसा / W_1

→ Initial money (initial size) W_0

→ r : Rate of interest : 6% / 7% / 8% : (r)

→ t : 2 years / 3 years.

W_1 (FINAL PAISA/SIZE) after FIXED DEPOSIT.

Quantitative comparisons between the growth of living system can also be made in two ways : (i) measurement and the comparison of total growth per unit time is called the absolute growth rate. (ii) The growth of the given system per unit time expressed on a common basis, e.g., per unit initial parameter is called the relative growth rate. In Figure 13.7 two leaves, A and B are drawn that are of different sizes but shows absolute increase in area in the given time to give leaves, A^1 and B^1. However, one of them shows much higher relative growth rate. Which one and why?

Leaf A > leaf B

absol. growth Rate: same 5cm^2

Bz leaf A initial size is small.

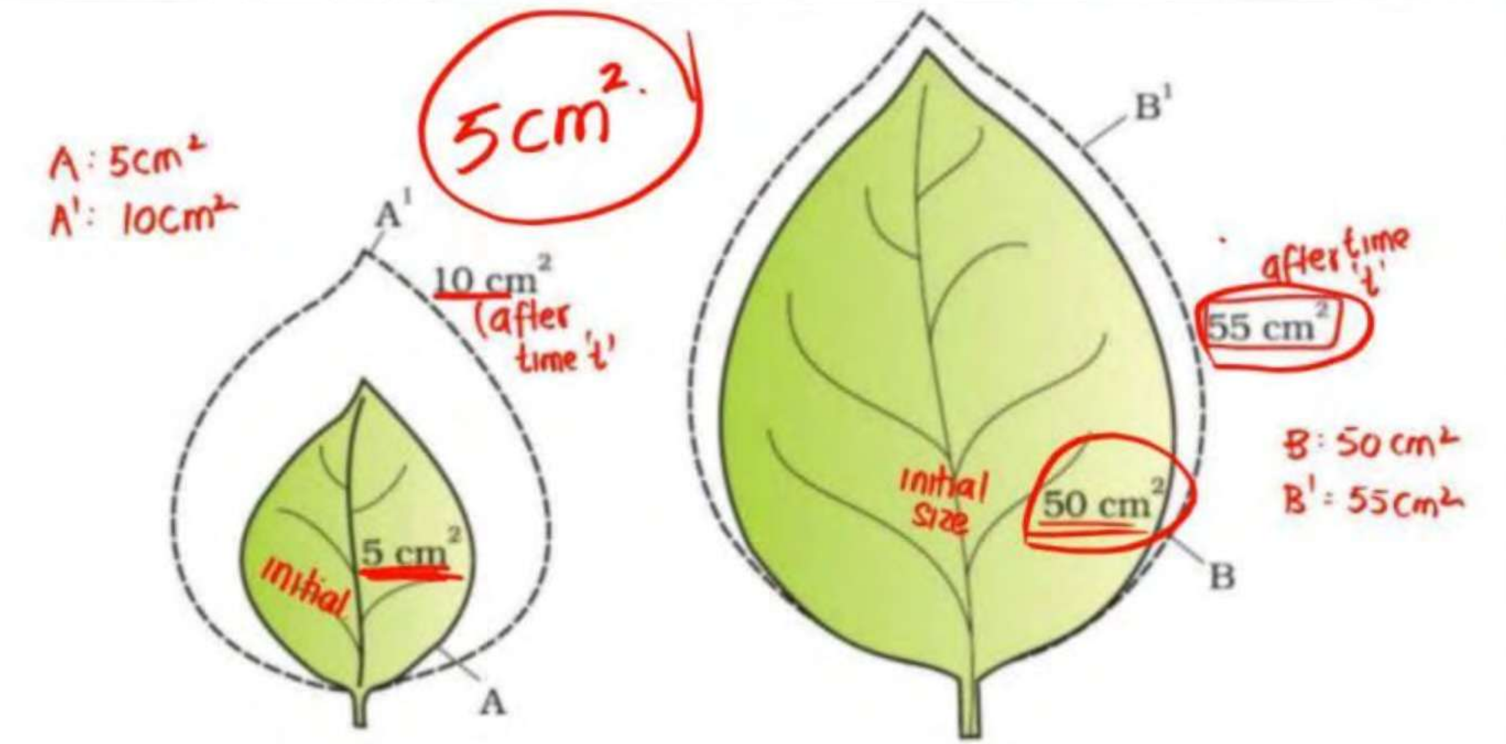


Figure 13.7 Diagrammatic comparison of absolute and relative growth rates. Both leaves A and B have increased their area by 5 cm² in a given time to produce A¹, B¹ leaves.

(AGR)
Absolute growth Rate

A: growth/per unit Time
5cm²

B: 5 cm²

⇒ AGR of Both A & B leaf are same

Relative growth Rate :
$\frac{\text{growth}}{\text{initial growth}}$

A: $\frac{5}{5cm^2} \times 100 \Rightarrow 100\%$

B: $\frac{5 \times 1\cancel{0}\cancel{0}}{5\cancel{0}} \Rightarrow 10\%$

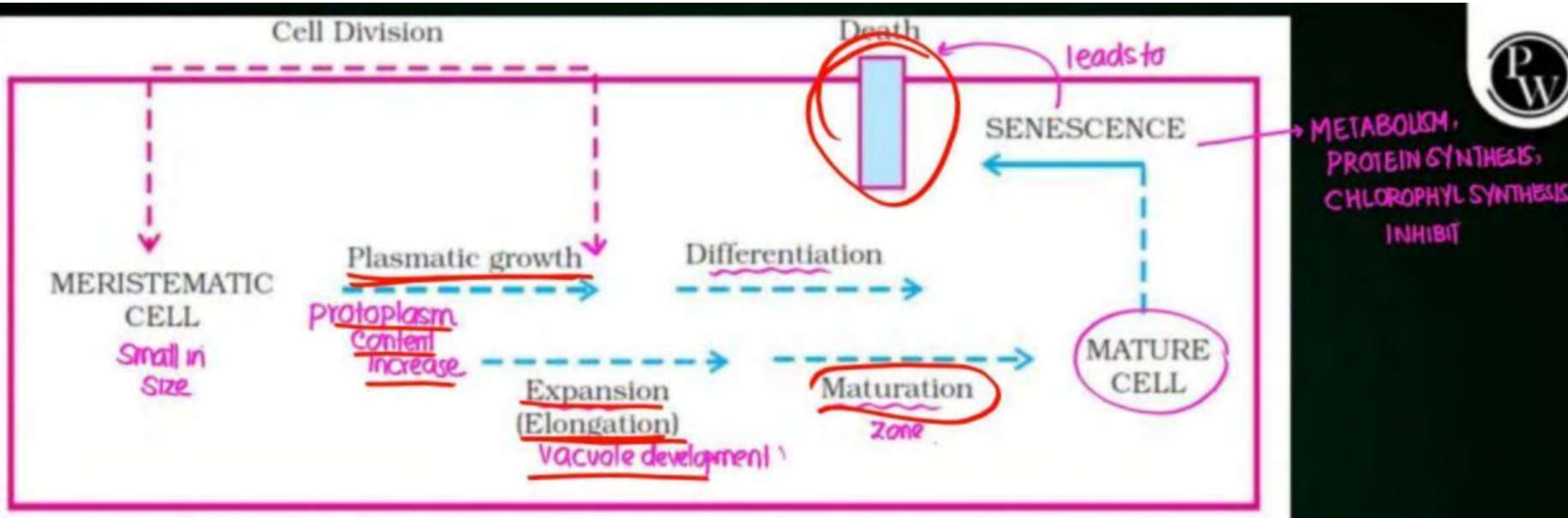


Figure 13.8 Sequence of the developmental process in a plant cell

Leaves

External

Plants follow different pathways in response to environment or phases of life to form different kinds of structures. This ability is called **plasticity**, e.g., heterophylly in cotton, coriander and larkspur. In such plants, the leaves of the juvenile plant are different in shape from those in mature plants. On the other hand, difference in shapes of leaves produced in air and those produced in water in buttercup also represent the heterophyllous development due to environment (Figure 13.9). This phenomenon of heterophylly is an example of plasticity.

Internal Factor (gene / DNA)

diff type of leaf on same plant

aquatic Habitat

ext. Factor

Outside H_2O (Terrestrial)

Internal Factor

gene

Plant growth Regulator

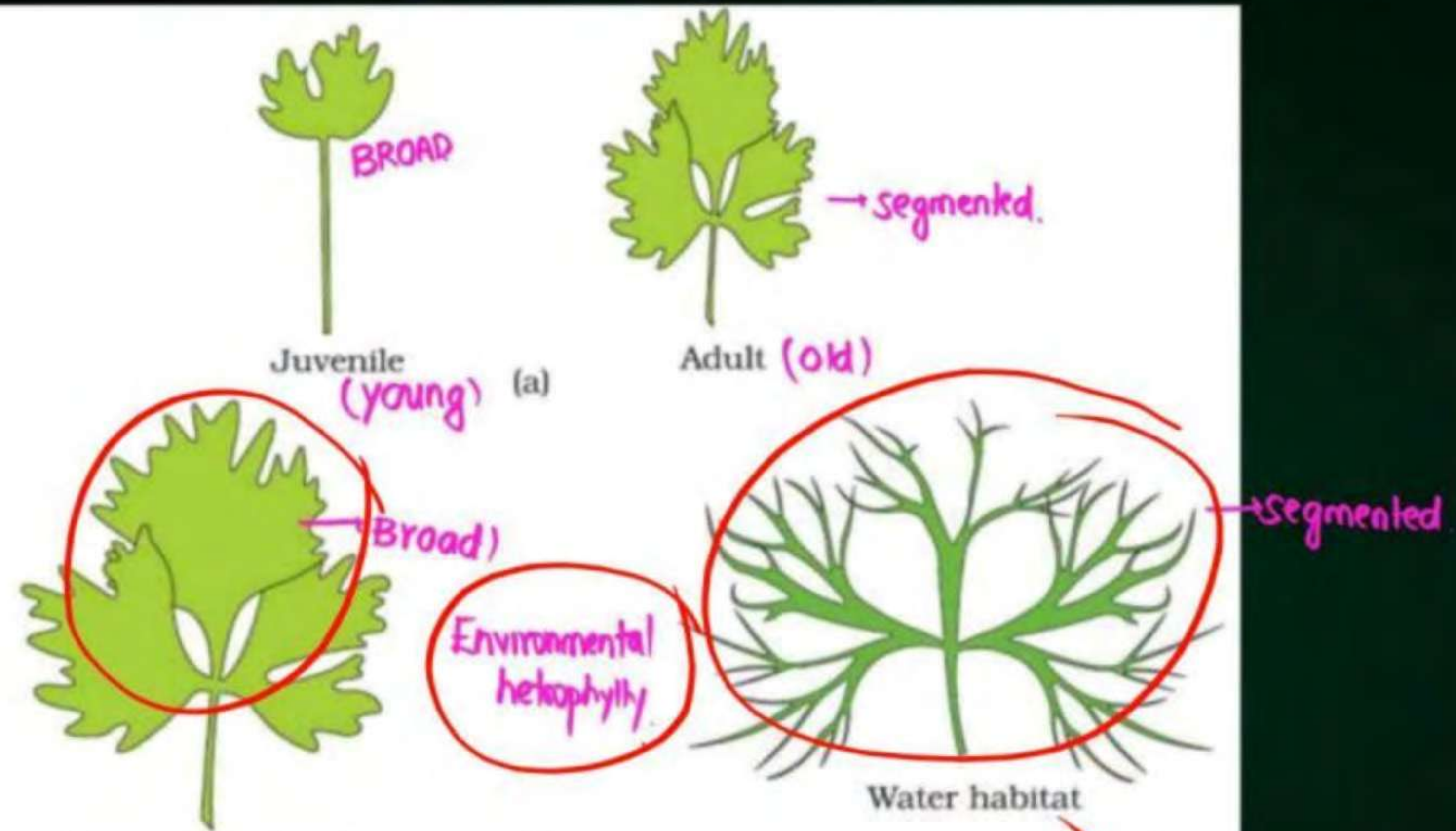
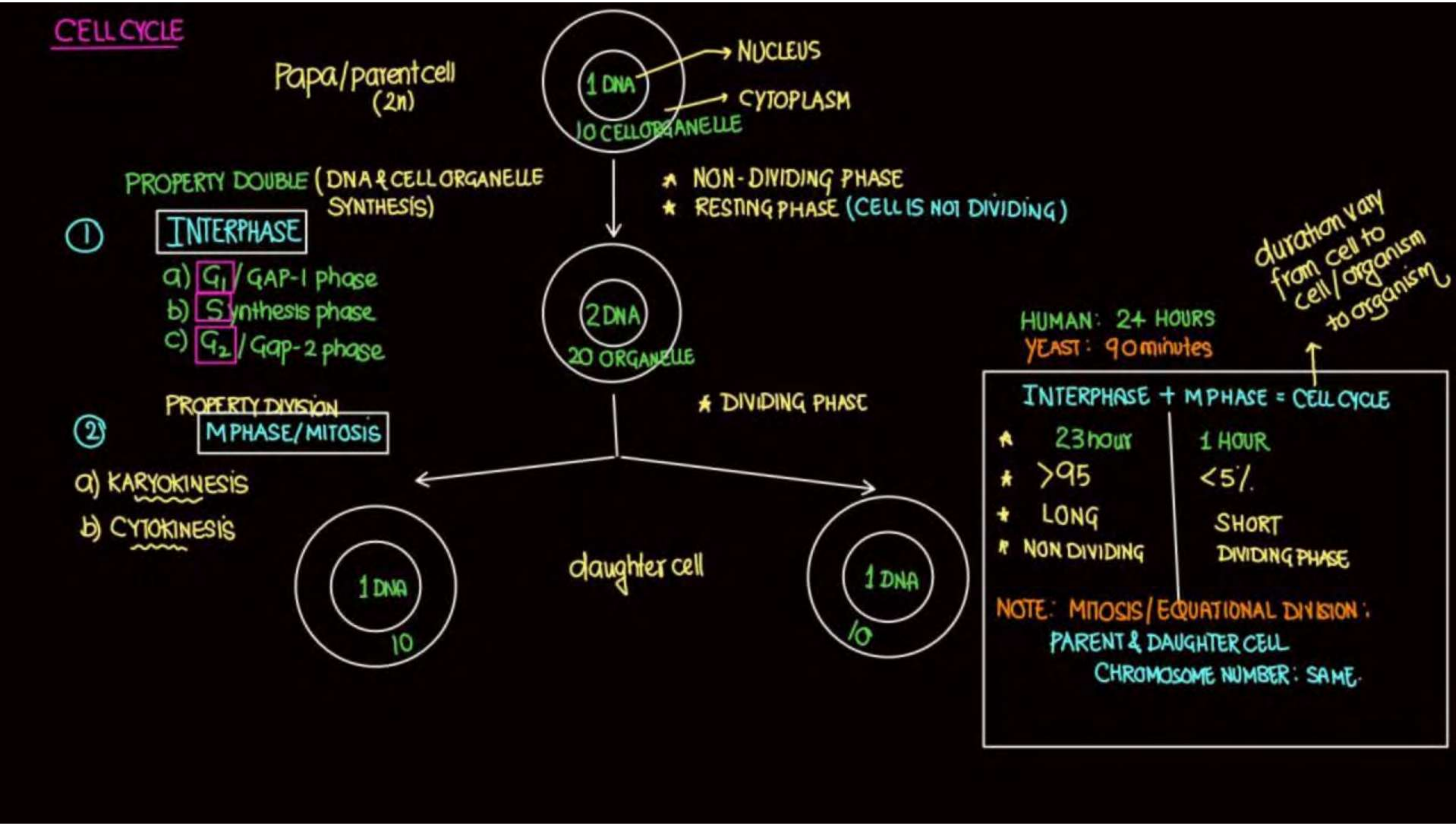


Figure 13.9 Heterophylly in (a) larkspur and (b) buttercup (Rananculus)

Thus, growth, differentiation and development are very closely related events in the life of a plant. Broadly, development is considered as the sum of growth and differentiation. Development in plants (i.e., both growth and differentiation) is under the control of intrinsic and extrinsic factors. The former includes both intracellular (genetic) or intercellular factors (chemicals such as plant growth regulators) while the latter includes light, temperature, water, oxygen, nutrition, etc.

DNA.


RUPESH SIR
JOIN MY OFFICIAL TELEGRAM CHANNEL
Physics Wallah
@PWRUPESHSIR


CELL CYCLE
Papa/parent cell (2n)
1 DNA
NUCLEUS
CYTOPLASM
10 CELL ORGANELLE
PROPERTY DOUBLE (DNA & CELL ORGANELLE SYNTHESIS)
★ NON-DIVIDING PHASE
★ RESTING PHASE (CELL IS NOT DIVIDING)
① INTERPHASE
a) G1 / GAP-1 phase
b) Synthesis phase
c) G2 / Gap-2 phase
2 DNA
20 ORGANELLE
duration vary from cell to cell / organism to organism
HUMAN: 24 HOURS
YEAST: 90 minutes
PROPERTY DIVISION
② MPHASE/MITOSIS
★ DIVIDING PHASE
a) KARYOKINESIS
b) CYTOKINESIS
1 DNA
10
daughter cell
1 DNA
10
INTERPHASE + MPHASE = CELL CYCLE
★ 23 hour
1 HOUR
★ >95
<5%
★ LONG
SHORT
★ NON DIVIDING
DIVIDING PHASE
NOTE: MITOSIS/EQUATIONAL DIVISION:
PARENT & DAUGHTER CELL
CHROMOSOME NUMBER: SAME.

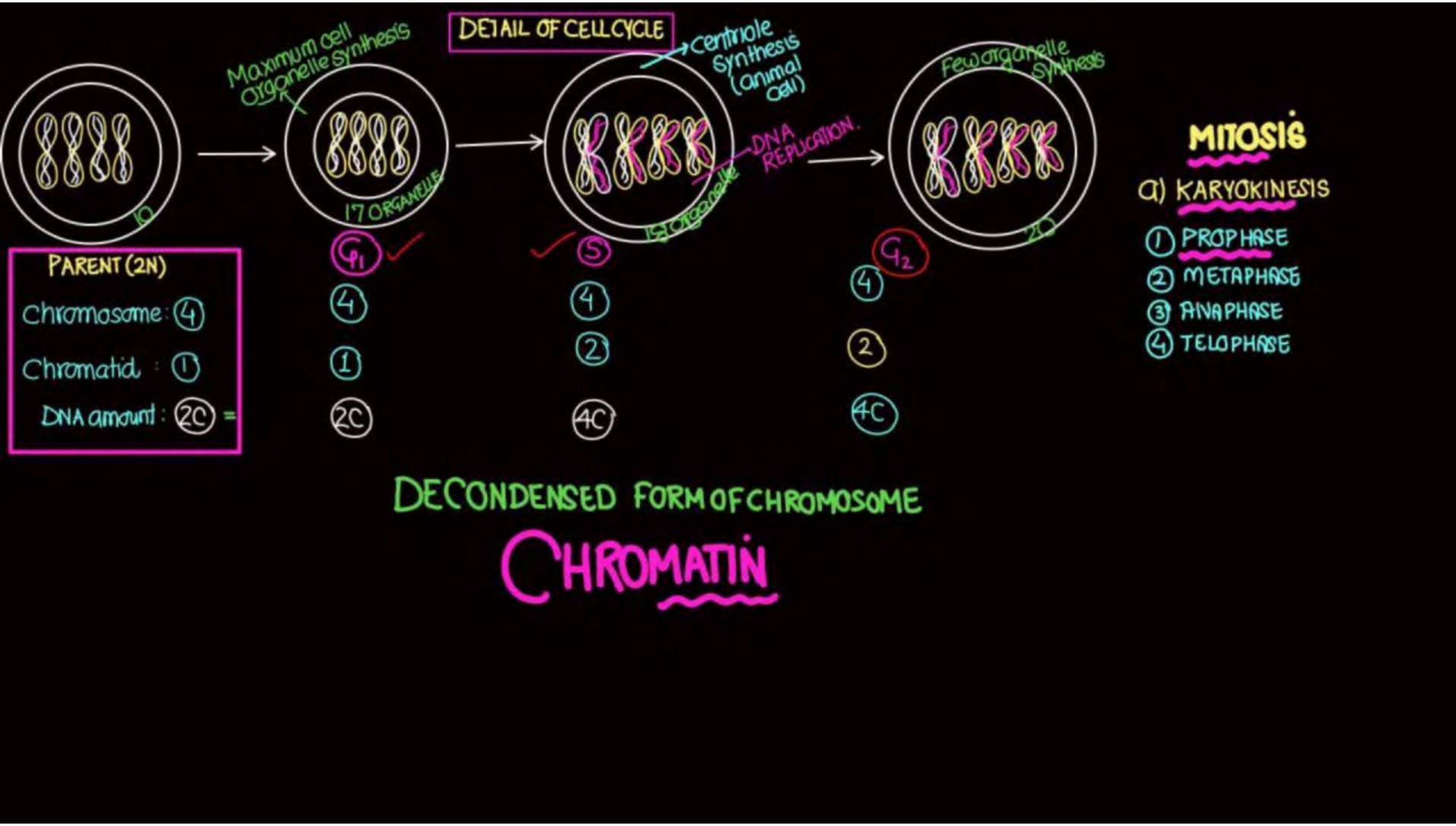
Definition of cell cycle

The sequence of events by which cell duplicates its genome / DNA (NUCLEUS) → DNA
and
Other constituent of cell. (cytoplasm) → CELL ORGANELLE

[INTERPHASE]

Equal distribution in TWO DAUGHTER CELL → M PHASE / MITOSIS

All events: ORDER / SEQUENCE
UNDER CONTROL OF GENE (PART OF DNA).

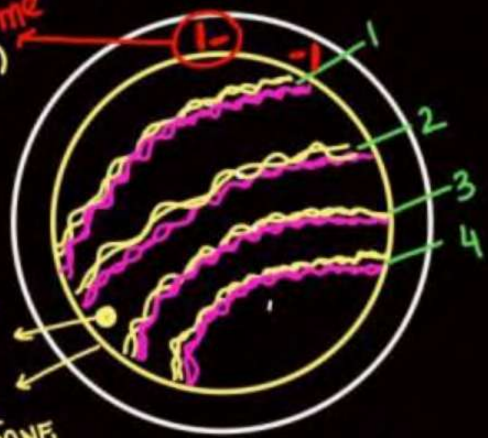


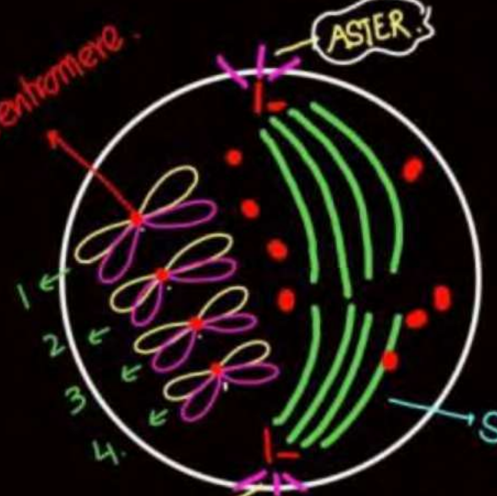
DETAIL OF CELLCYCLE
Maximum cell organelle synthesis
Centriole synthesis (animal cell)
Few organelle synthesis
DNA REPLICATION.
1O
17 ORGANELLE
1S organelle
2O
G1
S
G2
PARENT (2N)
Chromosome: 4
Chromatid: 1
DNA amount: 2C =
4
1
2C
4
2
4C
4
2
4C
MITOSIS
a) KARYOKINESIS
1 PROPHASE
2 METAPHASE
3 ANAPHASE
4 TELOPHASE
DECONDENSED FORM OF CHROMOSOME
CHROMATIN

	Chromosome	DNA amount
Parent cell	4	2C
G_1	4	2C
S	4	4C
G_2	4	4C
PROPHASE	4	4C
METAPHASE	4	4C
ANAPHASE	8	4C
TELOPHASE	4	2C

Equational DIVISION

PROPHASE



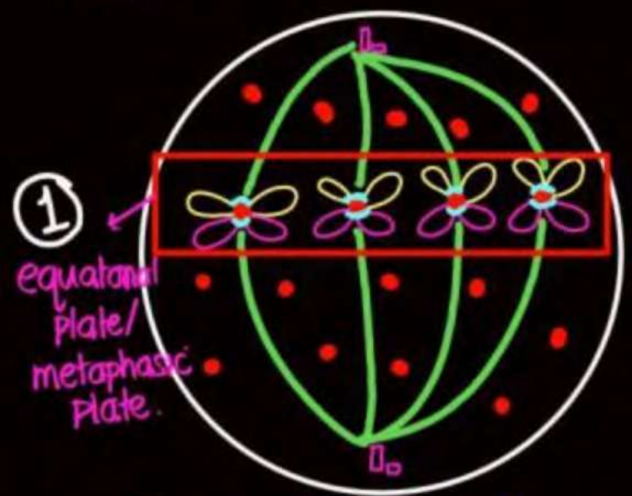


	EARLY PROPHASE	LATE PROPHASE
NUCLEOLUS, NM.	Starts disappearing	DISAPPEARED
Chromosome	decondensed form (Chromatin)	Condensed
Centriole	Starts moving Towards opposite pole	Reached at opposite pole.
DNA	TANGLED (VISIBILITY LOW)	UNTANGLED (VISIBILITY HIGH)

2 ASTER + SPINDLE FIBRE ⤳ MITOTIC APPARATUS.

- ⇒ Chromosomal material (DNA) OR CHROMATION → CONDENSATION.
- ⇒ CHROMATIN CONDENSED TO FORM CHROMOSOME.
- ⇒ BY END OF PROPHASE, NUCLEOLUS, NUCLEAR MEMBRANE, golgi BODY, ER: DISAPPEARED.
- ⇒ BOTH CHROMATID OF CHROMOSOME ATTACH AT CENTROMERE
- ⇒ CHROMOSOMAL MATERIAL (DNA) BECOME UNTANGLED.
- ⇒ CHROMOSOME NOT PRESENT ON SPINDLE FIBRE

METAPHASE

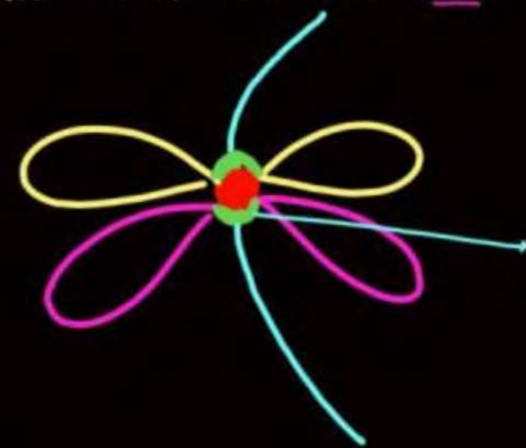


⇛ DISINTEGRATION OF 'N' & 'NM' IS BEGINING OF METAPHASE

⇛ All chromosome arrange on centre/ equator

⇛ Condensation of chromosome Completed (Maximum)
Visibility : Very HIGH.

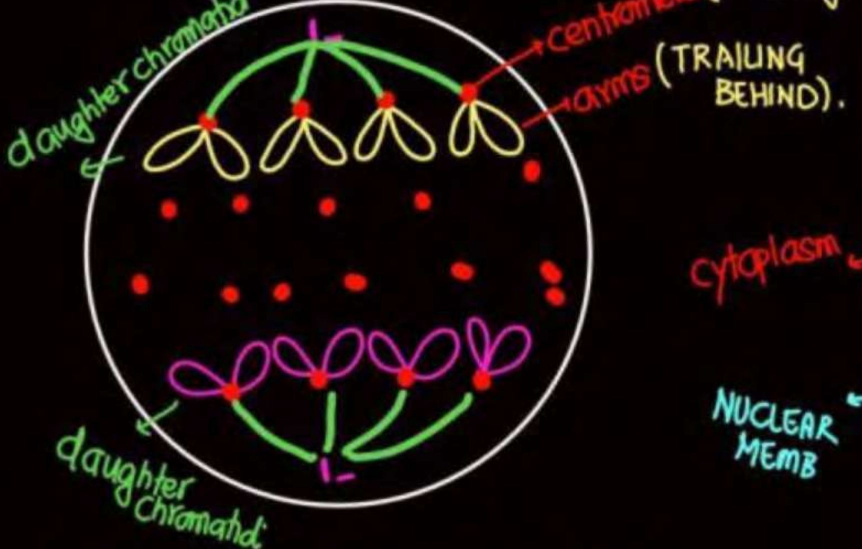
⇛ MORPHOLOGY (SIZE, NUMBER) : STUDY



Small protein disc (kinetochore) → provide attachment site to SPINDLE FIBRE / MICROTUBULE.
↓
PRESENT ON CENTROMERE

★ Plane of alignment of Chromosome : METAPHASIC PLATE.
↓
PRESENT IN CYTOPLASM.

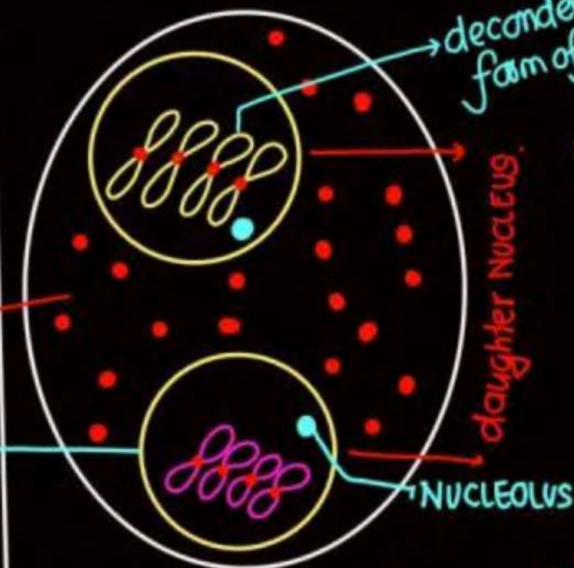
ANAPHASE



- Chromosome/centromere: splitting
- daughter chromatid of each Chromosome moves towards opposite pole

⇒ NOW EACH DAUGHTER CHROMATID CALLED DAUGHTER CHROMOSOME.

TELOPHASE



spindle fibre disappear

Visibility of chromosome: गायब

⇒ Karyokinesis completed.

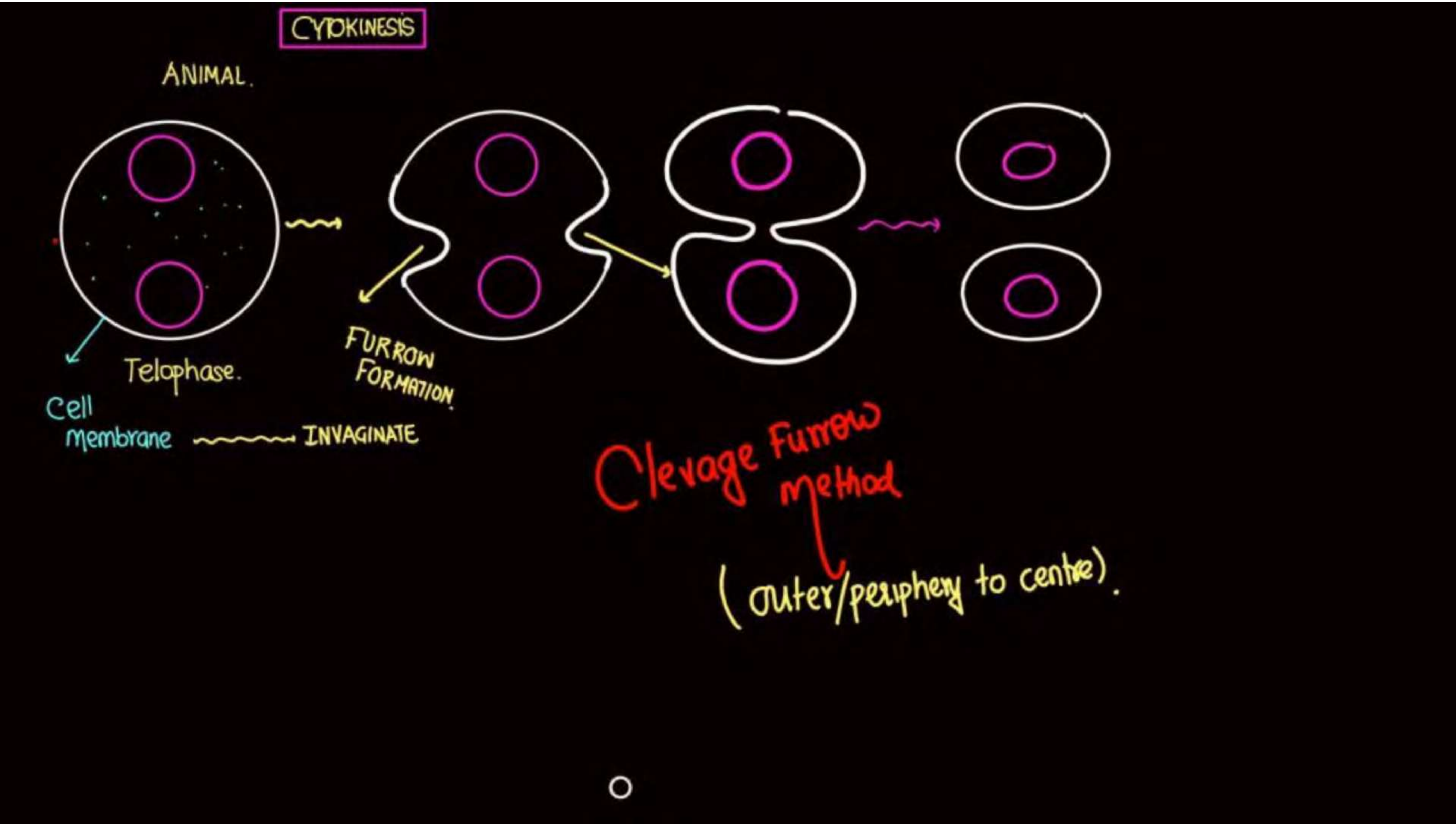
⇒ NM, NUCLEOLUS REAPPEAR.

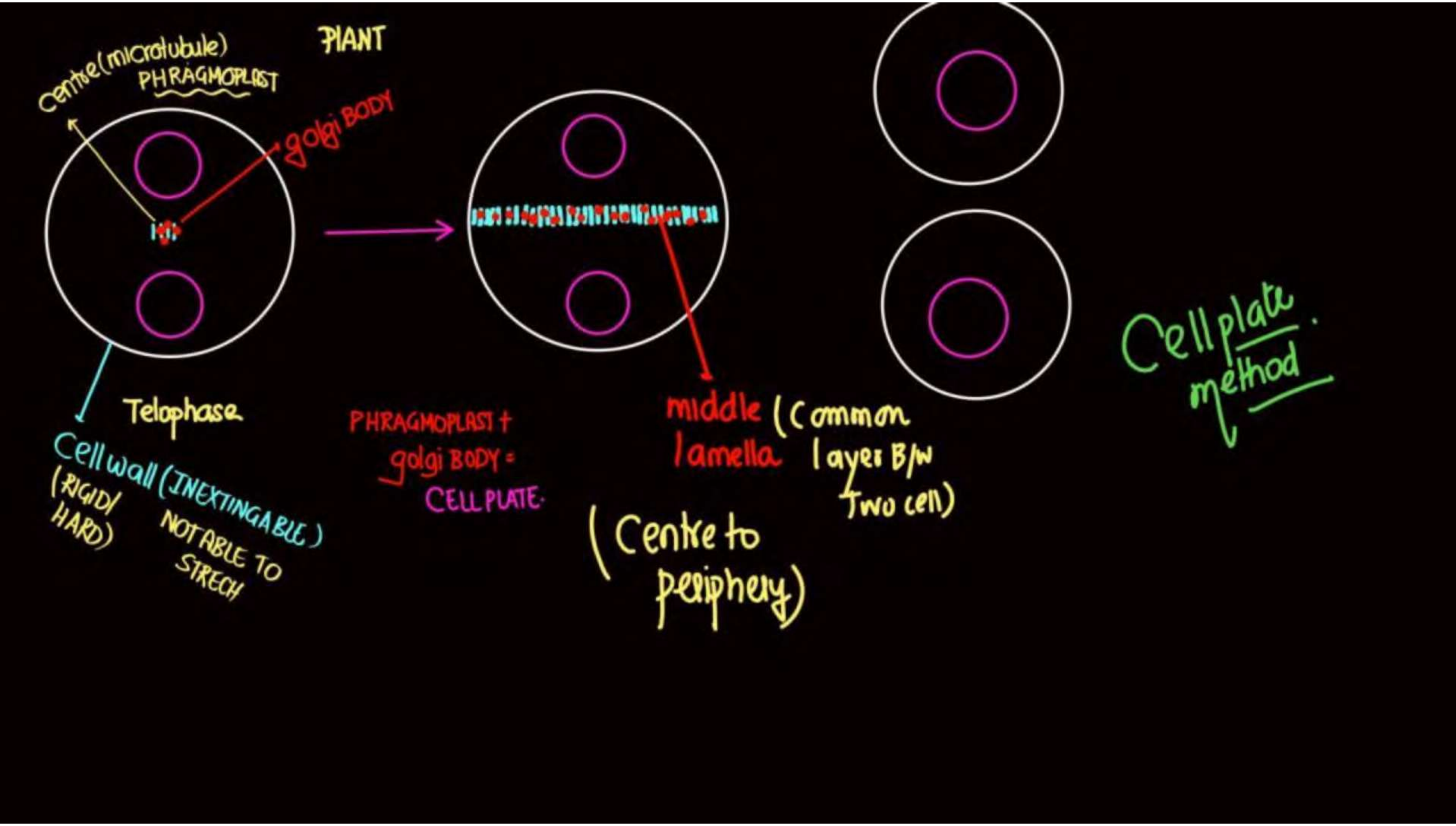
⇒ Chromosome $\xrightarrow[\text{decondensation}]{}$ chromatin

after karyokinesis cytokinesis

CHROMOSOME: IDENTITY LOST.

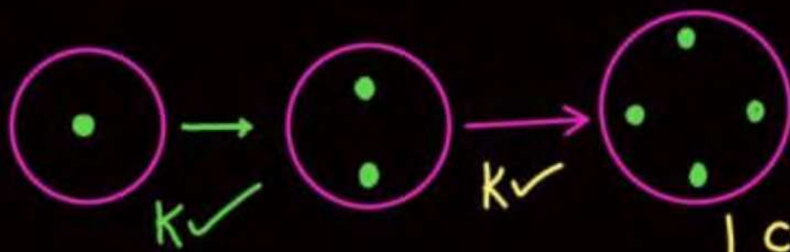
Two cells are formed


CYTOKINESIS
ANIMAL.
Telophase.
Cell membrane
INVAGINATE
FURROW FORMATION.
Clevage Furrow method
(outer/periphery to centre).



PLANT
Centre (microtubule)
PHRAGMOPLAST
golgi BODY
Telophase
Cell wall (INEXTINGABLE)
(RIGID/ HARD)
NOT ABLE TO STRECH
PHRAGMOPLAST + golgi BODY = CELL PLATE.
middle lamella (common layer B/W two cell)
(Centre to periphery)
Cell plate method.

NOTE :



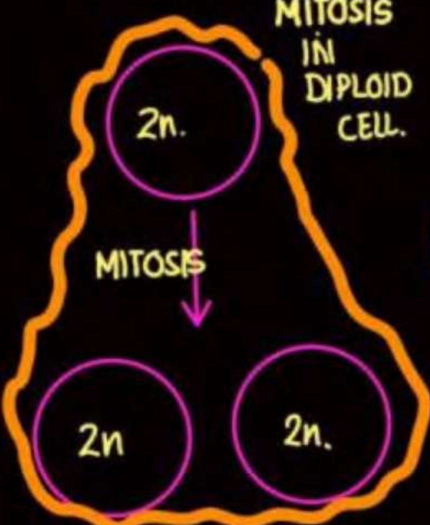
1 cell
NUCLEUS INCREASE
(MULTINUCLEATED)
CONDITION

K: Karyokinesis
C: cytokinesis

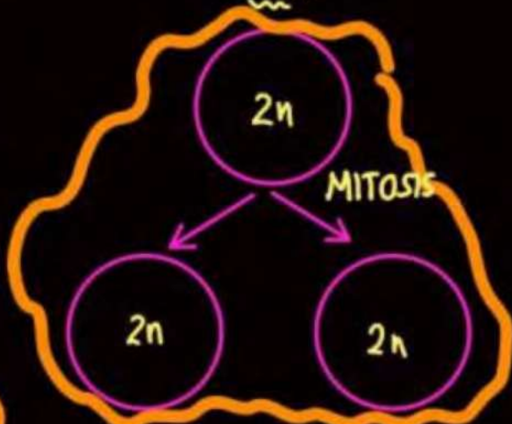
Karyokinesis not Followed By cytokinesis

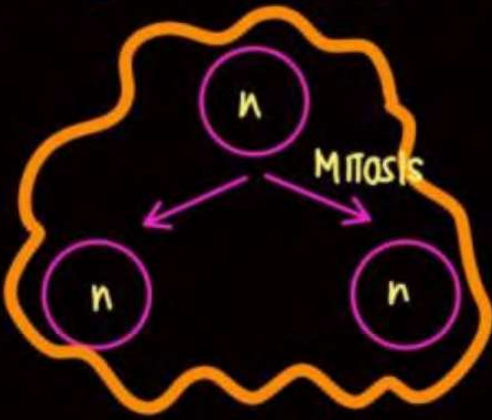
Syncytium → COCONUT: Liquid (Endosperm).
1000 nucleus.

ANIMAL (USUALLY)



Plant





exception

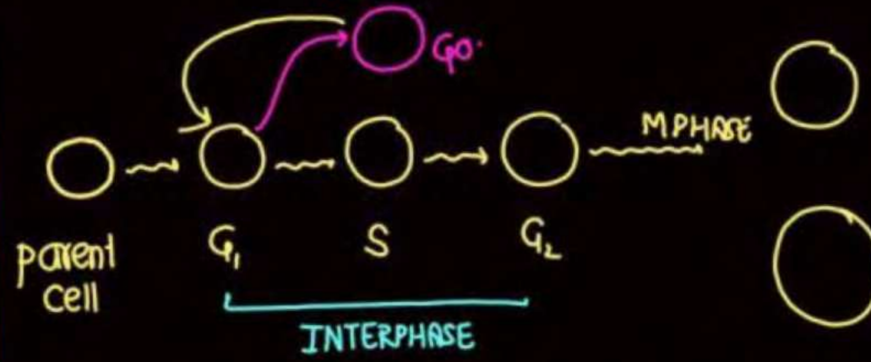
Honey Bee → Female

Queen (2n)

Male/DRONE (n) → mitosis

SOCIAL INSECT

Go phase



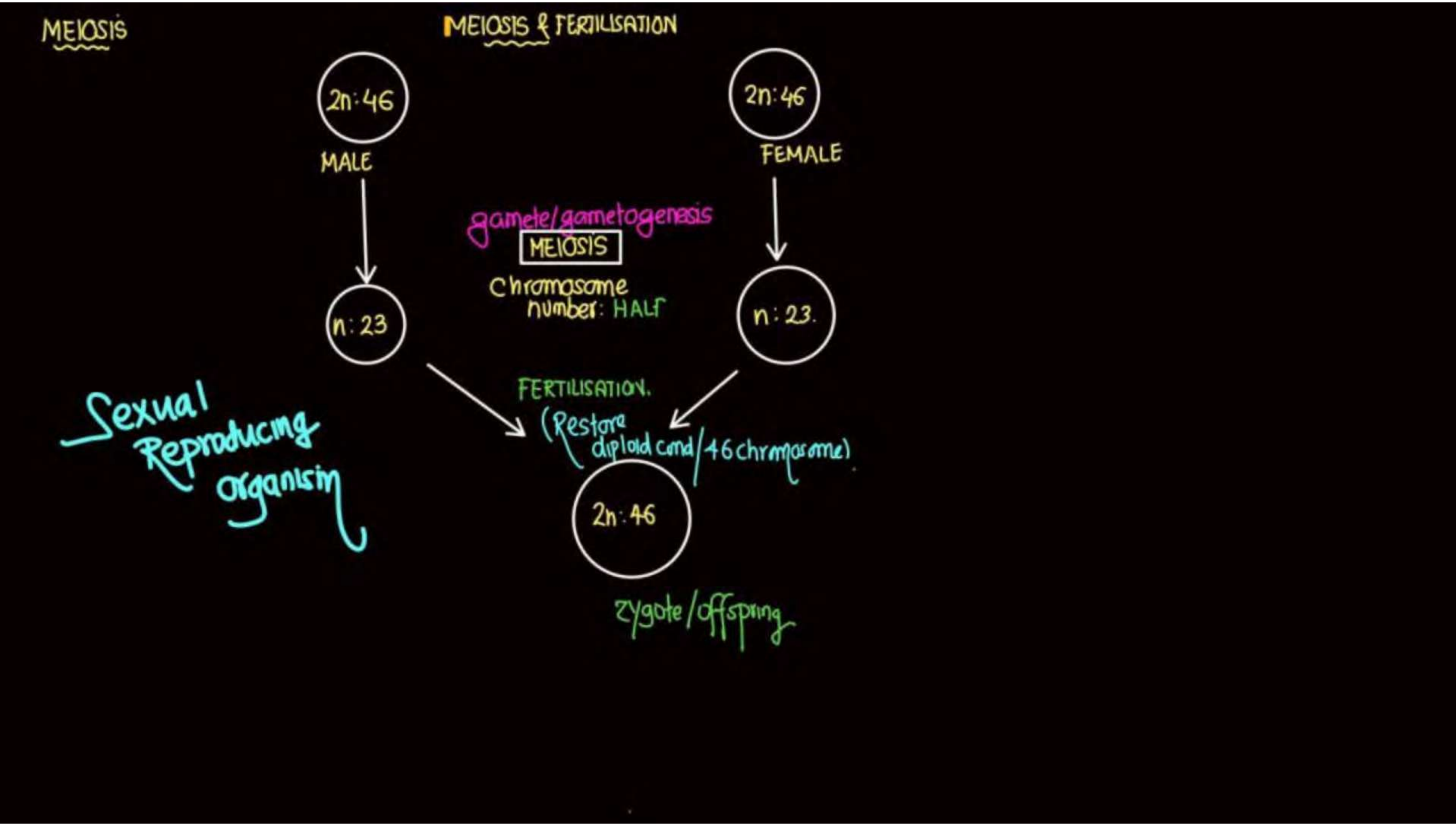
⇒ G_0: NOT A PART OF INTERPHASE / CELL CYCLE.

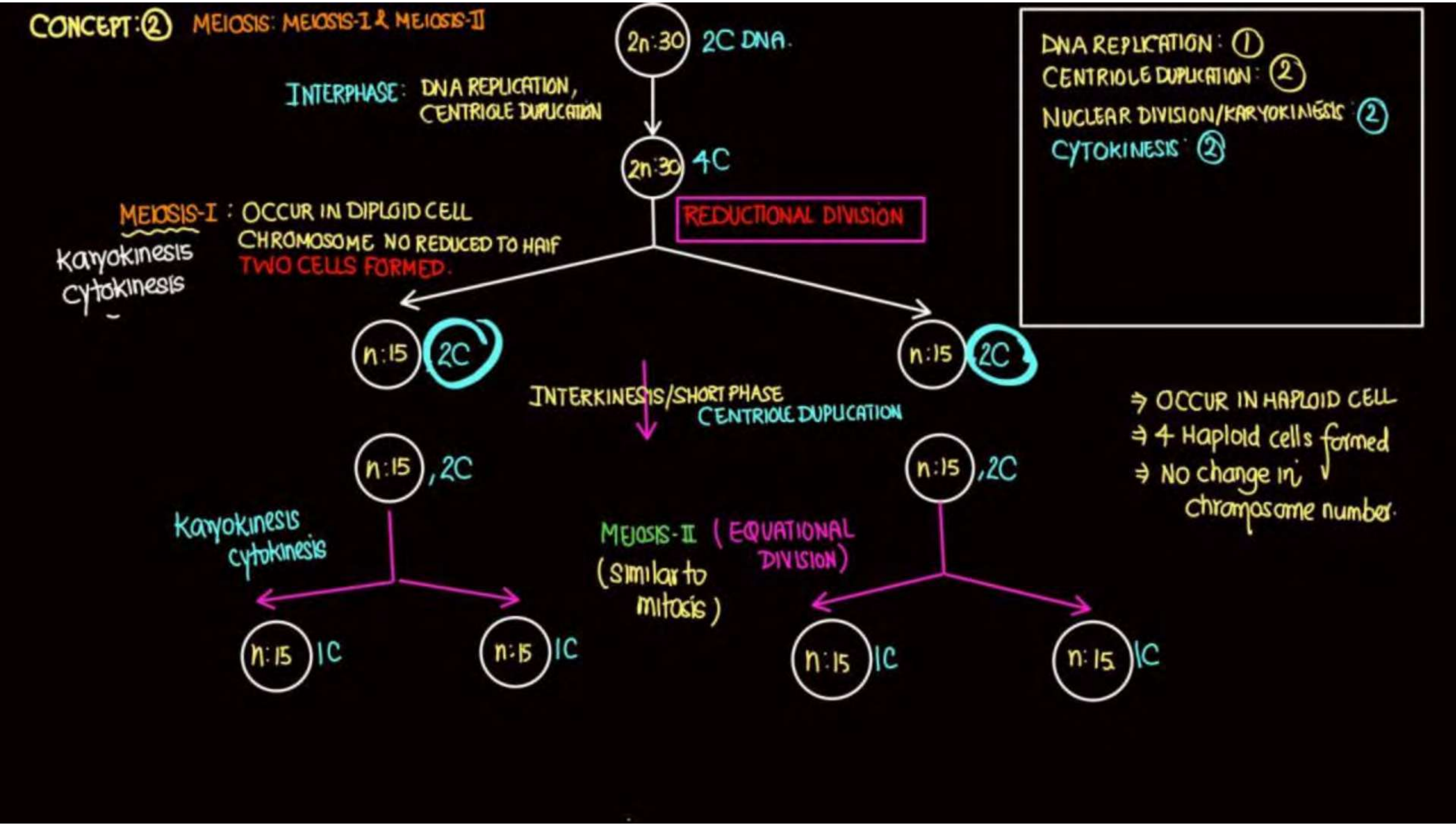
⇒ G_0: EXIT THE CELL CYCLE.
: NOT DIVIDE / INACTIVE STAGE / QUIESCENT STAGE

⇒ G_0: cell: metabolically active

- Permanent: cell never ever Back to G_1
  NEVER DIVIDE (HEART CELL / NERVE CELL)
- Temporary: Can back to G_1
  & then follow normal path.

(depend upon Requirement)


MEIOSIS
MEIOSIS & FERTILISATION
2n: 46
MALE
2n: 46
FEMALE
gamete/gametogenesis
MEIOSIS
Chromosome number: HALF
n: 23
n: 23.
Sexual Reproducing organism
FERTILISATION.
(Restore diploid cond/46 chromosome)
2n: 46
zygote/offspring


CONCEPT: 2 MEIOSIS: MEIOSIS-I & MEIOSIS-II
2n:30 2C DNA.
INTERPHASE: DNA REPLICATION, CENTRIOLE DUPLICATION
2n:30 4C
MEIOSIS-I : OCCUR IN DIPLOID CELL
CHROMOSOME NO REDUCED TO HALF
TWO CELLS FORMED.
Karyokinesis
cytokinesis
REDUCTIONAL DIVISION
DNA REPLICATION: 1
CENTRIOLE DUPLICATION: 2
NUCLEAR DIVISION/KARYOKINESIS: 2
CYTOKINESIS: 2
n:15 2C
n:15 2C
INTERKINESIS/SHORT PHASE
CENTRIOLE DUPLICATION
⇒ OCCUR IN HAPLOID CELL
⇒ 4 Haploid cells formed
⇒ No change in chromosome number.
n:15 ,2C
n:15 ,2C
Karyokinesis
cytokinesis
MEIOSIS-II (EQUATIONAL DIVISION)
(similar to mitosis)
n:15 1C
n:15 1C
n:15 1C
n:15 1C

INTERPHASE
MEIOSIS-I → PROPHASE-I
INTERKINESIS
MEIOSIS-II

INTERPHASE

$\left.\begin{array}{l}\text{PROPHASE-I}\\ \text{METAPHASE-I}\\ \text{ANAPHASE-I}\\ \text{TELOPHASE-I}\end{array}\right\} \rightarrow$ MEIOSIS-I

INTERKINESIS

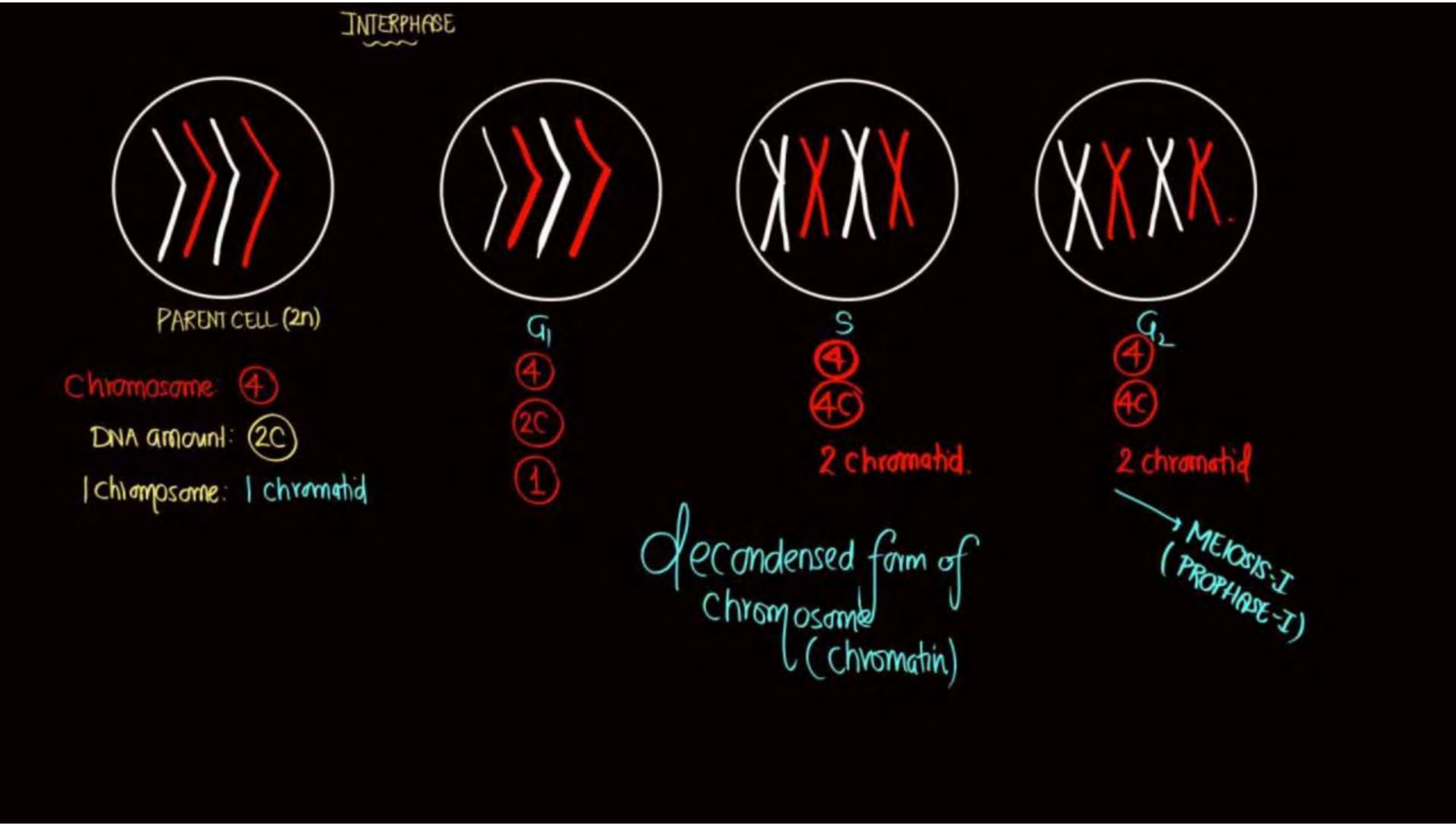
$\left.\begin{array}{l}\text{PROPHASE-II}\\ \text{METAPHASE-II}\\ \text{ANAPHASE-II}\\ \text{TELOPHASE-II}\end{array}\right\} -$ MEIOSIS-II

MEIOSIS-I

PROPHASE-I
↓
DIVIDED INTO 5 STAGES.

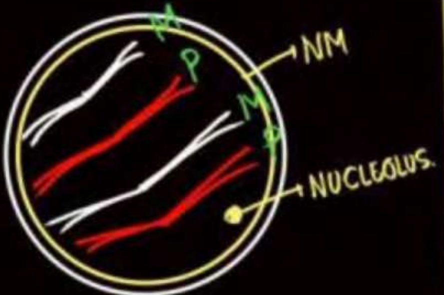
1. Leptotene
2. Zygotene
3. pachytene
4. diplotene
5. Diakinesis

MITOSIS < $\boxed{\text{MEIOSIS-I}}$
↓
PROPHASE-I
LONG, COMPLEX.



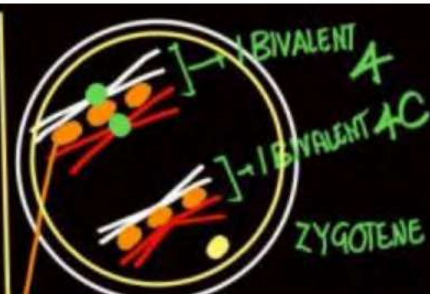
INTERPHASE
PARENT CELL (2n)
Chromosome: 4
DNA amount: 2C
1 Chromosome: 1 chromatid
G_1
4
2C
1
S
4
4C
2 chromatid.
G_2
4
4C
2 chromatid
MEIOSIS-I
(PROPHASE-I)
decondensed form of chromosome
(chromatin)

4
4C



LEPTOTENE

* COMPACTION/CONDENSATION OF CHROMOSOME
* CHROMOSOME VISIBLE IN LIGHT MICROSCOPE
* M: Maternal
* P: Paternal.



ZYGOTENE

* SYNAPTONEMAL COMPLEX (PROTEIN) HOLD 'M' & 'P' CHROMOSOME
* PAIRING OF HOMOLOGOUS CHROMOSOME : SYNAPSIS
* BIVALENT FORMED / TETRAD.
* 1 BIVALENT · 2 CHROMOSOME · $\boxed{\text{4 CHROMATID}}$
* ALL 4 CHROMATID OF ONE BIVALENT CLEARLY VISIBLE AT PACHYTENE STAGE
* SO TETRAD BETTER TO USE IN PACHYTENE.

Q Parent cell: 40 chromosome

Zygotene: BIVALENT : 20

CHROMATID: 40x2

⇒ 80.

4
4C

PACHYTENE

* EXCHANGE DNA OF NON-SISTER CHROMATID OF HOMOLOGOUS CHROMOSOME CROSSING OVER / RECOMBINATION.
* RECOMBINASE ENZYME.
* RECOMBINATION (RN) NODULE : SITE WHERE CROSSING OVER.

DIPLOTENE
(LONGEST)

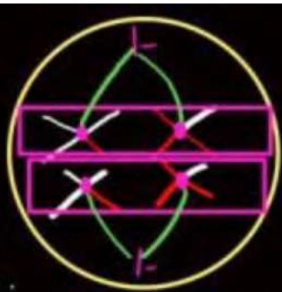
* Synaptonemal complex Begins to dissappear.
* Homologous Chromosome Begins to seperate except at the Region where CROSSING OVE OCCUR CALLED CHIASMATA. CROSS LIKE STRUCTURE
* This stage SUSPEND FOR MONTH/YEAR IN OOCYTE OF VERTEBRAE.

DIAKINESIS

* NUCLEOLUS, NM DISAPPEAR.
* TRANSITION TO METAPHASE
* TERMINALISATION OF CHIASMATA.
* SPINDLE FORMATION
* CHROMOSOME CONDENSED

4

4C.



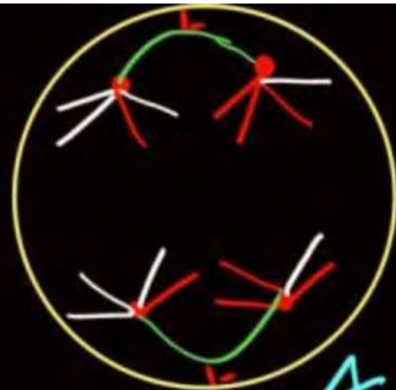
2 equ. plate.

METAPHASE-I

⇛ BIVALENT ON EQUATORIAL PLATE.

4

4C



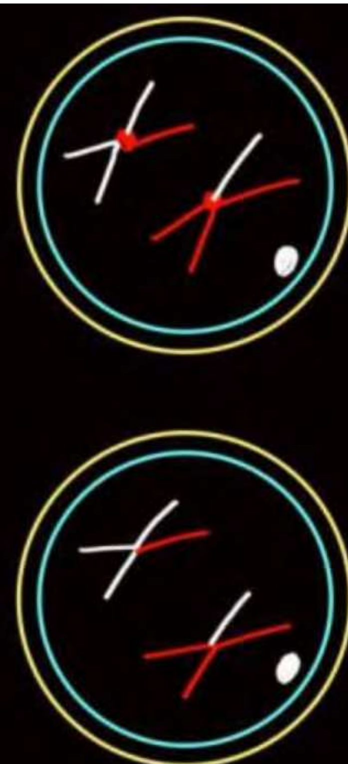
ANAP-I

4

4C

⇛ SEPERATION/ SEGREGATION OF HOMOLOGOUS CHROMOSOME

⇛ HOMOLOGOUS CHROMOSOME MOVE OPPOSITE POLE



Telop-I

2 chromosome

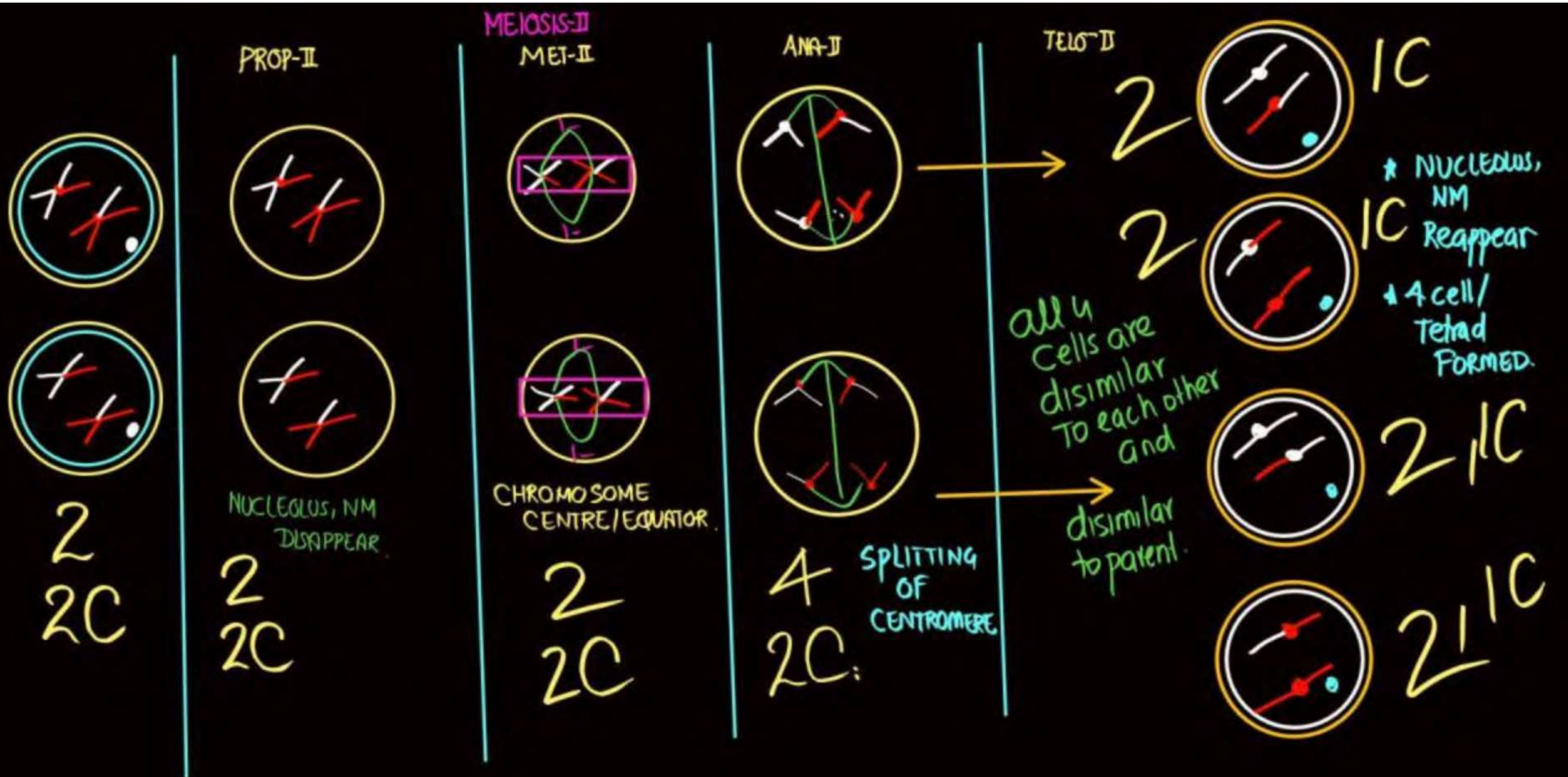
2C DNA.

⇛ dyad of cells formed

⇛ NUCLEOLUS, NM REAPPEAR.

2 chromo

2C DNA



MEIOSIS-II
PROP-II
MET-II
ANA-II
TELO-II
2
2C
NUCLEOLUS, NM DISAPPEAR
2
2C
CHROMOSOME CENTRE/EQUATOR.
2
2C
4
2C
SPLITTING OF CENTROMERE
2
1C
2
1C
2
1C
2
1C
all 4 cells are disimilar To each other and disimilar to parent.
* NUCLEOLUS, NM Reappear
* 4 cell/ Tetrad FORMED.

	Chromosome	DNA amount
Parent cell	4	2C/60
G_1	4	2C/60
S	4	4C/120
G_2	4	4C/120
LEPTOTENE (PROPHASE-I)	4	4C/120
ZYGOTENE (PROPHASE-I)	4	4C/120
PACHYTENE (PROPHASE-I)	4	4C/120
DIPLOTENE (PROPHASE-I)	4	4C/120
DIAKINESIS (PROPHASE-I)	4	4C/120
METAPHASE-I	4	4C/120
ANAPHASE-I	4	4C/120
TELOPHASE-I/MEIOSIS-I	2 ⇒ 2 chromatid	2C/60
PROPHASE-II	2	2C
METAPHASE-II	2	2C
ANAPHASE-II	4	2C
TELOPHASE-II/MEIOSIS-II	2 ⇒ 1 chromatid	1C

Chromosome DOUBLE नहीं होता

Half

Half

Half

Q: Parent cell: 60 Pg DNA

Meios-I ⇒ 60

Meios-II ⇒ 30

DOUBLE करके दो बार Half करता है

G_1 : 80
S : 160
G_2 : 160
M-I : 80
M-II : 40

Q Parent : 100 chromosome

M-I : 50

M-II : 50

Double नहीं करता

BUS EK बार Half करता

Q Meiosis-II :
In each cell : 60 chromosome.

Parent cell : G_1 = ? 120

Q Meiosis-II
DNA : 40 Pg
G_1 =

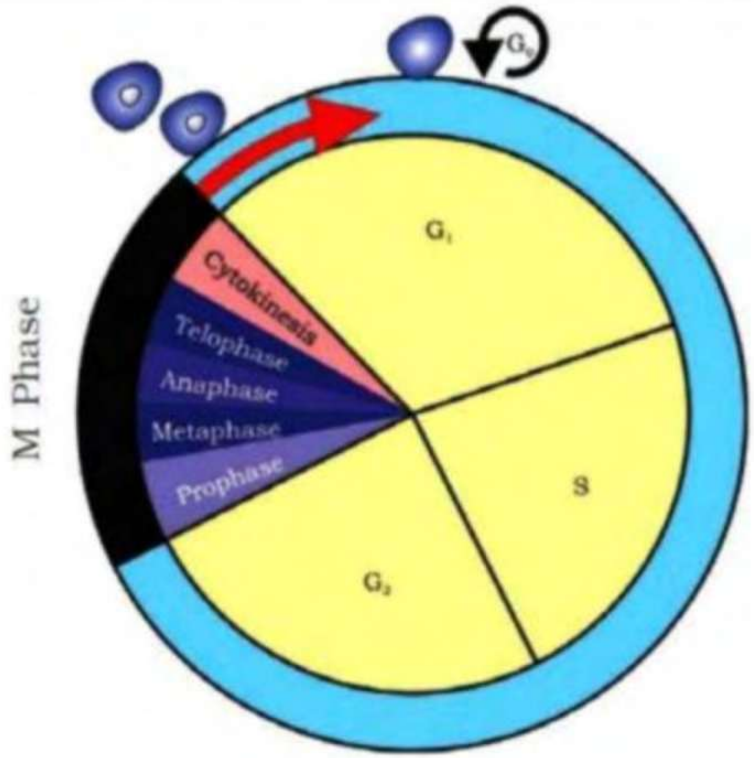


Figure 10.1 A diagrammatic view of cell cycle indicating formation of two cells from one cell

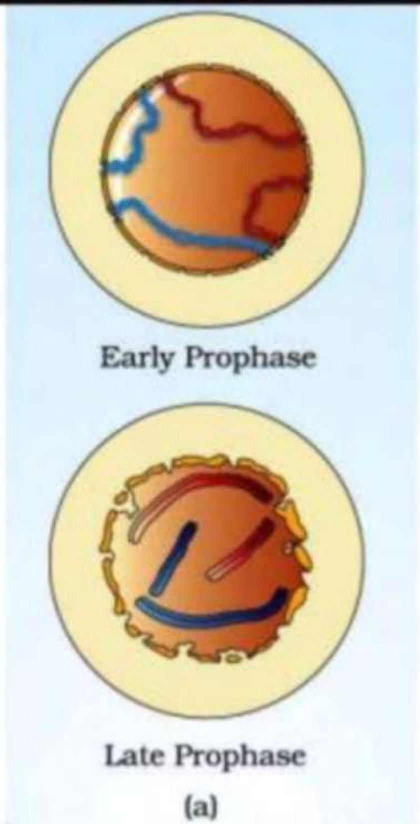


Figure 10.2 a and b : A diagrammatic view of stages in mitosis

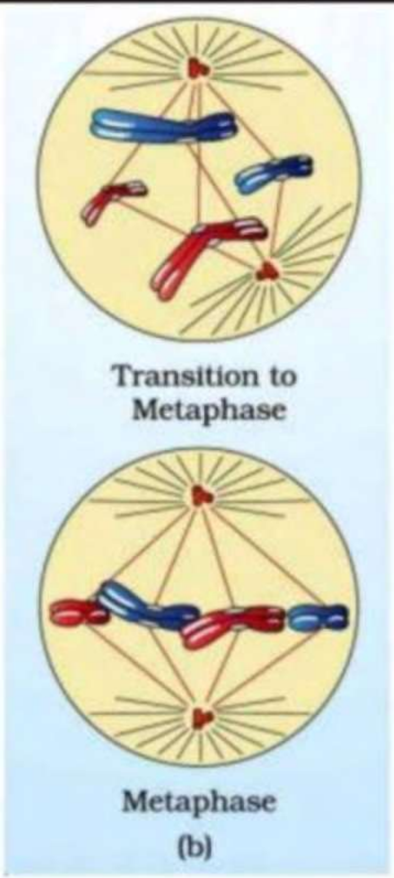
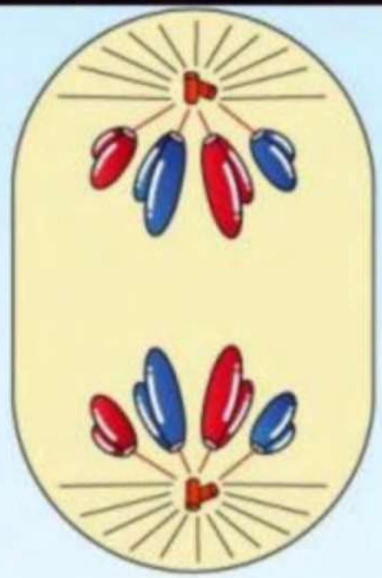


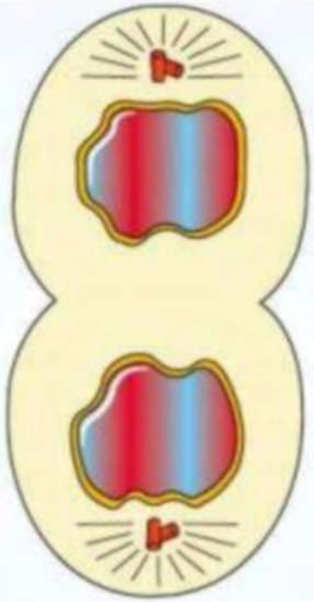
Figure 10.2 a and b : A diagrammatic view of stages in mitosis



Anaphase

(c)

Figure 10.2 c to e : A diagrammatic view of stages in Mitosis



Telophase

(d)

Figure 10.2 c to e : A diagrammatic view of stages in Mitosis

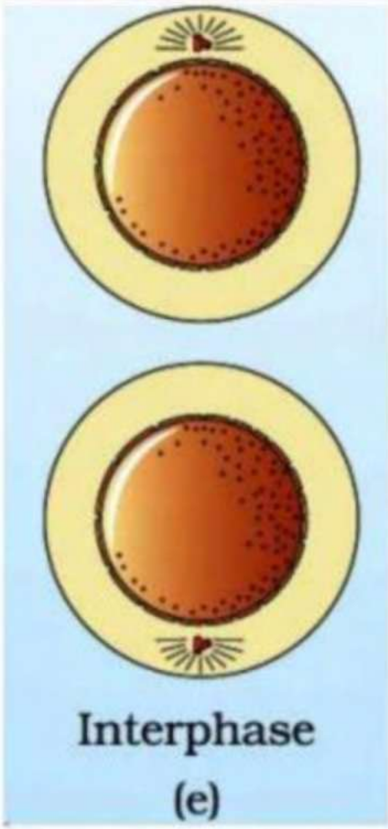


Figure 10.2 c to e : A diagrammatic view of stages in Mitosis

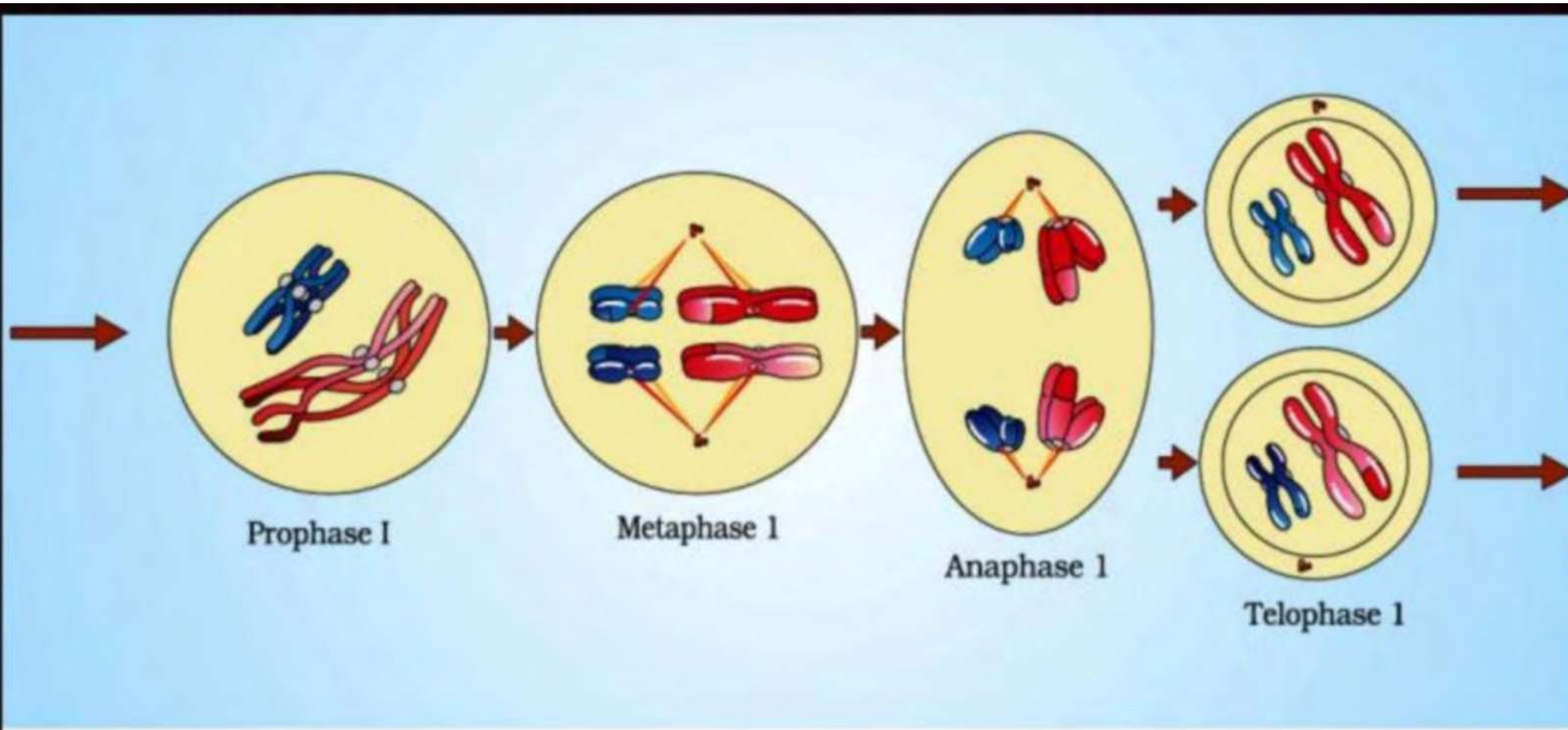


Figure 10.3 Stages of Meiosis I

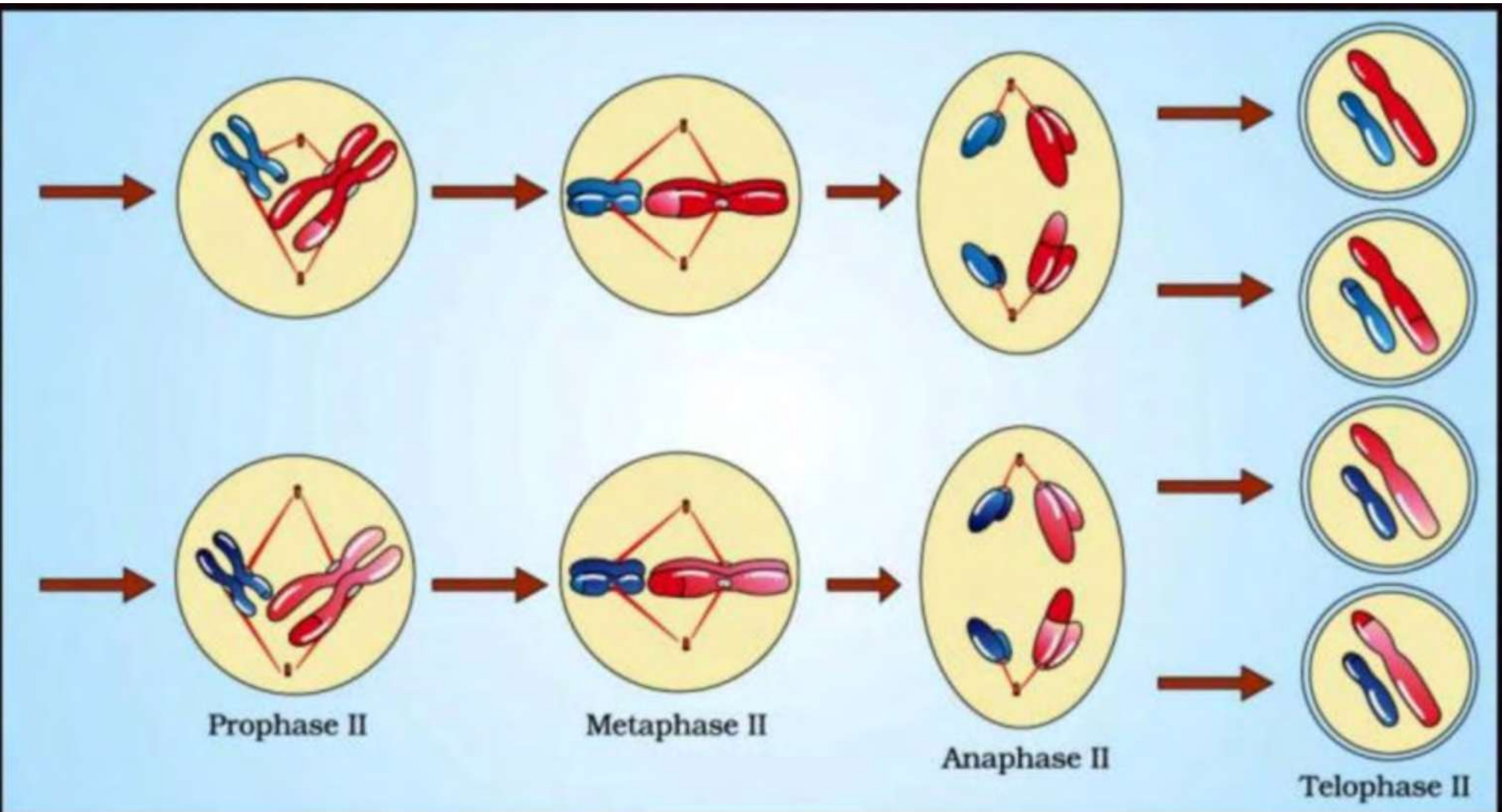


Figure 10.4 Stages of Meiosis II

TISSUE

★ GROUP OF CELL: COMMON ORIGIN, & FUNCTION.

TYPES

① MERISTEMATIC TISSUE

★ Cells: actively dividing

★ Cell wall: PRIMARY WALL

★ Immature cell

② PERMANENT TISSUE

★ Cells usually do not Divide

★ mature cell

NOTE: TERMINOLOGY

meristematic cell / TISSUE (DIVIDING) — UNDIFFERENTIATION.

↓ Cells stop Division — (DIFFERENTIATION)

PERMANENT TISSUE

↓ Cells Regain Capacity of Division — DEDIFFERENTIATION

NEET 2024

MERISTEMATIC CELL/ TISSUE

↓ Cell stop division — REDIFFERENTIATION

PERMANENT TISSUE

PRIMARY MERISTEM

↓

PRIMARY PERM. TISSUE

↓

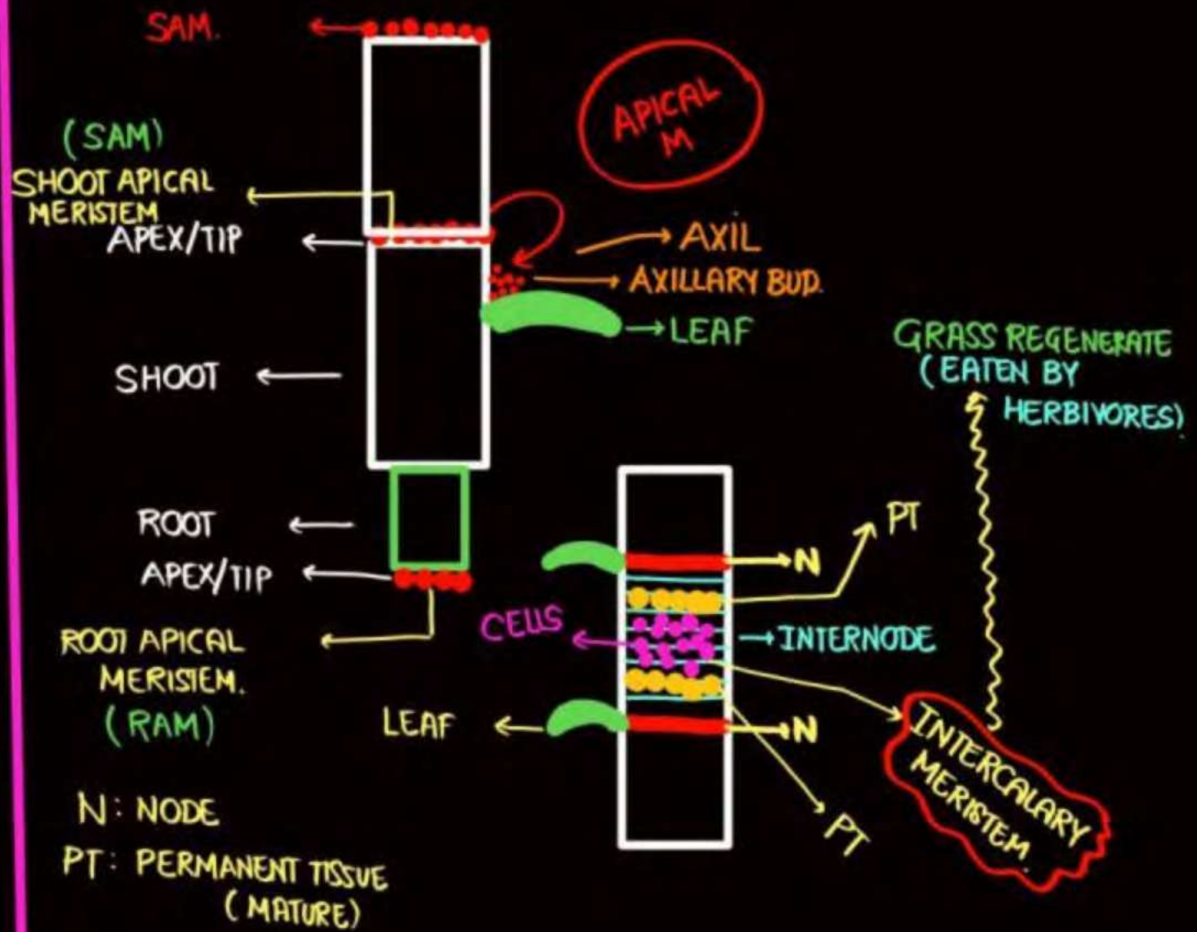
SECONDARY MERISTEM

↓

SECONDARY PERMAN. TISSUE

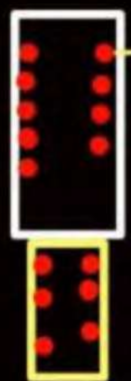
	PM	SM
FORMED:	EARLY	LATER.
FUNCTION:	LENGTH (ROOT, STEM) INCREASE	GIRTH/THICKNESS/ DIAMETER INCREASE
	PRIMARY GROWTH (EARLY)	SECONDARY GROWTH (LATER)
	PRIMARY XYLEM & PRIMARY PHLOEM FORMED (PRIMARY TISSUE)	SECONDARY XYLEM, SECONDARY PHLOEM (SECONDARY TISSUE)
eg:	APICAL M → SAM, RAM INTERCALARY M.	eg LATERAL MERISTEM

SOME CELLS SEPERATED FROM SAM AND COLLECTED IN AXIL REGION CALLED AXILLARY BUD → FORM → BRANCH, FLOWER.



STEM

ROOT



LATERAL SIDE
↓
MERIST. CELL
(LATERAL M.)
↓
SECONDARY GROWTH
(LATER)

eg ★ INTRAFASCICULAR CAMBIUM / FASCICULAR CAMBIUM → EARLY FORMED → $\boxed{\text{PRIMARY MERISTEM}}$ → GIRTH INCREASE → SECONDARY GROWTH

(ORIGIN) EXCEPTION FUNCTION (LATER)

★ INTERFASCICULAR CAMBIUM

★ CORK CAMBIUM

→ LATER FORMED → SEC. GROWTH

$\boxed{\text{SECONDARY MERISTEM}}$

★ All LATERAL M ARE SECONDARY M. (FALSE)

★ ALL SECON. MERISTEM ARE LATERAL MERISTEM. (TRUE)

PERMANENT TISSUE (P.T)

NEET 2024.

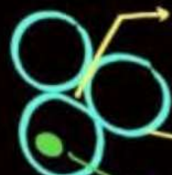
SIMPLE P.T

⇒ ONE TYPE OF CELL : PERFORM COMMON FUNCTION.

PARENCHYMA, COLLENCHYMA → CELLS DO NOT LOSE PROTOPLASM → LIVING

SCLERENCHYMA → CELLS LOSE PROTOPLASM → DEAD

PARENCHYMA



→ EITHER CLOSELY PACKED OR LITTLE INTERCELLULAR SPACE

→ CELL WALL : THIN, CELLULOSE

→ CHLOROPLAST
- → PHOTOSYNTHESIS
- → FOOD STORAGE
- → SECRETE OIL, RESIN, TANIN, MUCILAGE, LATEX.

* Cells isodiametric

COLLENCHYMA

INTERCELLULAR SPACE ABSENT.

→ CHLOROPLAST (PHOTOSYNTHESIS)

→ CELL WALL (CELLULOSE, HEMICELLULOSE, PECTIN)

↑ deposition more at CORNERS → THICK

⇒ YOUNG STEM, PETIOLE OF LEAF (MECHANICAL STRENGTH).

⇒ most of dicot stem. (BELOW EPIDERMIS)

→ epidermis

→ HYPODERMIS (COLLENCHYMA)

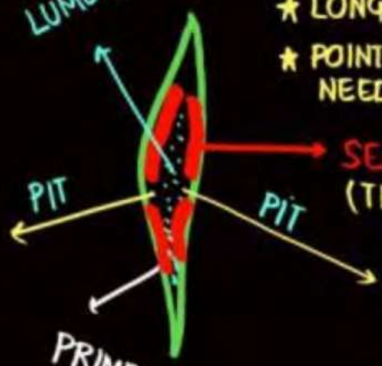
MONOCOT STEM : HYPODERMIS (SCLERENCHYMA).

ROOT : HYPODERMIS ABSENT.

SCLERENCHYMA

FIBRE (DEAD).

* LONG
* POINTED END/ NEEDLE LIKE



PW + SW → CELL WALL

USULALLY FOUND IN BUNDLES.

SCEREIDS (DEAD).

* SPHERICAL, OVAL, POLYGONAL.
* SINGLE/ GROUP.
* FRUIT WALL OF NUTS.
* SAPOTA. PEAR, GUAVA (PULP/SOFT PART)
* SEED COAT OF LEGUMES.
* LEAVES OF TEA.
* LIGNIFIED CELL WALL.
* NARROW LUMEN.

COMPLEX PER. TISSUE (NEET 2024)

★ MORE THAN ONE TYPE OF CELL.

① XYLEM :

★ water & minerals conduction.

★ PROVIDE MECHANICAL STRENGTH.

★ TRACHEID
★ VESSEL
★ XYLEM FIBRE
→ LOOSE PROTOPLASM (DEAD)

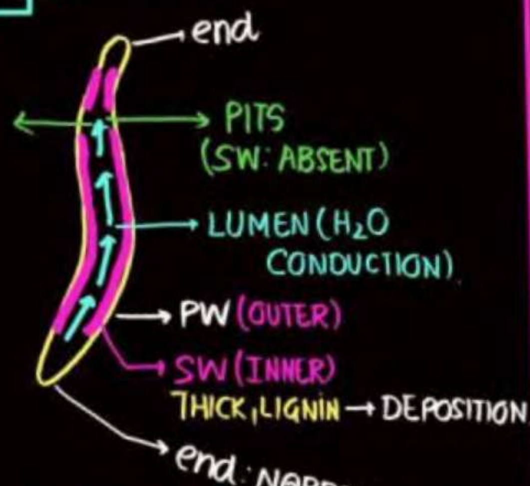
★ XYLEM PARENCHYMA → LIVING

TRACHEID → elongated, TUBE LIKE CELL.

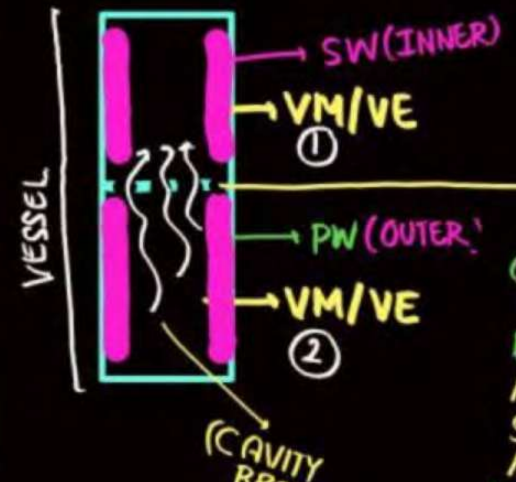
PTERIDO, GYMNO, ANGIOSPERM

VESSEL

ANGIOSPERM → FLOWERING PLANT.



TRACHEID



COMMON WALL/ END WALL B/W TWO VM ARE DISSOLVED SO PORES ARE FORMED (PERFORATION)

H_2O CONDUCTION.

★ LONG, CYLINDRICAL TUBE LIKE CELL

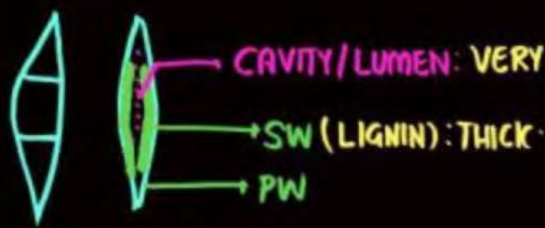
VESSELS

VM: VESSEL MEMBER

VE: VESSEL ELEMENT

★ VESSEL MADE UP OF MANY CELL & EACH CELL: VM/VE

XYLEM FIBRE



THICK, LIGNIFIED CELL WALL,
DEAD

XYLEM PARENCHYMA.

* LIVING, THIN WALL, CELLULOSE.
* FOOD: STORE: STARCH/FAT
* STORE: TANIN
* RADIAL COND^N OF H_2O: RAY PARENCHYMA.

WAIT ?

ENDARCH (STEM)

EXARCH. (ROOT)

TYPES OF XYLEM

PRIMARY X.
* EARLY FORMED DURING PRIMARY GROWTH

SEC. XYLEM.
* LATER
* DURING SEC. GROWTH.

PROTOXYLEM
⇒ FIRST FORMED
⇒ NARROW/SMALL VESSELS

METAXYLEM.
⇒ LATER.
⇒ BROAD/LARG VESSELS.

PHLOEM

★ FOOD CONDN.

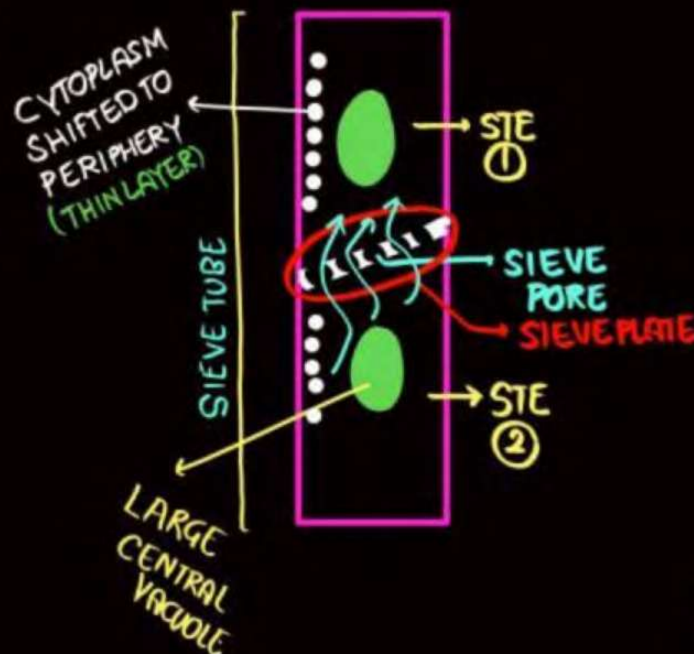
- SIEVE TUBE → ANGIOSPERM
- COMPANION CELL. → ANGIOSPERM
- PHLOEM PARENCHYMA.

SIEVE TUBE, COMPANION CELL, PHLOEM PARENCHYMA → LIVING

- PHLOEM FIBRE → DEAD.

- SIEVE CELL
- ALBUMINOUS CELL.

SIEVE CELL, ALBUMINOUS CELL → Gymnosperm.



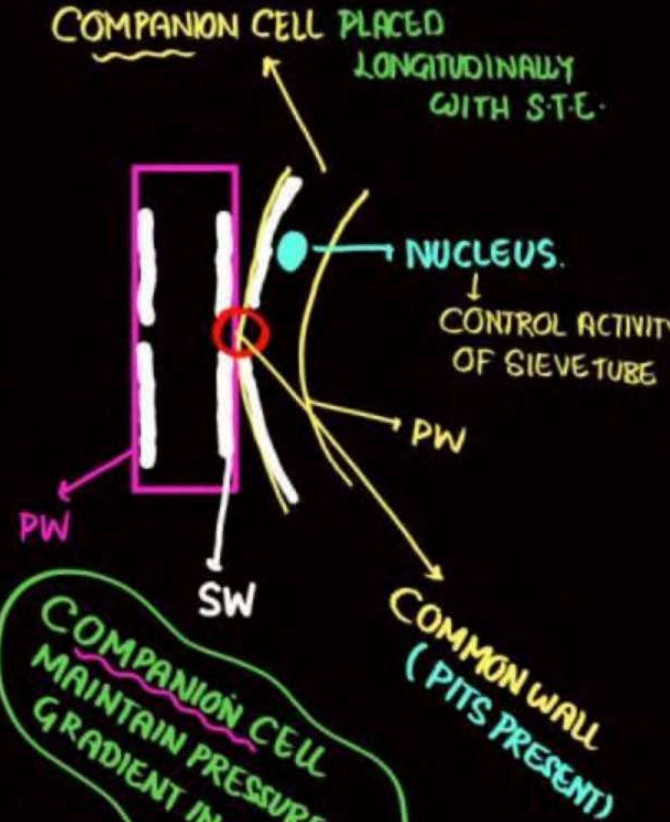
SIEVE TUBE

★ MADE UP OF STE (SIEVE TUBE ELEMENT)

★ CELL WALL : CELLULOSE

★ NUCLEUS ABSENT.

★ FOOD CONN FROM ONE STE TO ANOTHER THROUGH SIEVE PORE



COMPANION CELL MAINTAIN PRESSURE GRADIENT IN SIEVE TUBE

Phloem fibres (bast fibres) are made up of sclerenchymatous cells. These are generally absent in the primary phloem but are found in the secondary phloem. These are much elongated, unbranched and have pointed, needle like apices. The cell wall of phloem fibres is quite thick. At maturity, these fibres lose their protoplasm and become dead. Phloem fibres of jute, flax and hemp are used commercially. The first formed primary phloem consists of narrow sieve tubes and is referred to as **protophloem** and the later formed phloem has bigger sieve tubes and is referred to as **metaphloem**.

Explanation

EARLY (PRIMARY GROWTH)

LIGNIN (SEC. WALL).

PRIMARY PHLOEM
⇒ EARLY (PRIMARY GROWTH)

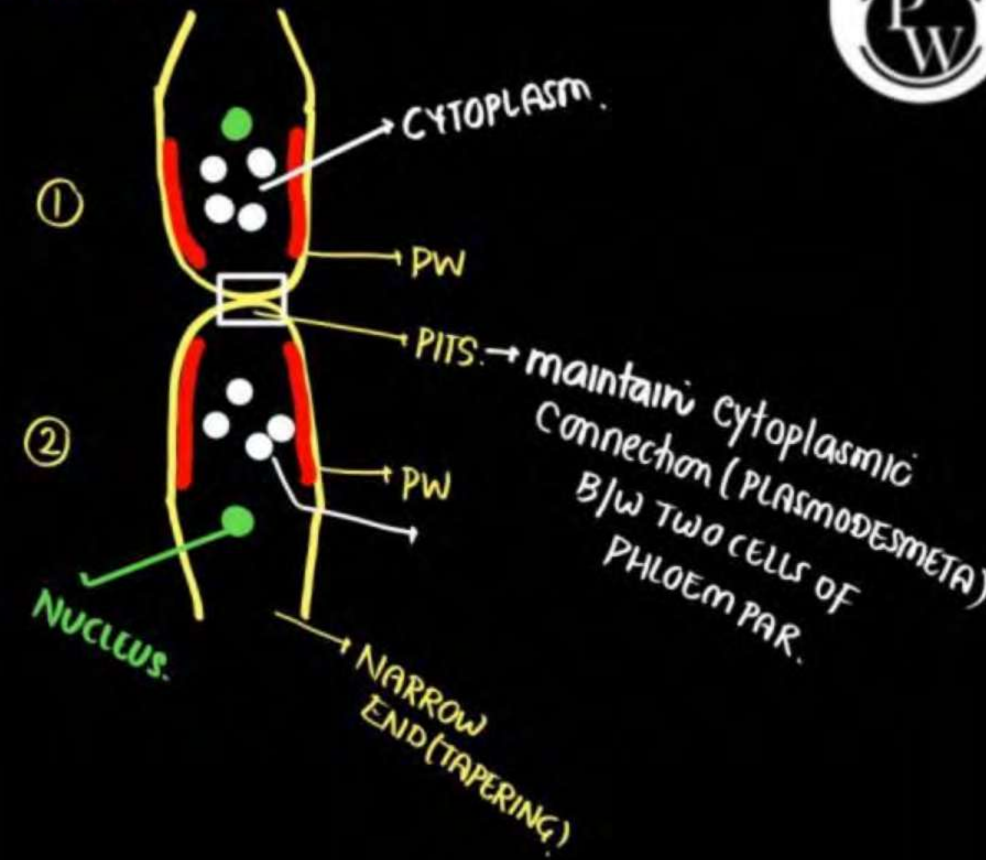
SEC. PHLOEM.
⇒ LATER.
⇒ SECONDARY GROWTH.

PROTOPHLOEM
FIRST FORMED
SMALL/NARROW SIEVE TUBE

METAPHLOEM.
LATER.
LARGE/BROAD SIEVETUBE.

Phloem parenchyma is made up of elongated, tapering cylindrical cells which have dense cytoplasm and nucleus. The cell wall is composed of cellulose and has pits through which plasmodesmatal connections exist between the cells. The phloem parenchyma stores food material and other substances like resins, latex and mucilage. Phloem parenchyma is absent in most of the monocotyledons. Stem.

Explanation



TISSUE SYSTEM.

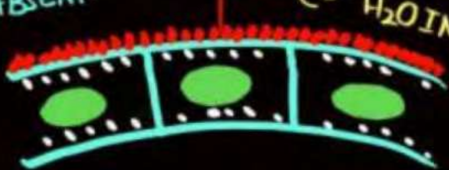
EPIDERMAL TISSUE SYSTEM.

→ EPIDERMIS ✓
→ STOMATA ✓
→ EPIDERMAL APPENDAGES.

a) EPIDERMIS

ROOT ABSENT. ← CUTICLE (CUTIN) → STEM, LEAF

H_2O IMPERMEABLE (minimise H_2O LOSS/ TRANSPIRATION)



⇒ CELLS : ELONGATED, COMPACTLY ARRANGE

⇒ GENERALLY SINGLE LAYER.

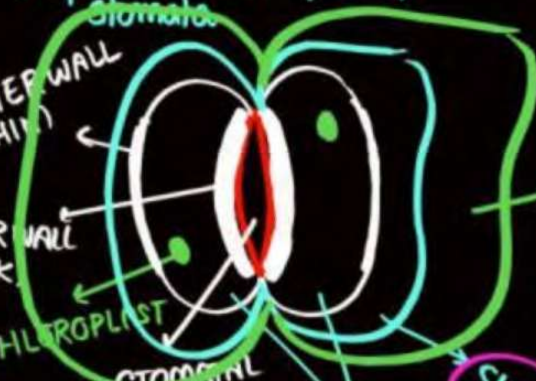
⇒ CONTINUOUS

⇒ CENTRE : LARGE VACUOLE.

⇒ cytoplasm : periphery : THIN LAYER.

b) STOMATA

⇒ epidermis interrupted By stomata

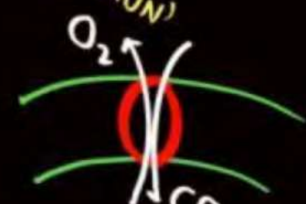


SUBSIDIARY CELL → some epid. cell change their shape covered guard cell.

(GUARD CELL) BEAN/KIDNEY SHAPE CELL COVERED STOMATAL PORE

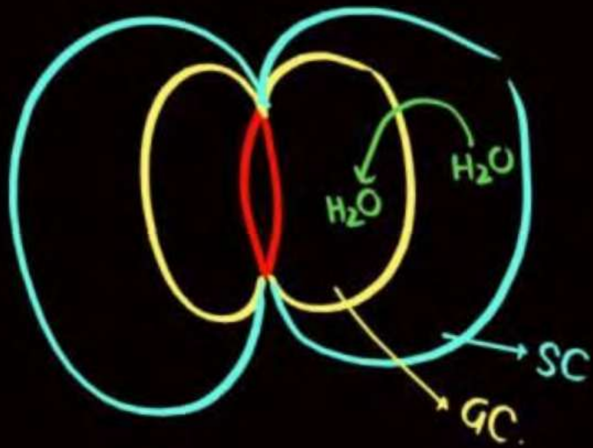
① STOM. PORE
② GUARD CELL
③ SUBSIDIARY CELL

↓ STOMATAL APPARATUS.



* gaseous exchange
* TRANSPIRATION

monocot (grass) dumbell shape (guard cell)



SC $\xrightarrow{H_2O}$ GC → SWELL/TURGID → STOMATA PORE OPEN.

GC $\xrightarrow{H_2O}$ SC

→ SHRINK/FLACCID → STOMATA CLOSED.

EPIDERMAL APPENDAGES

⇒ some outgrowth/structure arise from epidermis

ROOT

* UNICELLULAR.
* absorption of H_2O/mineral.

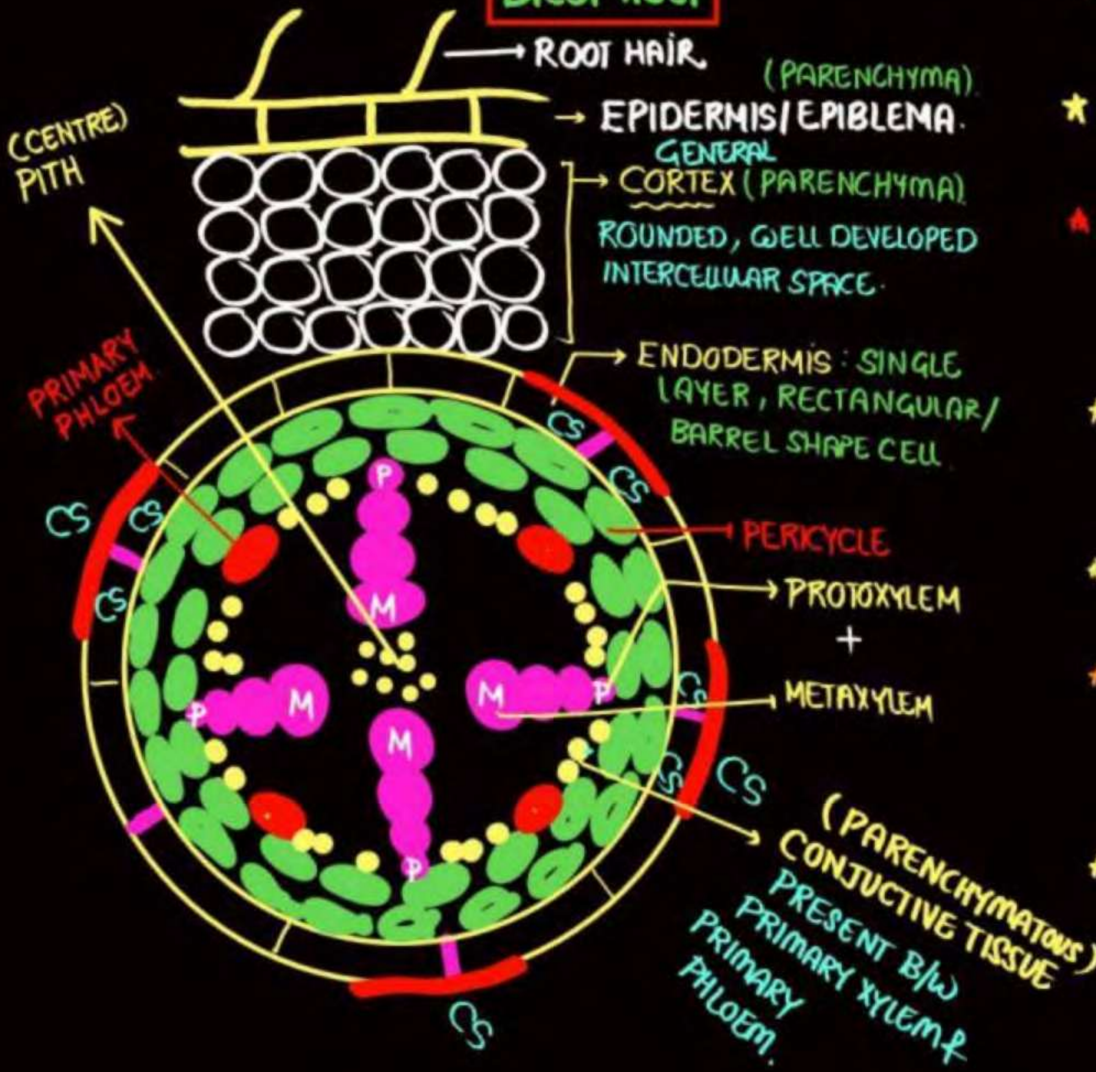
STEM

* MULTICELLULAR (MOSTLY) OR UNICELLULAR.
* SOFT / STIFF
* BRANCHED / UNBRANCHED.
* SECRETE OIL
* TRANSPIRATION / H_2O LOSS PREVENT

VASCULAR TISSUE SYSTEM.

- → RADIAL VASCULAR BUNDLE & EXARCH (DICOT, MONOCOT ROOT)
- → CONJOINT VASCULAR BUNDLE & ENDARCH. (DICOT, MONOCOT STEM).

DICOT ROOT



★ RADIAL & TANGENTIAL WALL: WATER IMPERMEABLE SUBSTANCE (SUBERIN) PRESENT: **CASPARIAN STRIPS (CS).**

★ CORTEX → GENERAL CORTEX (OUTER LAYER)
→ ENDODERMIS (INNER LAYER)

★ PERICYCLE (THICK WALLED PARENCHYMA) (PERMANENT TISSUE) —dedifferentiation→ meristematic cell. OR SECONDARY MERISTEM. (VASCULAR CAMBIUM) ↓ INCREASE THICKNESS OF ROOT.

→ FORM LATERAL ROOT (SECONDARY & TERTIARY ROOT)

★ PITH/CENTRE: PARENCHYMA IS NOT WELL DEVELOPED

★ PITH INCONSPICUOUS, SMALL.

EXARCH.

★ METAXYLEM TOWARDS: PITH/CENTRE
PROTOXYLEM TOWARDS: PERIPHERY/OUTER

★ PROTOXYLEM + METAXYLEM → PRIMARY XYLEM

★ PRIMARY XYLEM & PRIMARY PHLOEM: DIFFERENT LINE/RADIUS, ALTERNATE
RADIAL VASCULAR BUNDLE

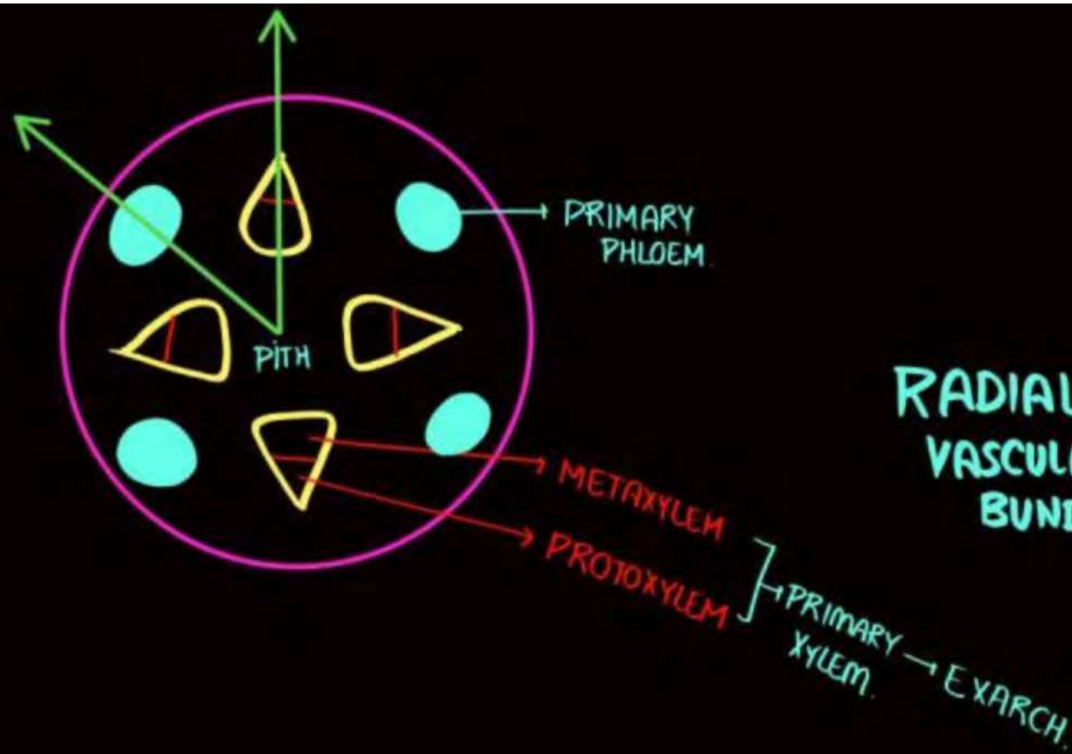
STELE

PITH → XYLEM, PHLOEM → PERICYCLE
(VASCULAR TISSUE)

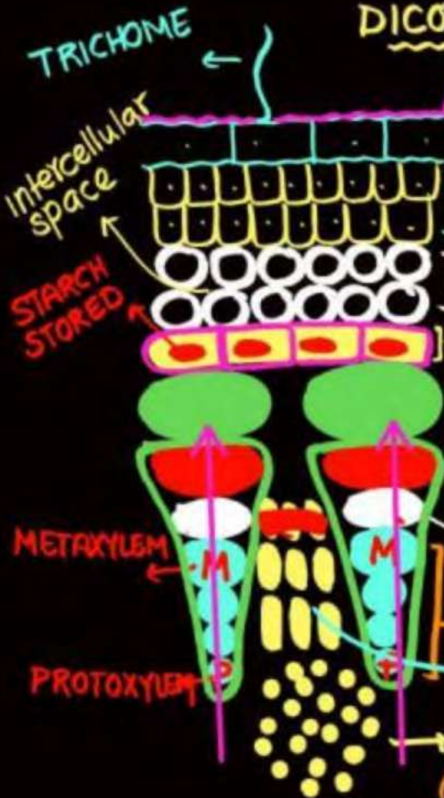
★ 4 : XYLEM , 4 : PHLOEM
(TETRACH ROOT)

★ 2 → X, P
3 → X, P
4 → X, P → most common → DIARCH TO TETRACH
5 → X, P → PENTARCH
6 → X, P → HEXARCH

	DICOT ROOT	MONOCOT ROOT
PERICYCLE	VASCULAR CAMBIUM	ABSENT
	LATERAL ROOT	PRESENT
SECONDARY GROWTH (THICKNESS	✓	×
SECONDARY XYLEM	✓	×
PITH	small, inconspicuous (NOT WELL DEVELOPED)	LARGE, CONSPICUOUS (WELL DEVELOPED)
VASCULAR BUNDLE	2 TO 4	MORE THAN SIX (POLYARCH)
	FEWER	MORE
	EXARCH, RADIAL	EXARCH, RADIAL



RADIAL
VASCULAR
BUNDLE.



MEDULARY RAYS (PARENCHYMA) PERMANENT TISSUE $\xrightarrow{\text{dedifferentiation}}$ merist cell / secondary meristem / interfascicular cambium

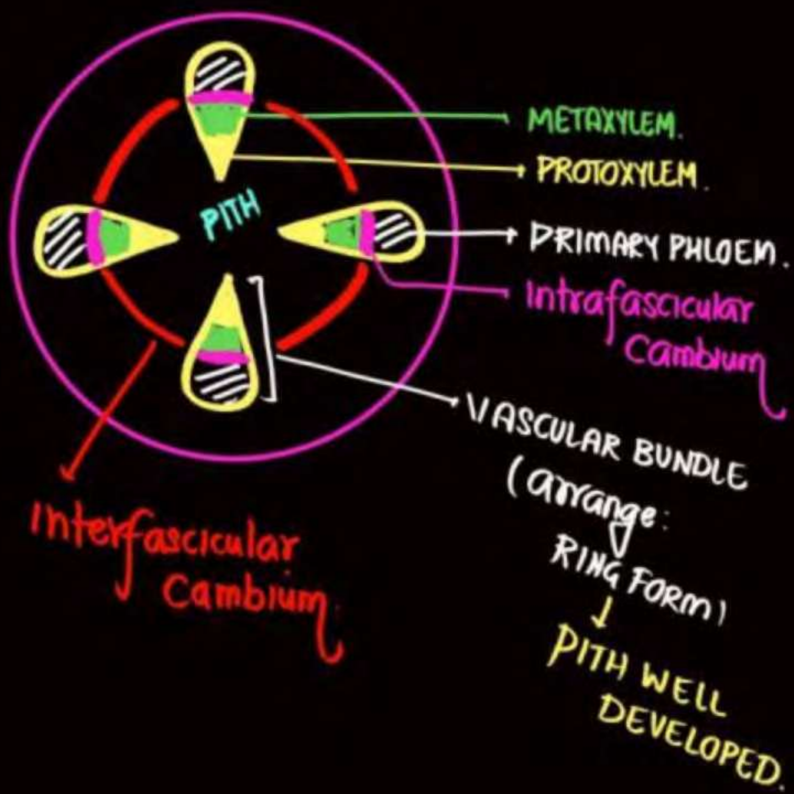
INTRAFASCICULAR CAMBIUM (PRIMARY MERISTEM) FORMED EARLY + interfas. cambium (SECON. MERISTEM) LATER FORMED → VASCULAR CAMBIUM

↓

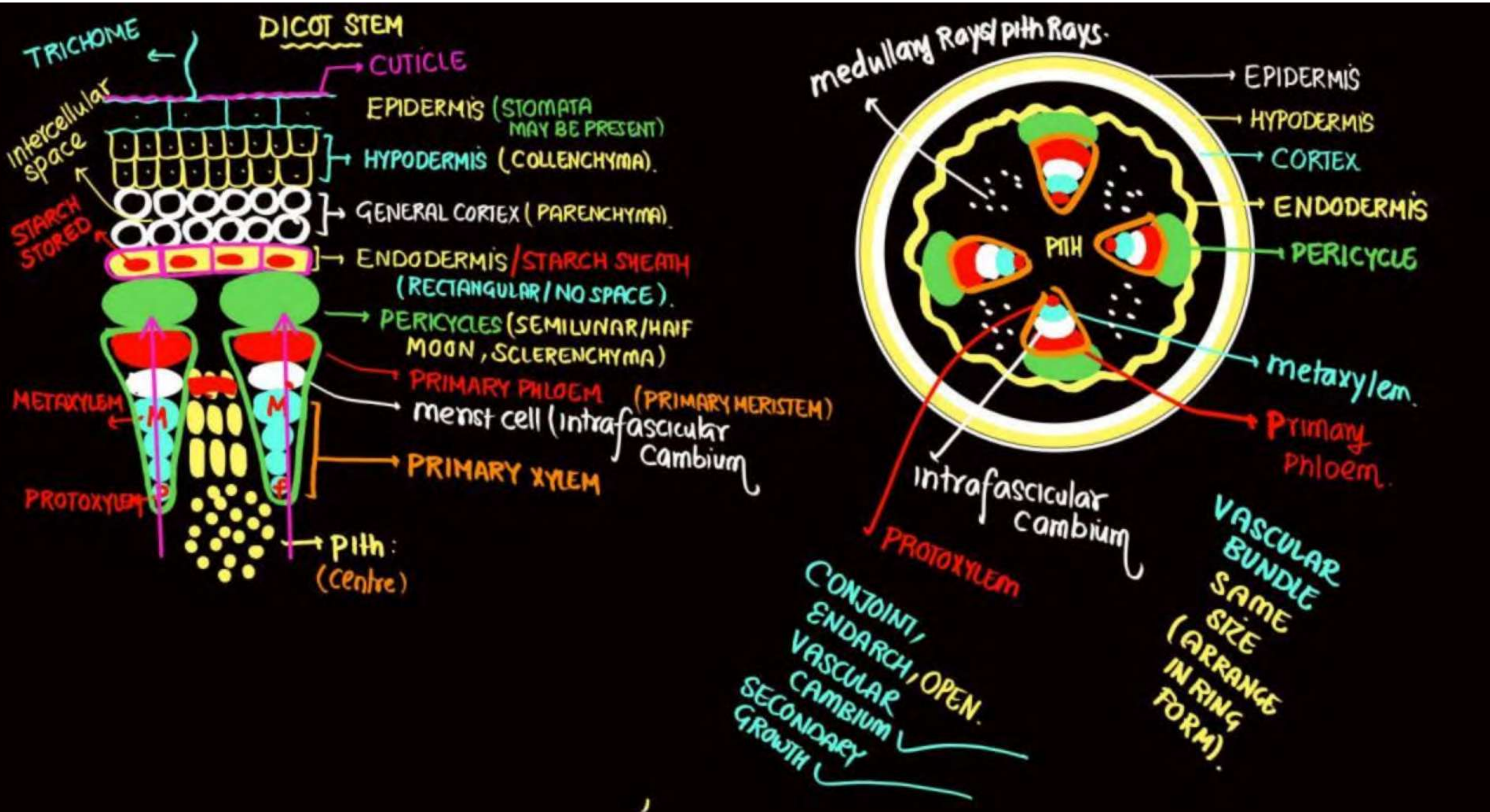
SECONDARY GROWTH. (FORMATION OF SECONDARY XYLEM & SECON. PHLOEM)

PROTOXYLEM: TOWARDS PITH
METAXYLEM: PERIPHERY/OUTER
ENDARCH

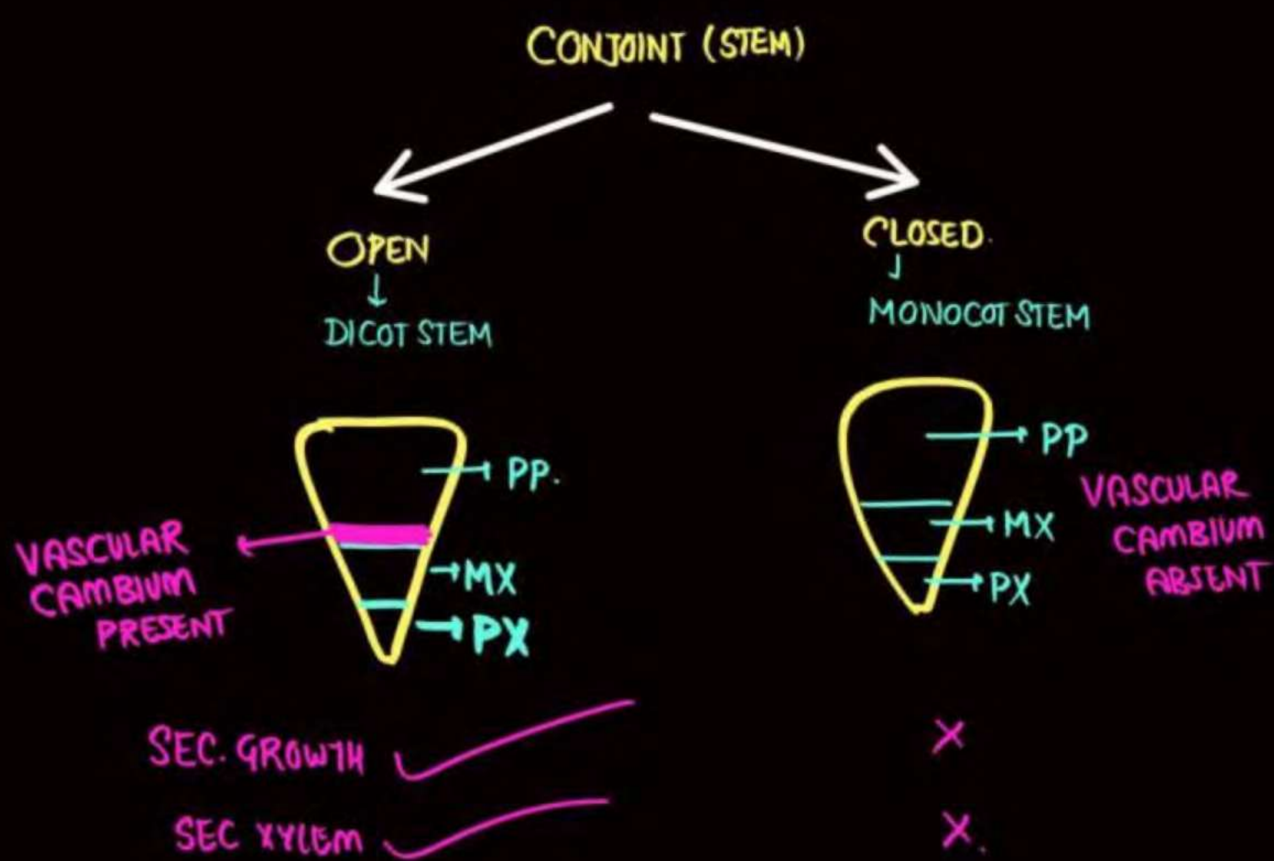
PRIMARY XYLEM & PRIMARY PHLOEM: SAME LINE /
PRIMARY XYLEM COVERED BY PRIMARY PHLOEM:
CONJOINT VASCULAR BUNDLE



METAXYLEM.
PROTOXYLEM.
PITH
PRIMARY PHLOEM.
Intrafascicular
Cambium
VASCULAR BUNDLE
(arrange:
RING FORM)
PITH WELL
DEVELOPED.
Interfascicular
Cambium.



DICOT STEM
TRICHOME
CUTICLE
EPIDERMIS (STOMATA MAY BE PRESENT)
intercellular space
HYPODERMIS (COLLENCHYMA).
GENERAL CORTEX (PARENCHYMA)
STARCH STORED
ENDODERMIS/STARCH SHEATH (RECTANGULAR/NO SPACE).
PERICYCLES (SEMILUNAR/HALF MOON, SCLERENCHYMA)
PRIMARY PHLOEM
(PRIMARY MERISTEM)
METAXYLEM
menst cell (intrafascicular Cambium
PRIMARY XYLEM
PROTOXYLEM
pith: (centre)
medullary Rays/pith Rays.
EPIDERMIS
HYPODERMIS
CORTEX
ENDODERMIS
PERICYCLE
PITH
metaxylem.
Primary Phloem.
intrafascicular cambium
PROTOXYLEM
CONJOINT, ENDARCH, OPEN. VASCULAR CAMBIUM SECONDARY GROWTH
VASCULAR BUNDLE SAME SIZE (ARRANGE IN RING FORM).


CONJOINT (STEM)
OPEN
DICOT STEM
CLOSED.
MONOCOT STEM
PP.
MX
PX
VASCULAR CAMBIUM PRESENT
PP
MX
PX
VASCULAR CAMBIUM ABSENT
SEC. GROWTH
SEC XYLEM
X
X.

2. The Ground Tissue System

All tissues except epidermis and vascular bundles constitute the **ground tissue**. It consists of simple tissues such as parenchyma, collenchyma and sclerenchyma. Parenchymatous cells are usually present in cortex, pericycle, pith and medullary rays, in the primary stems and roots. In leaves, the ground tissue consists of thin-walled chloroplast containing cells and is called **mesophyll.**

Explanation

EPIDERMIS ⟶ EPIDERMAL TISSUE SYSTEM.

XYLEM, PHLOEM ⟶ VASCULAR TISSUE SYSTEM.

HYPOD, CORTEX, ENDODE, PERICYCLE, PITH, PITH RAYS : GROUND TISSUE SYST.

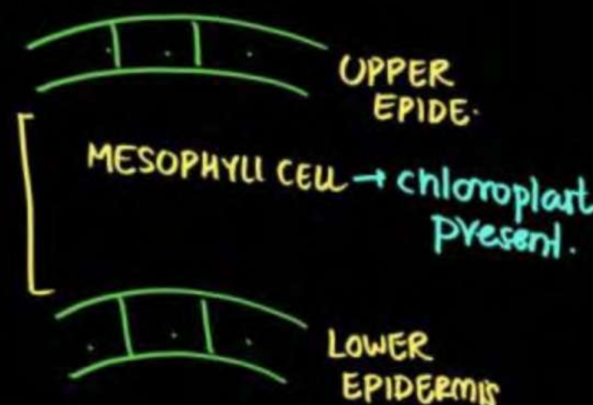
P P P P

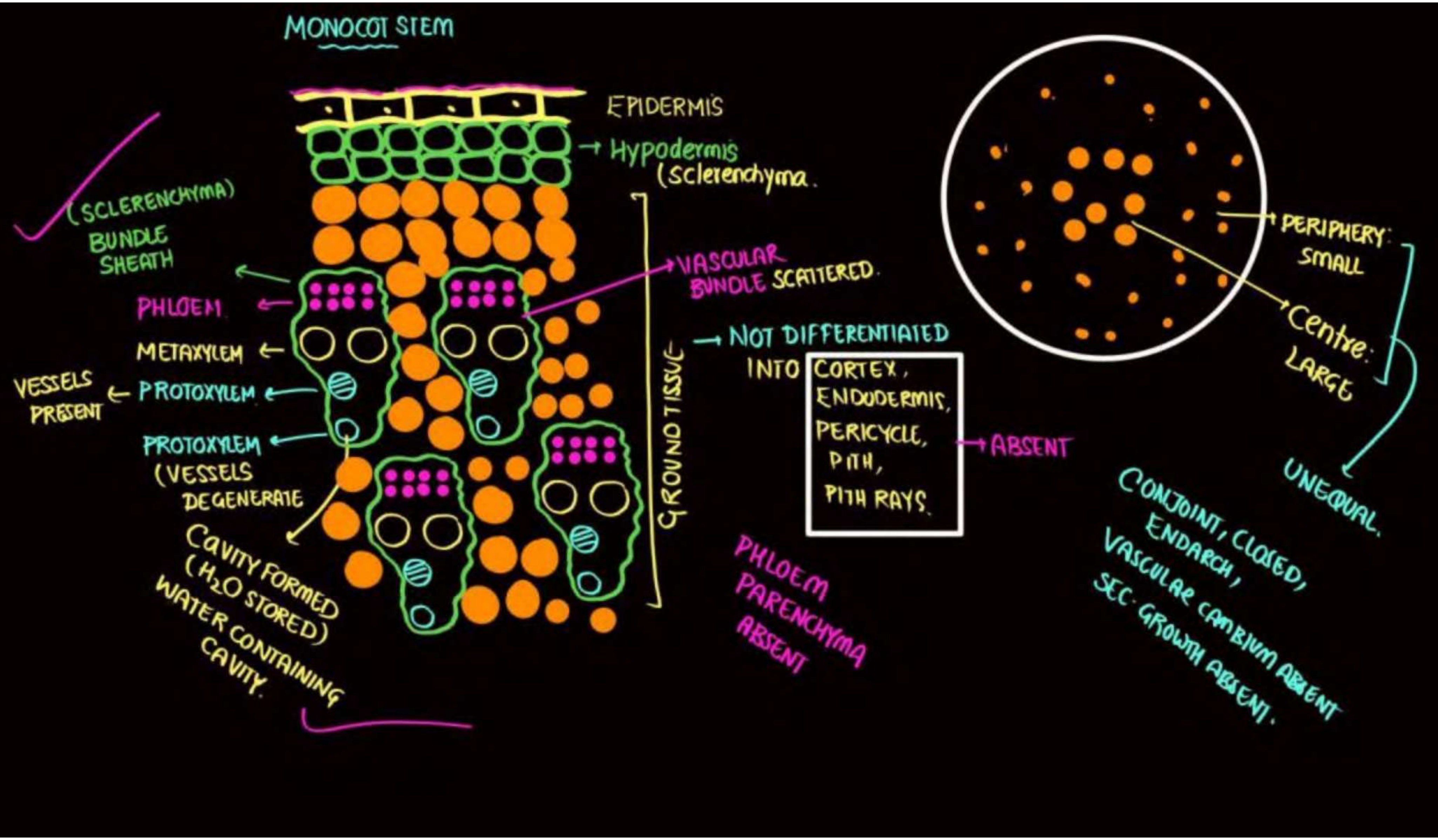
collenchyma (DICOT STEM)

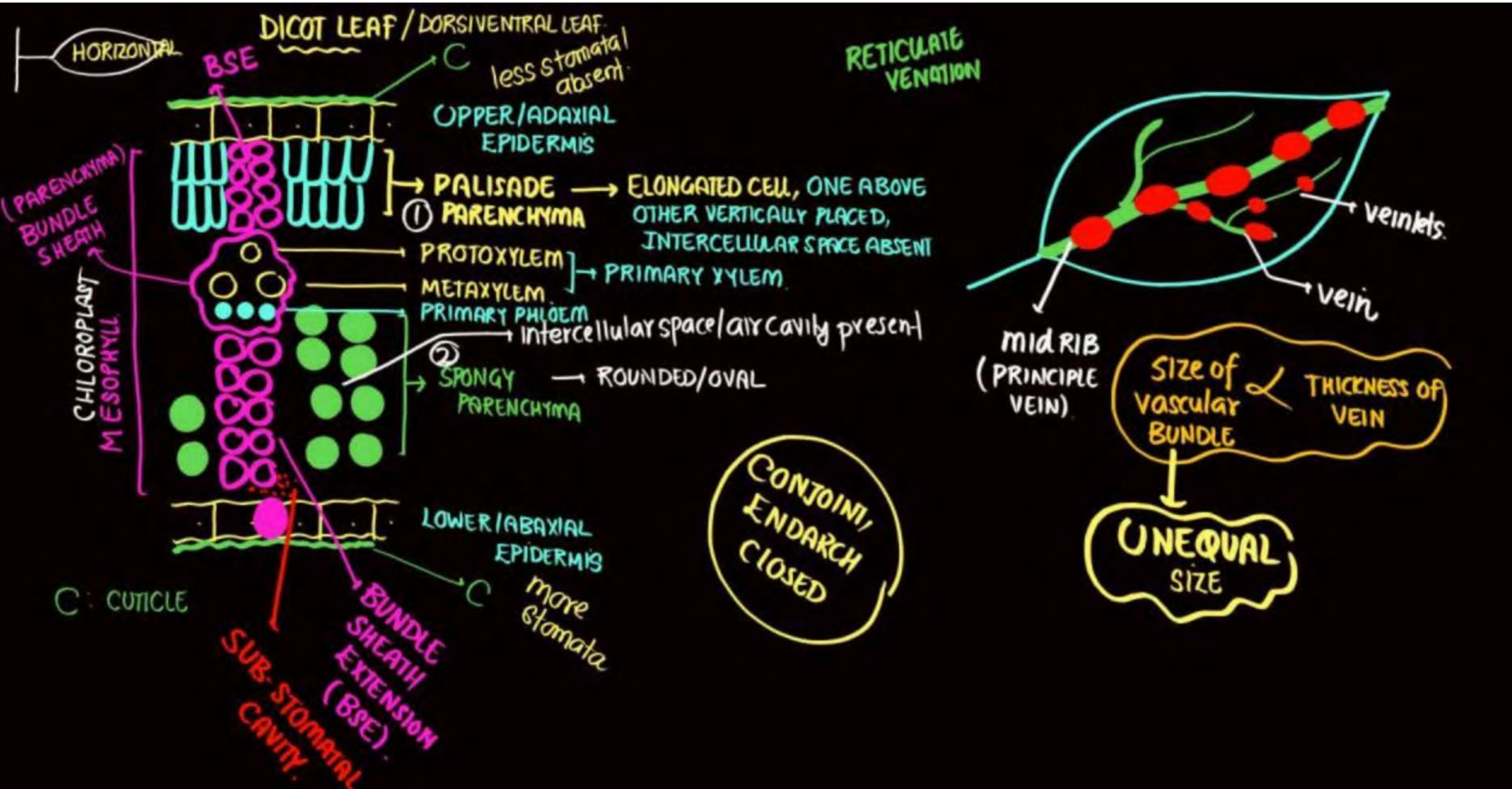
SCLERENCHYMA (MONOCOT STEM)

P: PARENCHYMA.

LEAF



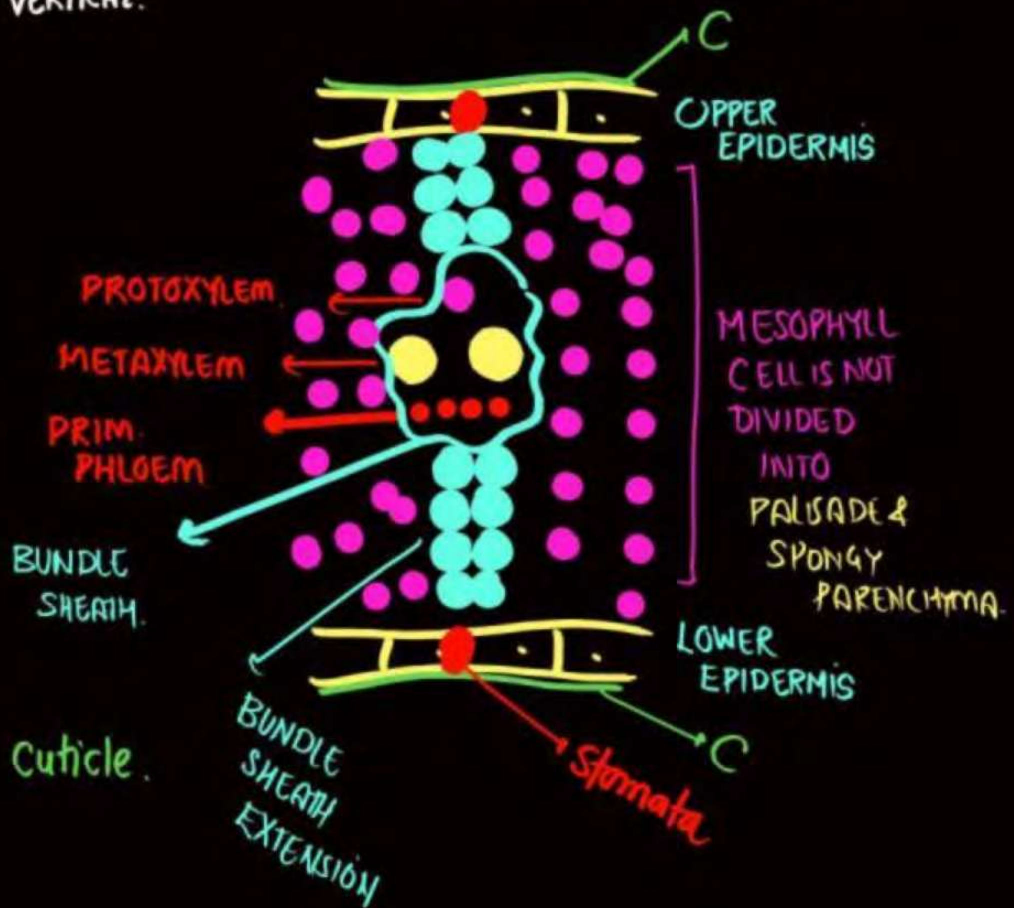

MONOCOT STEM
EPIDERMIS
Hypodermis (sclerenchyma.
(SCLERENCHYMA) BUNDLE SHEATH
PHLOEM
METAXYLEM
VESSELS PRESENT
PROTOXYLEM
PROTOXYLEM (VESSELS DEGENERATE
Cavity FORMED (H_2O STORED)
WATER CONTAINING CAVITY.
VASCULAR BUNDLE SCATTERED.
GROUND TISSUE
NOT DIFFERENTIATED INTO
CORTEX, ENDODERMIS, PERICYCLE, PITH, PITH RAYS.
ABSENT
PHLOEM PARENCHYMA ABSENT
PERIPHERY: SMALL
Centre: LARGE
UNEQUAL.
CONJOINT, CLOSED, ENDARCH,
VASCULAR CAMBIUM ABSENT
SEC. GROWTH ABSENT.



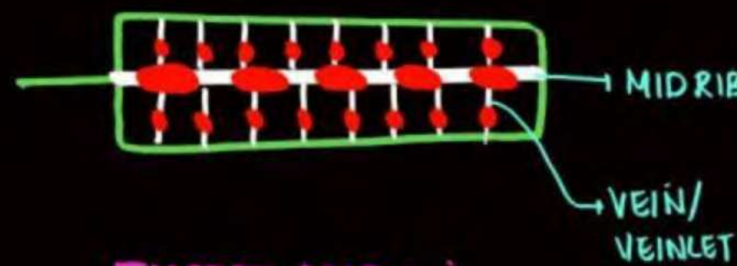
DICOT LEAF / DORSIVENTRAL LEAF
HORIZONTAL
BSE
C
less stomatal
absent
UPPER/ADAXIAL EPIDERMIS
(PARENCHYMA) BUNDLE SHEATH
CHLOROPLAST
MESOPHYLL
PALISADE PARENCHYMA
①
ELONGATED CELL, ONE ABOVE OTHER VERTICALLY PLACED, INTERCELLULAR SPACE ABSENT
PROTOXYLEM
METAXYLEM
PRIMARY XYLEM
PRIMARY PHLOEM
intercellular space/air cavity present
②
SPONGY PARENCHYMA
ROUNDED/OVAL
LOWER/ABAXIAL EPIDERMIS
C
more stomata
C : CUTICLE
SUB-STOMATAL CAVITY.
BUNDLE SHEATH EXTENSION (BSE).
CONJOINT, ENDARCH CLOSED
RETICULATE VENATION
veinlets.
vein
mid RIB (PRINCIPLE VEIN)
Size of vascular BUNDLE ∝ THICKNESS OF VEIN
UNEQUAL SIZE

VERTICAL.

MONOCOT LEAF. / ISOBILATERAL.



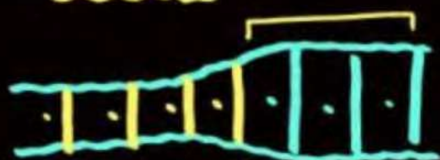
C : Cuticle.



EXCEPT MIDRIB

SIZE OF VASCULAR BUNDLE : EQUAL.

BULLIFORM CELL (B.C).

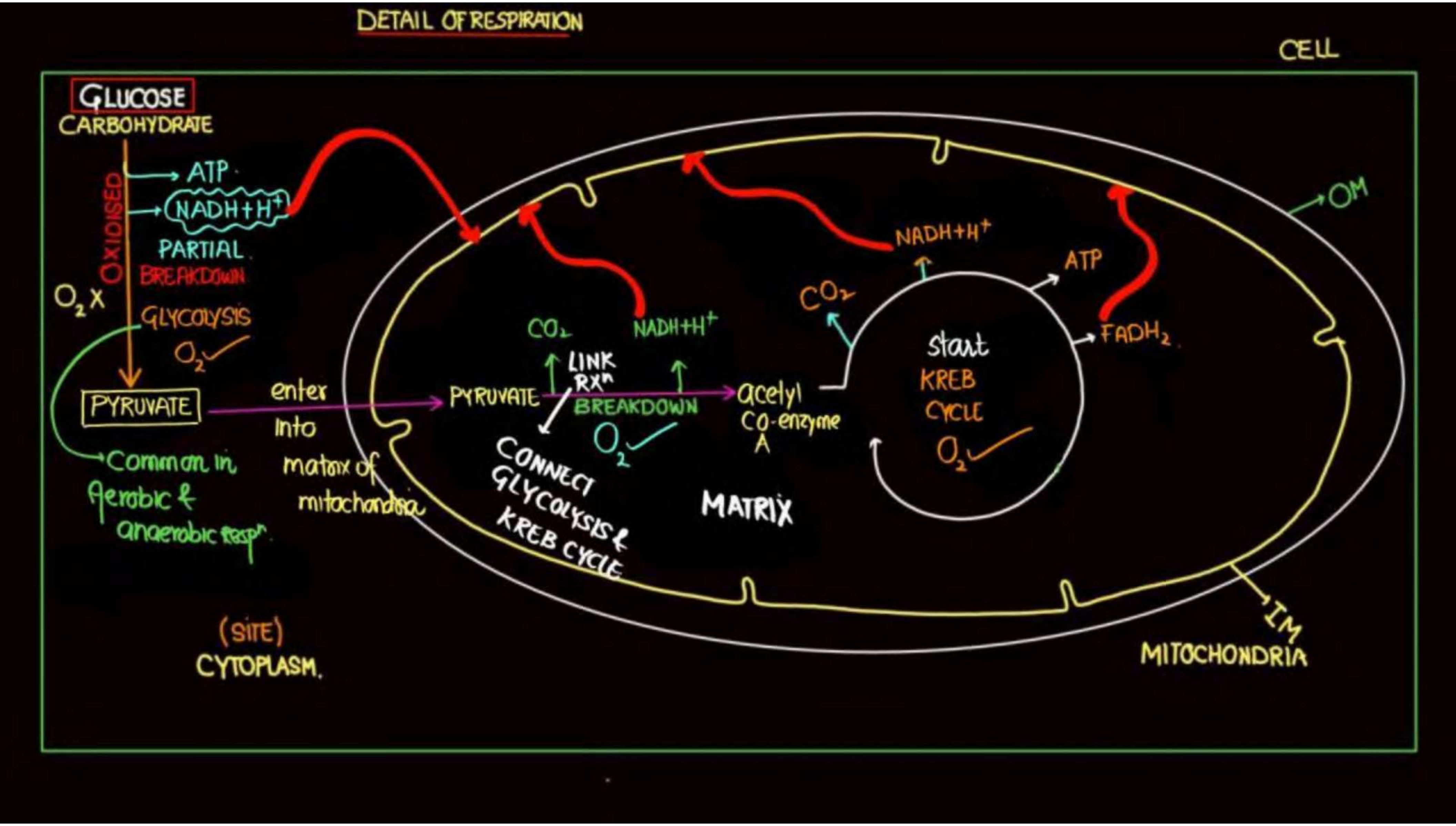


⇒ monocot leaf

UPPER EPIDERMIS.
LARGE CELL, GROUP,
COLOURLESS.,
EMPTY

B.C

	BC	BC	LEAF
H_2O available ⟶	WATER ✓	SWELL (TURGID)	EXPOSED.
H_2O NOT AVAILABLE	X	shrink (FLACCID)	CURL INWARD → SURFACE AREA DECREASE → TRANSPIRATION DECREASE



DETAIL OF RESPIRATION
CELL
GLUCOSE
CARBOHYDRATE
OXIDISED
ATP
NADH+H+
PARTIAL
BREAKDOWN
O2 X
GLYCOLYSIS
O2 ✓
PYRUVATE
Common in aerobic & anaerobic respn.
enter into matrix of mitochondria
PYRUVATE
LINK RXn
BREAKDOWN
CO2
NADH+H+
O2 ✓
CONNECT GLYCOLYSIS & KREB CYCLE
acetyl Co-enzyme A
MATRIX
CO2
NADH+H+
ATP
FADH2
Start KREB CYCLE
O2 ✓
OM
IM
MITOCHONDRIA
(SITE)
CYTOPLASM.

- ★ Glycolysis O_2 ✓, ATP, NADH, CYTOPLASM
- ★ LINK RX^n O_2 ✓, NADH, MATRIX
- ★ KREB CYCLE O_2 ✓, ATP, NADH, $FADH_2$, MATRIX

(O_2 PRESENT)

$\boxed{\text{AEROBIC RESPIRATION}}$

IM: INNER MEM. OF MITOCHOND.

Inner memb. of mitoch.

Participat in PROCESS.

ELECTRON TRANSPORT CHAIN

$$\boxed{\begin{array}{l} 1\ NADH \longrightarrow 3\ ATP \\ 1\ FADH_2 \longrightarrow 2\ ATP \end{array}}$$

HOW?

O_2 ——

GLYCOLYSIS

- ★ SPLITTING OF GLUCOSE
- ★ PARTIAL BREAKDOW OF GLUCOSE
- ★ GLUCOSE $\xrightarrow{\text{OXIDISED}}$ 2 PYRUVATE
  (1 mole : 6C) — 1 mol : 3C
  2 mol × 3C = 6C
- ★ CO_2 : ABSENT
- ★ DISCOVERED: EMBDEN, MEYERHOFF, PARANAS (EMP) pathway
- ★ CYTOPLASM → SITE → LIQUID REGION (CYTOSOL)
- ★ INDEPENDENT OF O_2

GLUCOSE   1 mole, 6C

Hexokinase, Mg^{+2} 1st

$\xrightarrow{\text{ATP} \rightarrow \text{ADP} + \text{ip}}$ (Energy consumed).

GLUCOSE - 6- Phosphate   1 mole, 6C, 1P

2nd

FRUCTOSE - 6- PHOSPHATE   1 mole, 6C, 1P

PHOSPHOFRUCTOKINASE Mg^{+2} 3rd.

$\xrightarrow{\text{ATP} \rightarrow \text{ADP} + \text{ip}}$ (Energy consumed).

FRUCTOSE 1, 6 BIS PHOSPHATE   1 mole, 6C, 2P.

aldolase   4th.

Dihydroxyacetone phosphate $\xrightleftharpoons{5^{th}}$ 3- Phosphoglyceraldehyde.

3C, 1mol, 1P   3C, 1mol, 1P

Energy Consuming PHASE / glucose activation phase

⇒ ATP CONSUMED: $\boxed{2}$

3 PHOSPHOGLYCERALDEHYDE , 2 mol, 3C+3C, 1P+1P.

$\boxed{2H_3PO_4}$ Oxidⁿ $\xrightarrow{2NAD^+ \rightarrow 2NADH + 2H^+}$ 6th step

SUBSTRATE ← 1,3 BISPHOSPHOGLYCERIC ACID 2 mol, 3C+3C, 2P+2P

$\xrightarrow{2IP + 2ADP \rightarrow 2ATP}$ 7th step SUBSTRATE LEVEL PHOSPHORYLATION

PRODUCT 3 PHOSPHOGLYCERIC ACID 2 mol, 3C+3C, 1P + 1P

8th step

2 PHOSPHOGLYCERIC ACID 2 mol, 3C+3C, 1P + 1P

9th

H_2O

PHOSPHOENOL PYRUVATE 2 mol, 3C+3C, 1P + 1P

Pyruvate kinase, K^+, Mg^{+2}.

$\xrightarrow{2IP + 2ADP \rightarrow 2ATP}$ 10th step SUBSTRATE LEVEL PHOSPHORYLATION

PYRUVATE 2 mol, 3C+3C, 0P + 0P

Q Total ATP in glycolysis (including ETC)

2+6 ⇒ $\boxed{8}$

★ 3 PGAL (1mol) → 2H ⇒ 2 Redox equivalent.

★ 3PGAL (2mol) → 2H + 2H

$\boxed{NAD^+ \quad NAD^+}$

$\boxed{NADH + H^+}$ $\boxed{NADH + H^+}$

★ ADP + IP → ATP

PHOSPHORYLATION.

★ DIRECT ATP / SUBSTRATE LEVEL PHOSPHORYLATION ATP

⇒ $\boxed{4\ ATP}$ → cytoplasm

★ CONSUMED: $\boxed{2\ ATP}$

★ NET GAIN OF ATP: 4-2 = $\boxed{2\ ATP}$

★ INDIRECT ATP/ETC:

2NADH X 3ATP: $\boxed{6ATP}$ → INNER MEMBRANE.

★ All steps are Reversible: 1st, 3rd, 10th.

★ PHOTOSYNTHESIS: GLUCOSE FORMED

↓ CHANGE

SUCROSE ✓

(END PRODUCT OF PHOTOSYNTHESIS)

↓ INVERTASE

GLUCOSE ✓ FRUCTOSE ✓

BOTH ENTER READILY (FAST) INTO GLYCOLYSIS

SUMMARISE

G $\xrightarrow{ATP \rightarrow ADP}$ G6P

↓

F6P $\xrightarrow{ATP \rightarrow ADP}$ F 1,6 BISP

DHAP ← F 1,6 BISP → 3-PGAL

3-PGAL $\xrightarrow{2NADH}$ 1,3 BISPGA

1,3 BISPGA $\xrightarrow{2ATP}$ 3PGA

3PGA → 2PGA → PEP

PEP $\xrightarrow{2ATP}$ PYRUVATE

FRUCTOSE $\xrightarrow{ATP \rightarrow ADP}$ F6P

tip

Q ONE MOLECULE OF FRUCTOSE ENTER INTO GLYCOLYSIS

DIRECT ATP: 4

Q ATP CONSUMED: 2

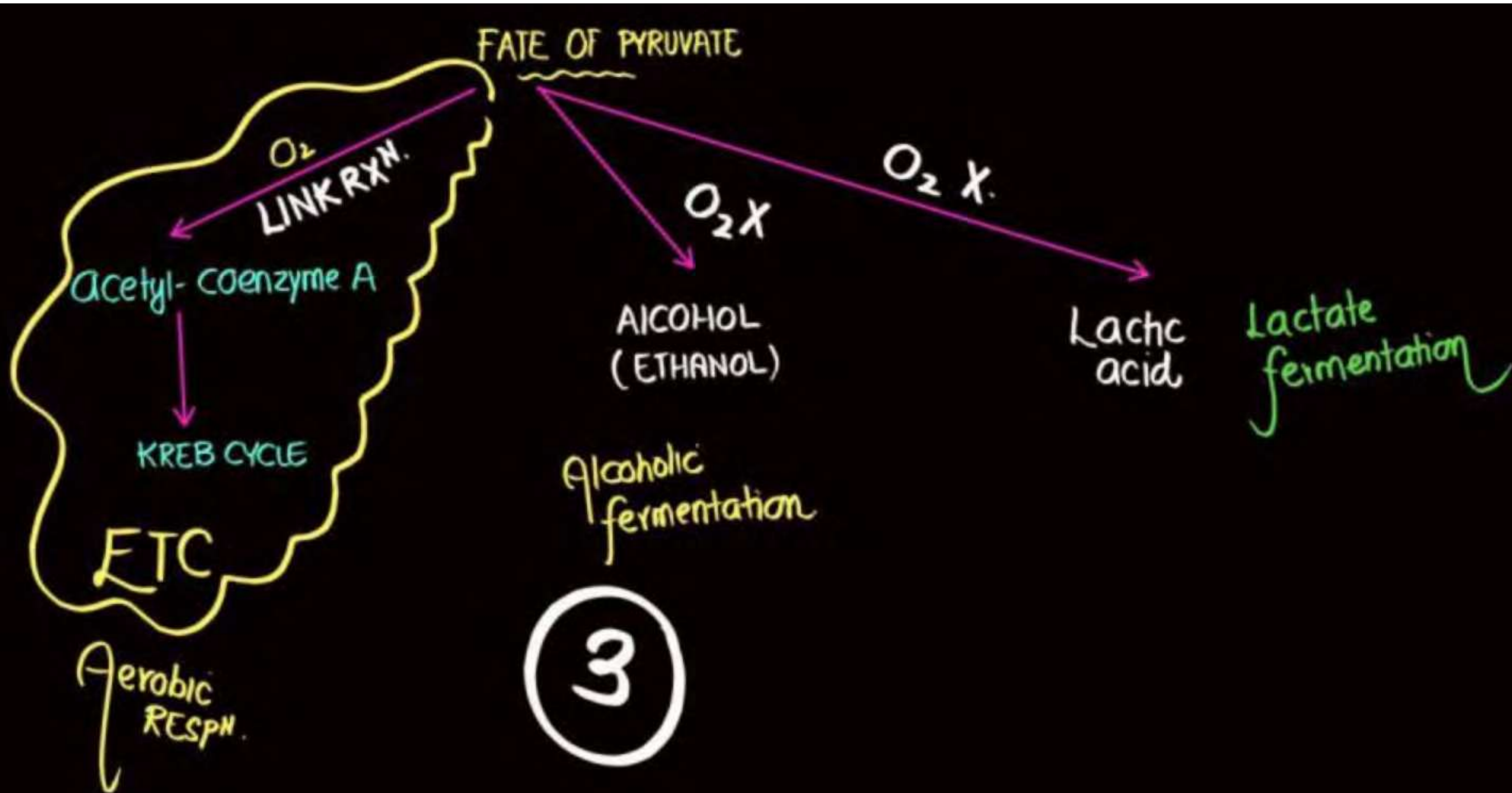
Q INDIRECT ATP: 2NADH×3 = 6

Q NET GAIN: 4 − 2 : 2

NOTE: STORAGE CARBOHYDRATE (STARCH) → GLUCOSE.

NOTE: 2H : 2 REDOX EQUIVALENT

NOTE: COMMON PATHWAY FOR AEROBIC & ANAEROBIC RESP^N.


FATE OF PYRUVATE
O_2
LINK RXN.
acetyl- coenzyme A
KREB CYCLE
ETC
Aerobic RESPN.
O_2 X
ALCOHOL
(ETHANOL)
Alcoholic fermentation
O_2 X.
Lactic acid
Lactate fermentation
3

(glycolysis)
PYRUVATE
(CYTOPLASM)

ENTER INTO MATRIX OF MITOCHONDRIA

$\boxed{\text{LINK RX}^N \text{ / OXIDATIVE DECARBOXYLATION}}$ → RELEASE OF CO_2.

$$2\text{PYRUVATE} + \boxed{\text{Coenzyme A} + 2NAD^+} \xrightarrow[\text{MULTISTEP REACTION}]{\text{PYRUVATE DEHYDROGENASE, } Mg^{+2} \text{ (MULTIENZYME COMPLEX)}} 2\text{ ACETYL CO-A} + 2CO_2 + 2NADH + 2H^+$$

*

1mol : 3C
3C+3C : 6C

1mol : 2C
2C+2C : 4C

2C

① DIRECT ATP FORMED: ZERO
(SUBSTRATE LEVEL PHOSPHORYLATION)

② INDIRECT ATP/ETC: 2NADH X 3ATP : $\boxed{6ATP}$

③ If one molecule of pyruvic acid enter into LINK RX^n

CO_2 → 1
NADH → 1
INDIRECT ATP → 3
ACETYL Co-A → 1.

KREB CYCLE

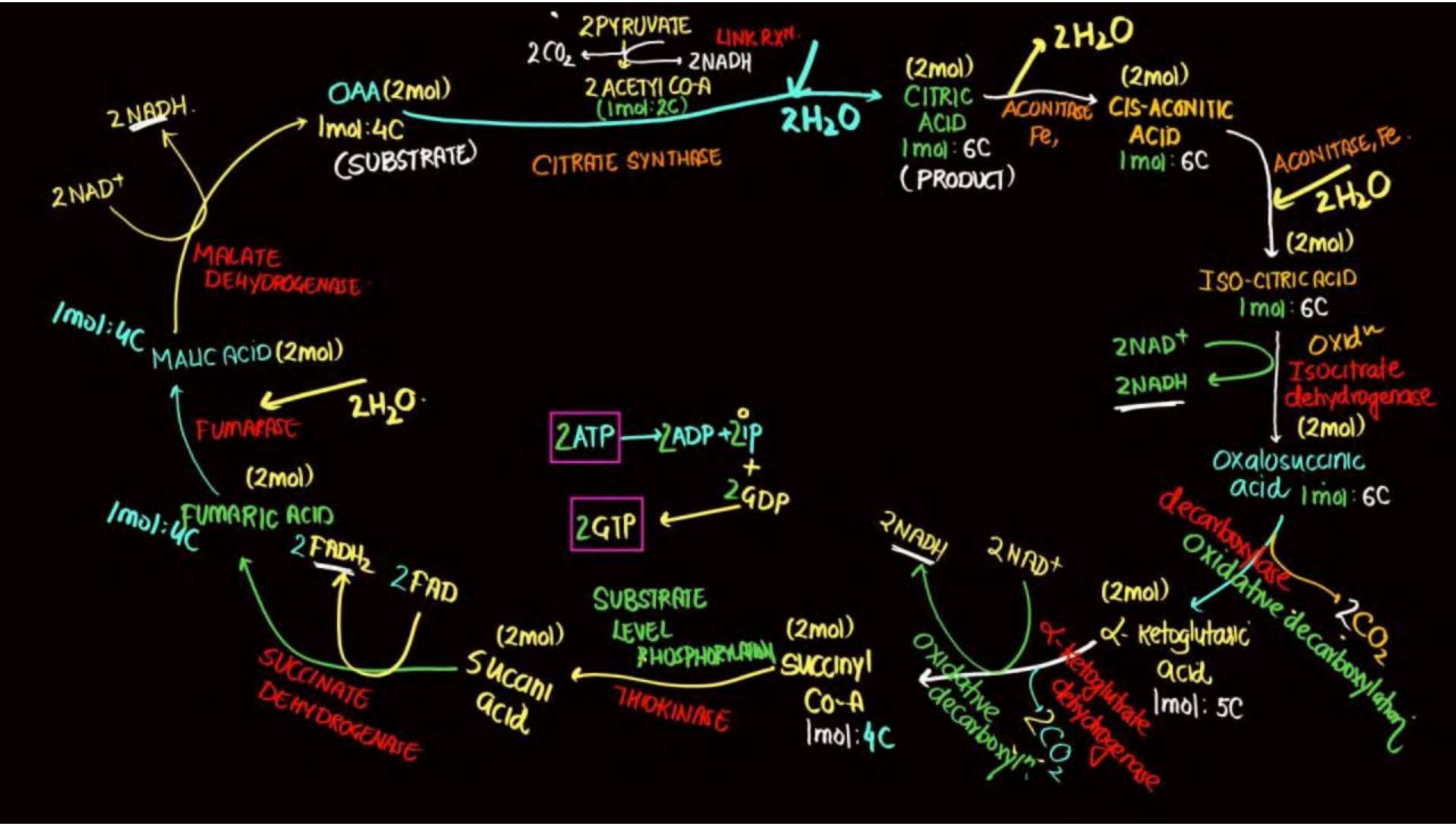
- MATRIX OF MITOCHONDRIA : SITE
- FIRST PRODUCT: CITRIC ACID = 6C. ⟶ 3COOH.
- CITRIC ACID CYCLE / TRICARBOXYLIC ACID CYCLE (TCA)
- All ENZYMES PRESENT IN MATRIX
  EXCEPT SUCCINATE DEHYDROGENASE → INNER MEMB

- FIRST STEP:

$$\text{2 ACETYL CO-A} + \text{2 Oxaloacetic acid} \xrightarrow[\text{CITRATE SYNTHASE}]{\text{CONDENSATION REACTION}} \text{2 CITRIC ACID}$$

2 H_2O CONSUMED.

2 ACETYL CO-A	2 Oxaloacetic acid	2 CITRIC ACID
1 mol: 2C	1 mol: 4C	1 mol: 6C
2C+2C: 4C	4C+4C: 8C.	6C+6C: 12C.



2PYRUVATE
LINK RXⁿ.
2CO₂
2NADH
2 ACETYl CO-A
(1mol:2C)
OAA(2mol)
1mol:4C
(SUBSTRATE)
CITRATE SYNTHASE
2H₂O
(2mol)
CITRIC
ACID
1mol: 6C
(PRODUCT)
2H₂O
ACONITASE
Fe,
(2mol)
CIS-ACONITIC
ACID
1mol: 6C
ACONITASE, Fe.
2H₂O
(2mol)
ISO-CITRIC ACID
1mol: 6C
2NAD⁺
2NADH
Oxidⁿ
Isocitrate
dehydrogenase
(2mol)
Oxalosuccinic
acid 1mol: 6C
decarboxylase
Oxidative decarboxylation
2CO₂
(2mol)
α-Ketoglutaric
acid
1mol: 5C
2NADH
2NAD⁺
α-Ketoglutarate
dehydrogenase
Oxidative
decarboxylⁿ.
2CO₂
(2mol)
Succinyl
Co-A
1mol: 4C
SUBSTRATE
LEVEL
PHOSPHORYLATION
THIOKINASE
(2mol)
Succini
acid
2FADH₂
2FAD
SUCCINATE
DEHYDROGENASE
(2mol)
FUMARIC ACID
1mol: 4C
FUMARASE
2H₂O
MALIC ACID (2mol)
1mol: 4C
MALATE
DEHYDROGENASE
2NAD⁺
2NADH
2ATP
2ADP + 2iP
+
2GDP
2GTP

* DIRECT ATP/ SUBSTRATE LEVEL PHOSPHORYLATION : 2 (MATRIX)
* TOTAL NADH : $\boxed{6}$
* TOTAL $FADH_2$: 2
* INDIRECT ATP (NADH) : 6 NADH X 3ATP ⇒ 18 ATP
  ($FADH_2$) : 2 $FADH_2$ X 2ATP ⇒ 4 ATP

  → 22 ATP (INNER MEM)

  → 24 ATP
* TOTAL CO_2 : 4
* If one molecule of Acetyl co-A enter into kreb cycle
  - NADH → 3
  - $FADH_2$ → 1
  - CO_2 → 2
  - ATP (DIRECT) → 1.

NAD⁺

FAD⁺

In addition it also requires regeneration of NAD^+ and FAD^+ from NADH and $FADH_2$ respectively. The summary equation for this phase of respiration may be written as follows:

$$\text{Pyruvic acid} + 4NAD^+ + FAD^+ + 2H_2O + ADP + Pi \xrightarrow{\text{Mitochondrial Matrix}} 3CO_2 + 4NADH + 4H^+ + FADH_2 + ATP$$

(1 molecu)

$NADH + H^+ \xrightarrow{\text{oxidised}} NAD^+$

$FADH_2 \xrightarrow{\text{oxidised}} FAD^+$

Kreb cycle

LINK Rxn + KREB CYCLE

$6H_2O$

$2H_2O$

$6 - 2$

$\Rightarrow \boxed{4H_2O}$

CALCULATION OF ATP

glycolysis

- TOTAL ATP / DIRECT ATP / SUBSTRATE LEVEL → 4
- CONSUMED ATP → 2
- NET GAIN OF ATP → 4 − 2 → $\boxed{2}$ (cytoplasm)
- INDIRECT ATP → 2 NADH × 3 → $\boxed{6}$ ETC

$\boxed{2}$ + $\boxed{6}$ → 8

LINK RXN

- DIRECT / SUBSTRATE LEVEL → ZERO
- INDIRECT ATP → 2 NADH × 3 → $\boxed{6}$ ETC → 6

KREB CYCLE

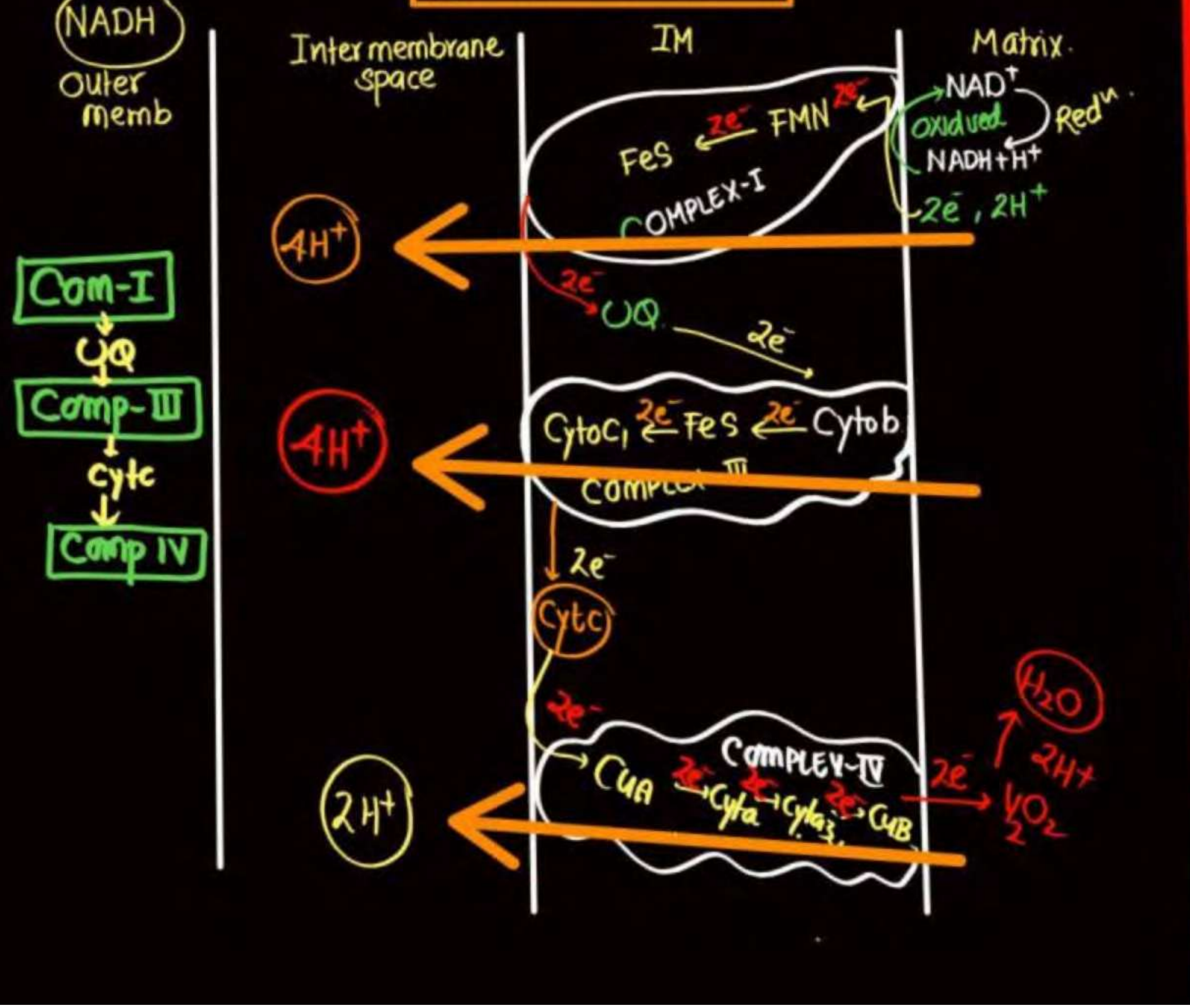
- DIRECT / SUBSTRATE LEVEL → $\boxed{2}$ matrix
- INDIRECT ATP → 6 NADH × 3 ATP → $\boxed{18}$ ETC
- INDIRECT ATP → 2 $FADH_2$ × 2 ATP → $\boxed{4}$ ETC

$\boxed{2}$ + $\boxed{18}$ + $\boxed{4}$ → 24

1 mole of glucose in aerobic Respn.

38

ELECTRON TRANSPORT CHAIN



⇒ FMN: FLAVIN MONO NUCLEOTIDE

⇒ COMPLEX: MAINLY PROTEIN. BUT HAVE NON PROTEIN PART (FMN, FeS) / NADH DEHYDROGENASE

⇒ UQ / Coenzyme Q: mobile e^- carrier
LIPID SOLUBLE

⇒ Cytochrome: protein.

⇒ Complex-III: Cyto bc_1 complex. / cyto c Reductase.

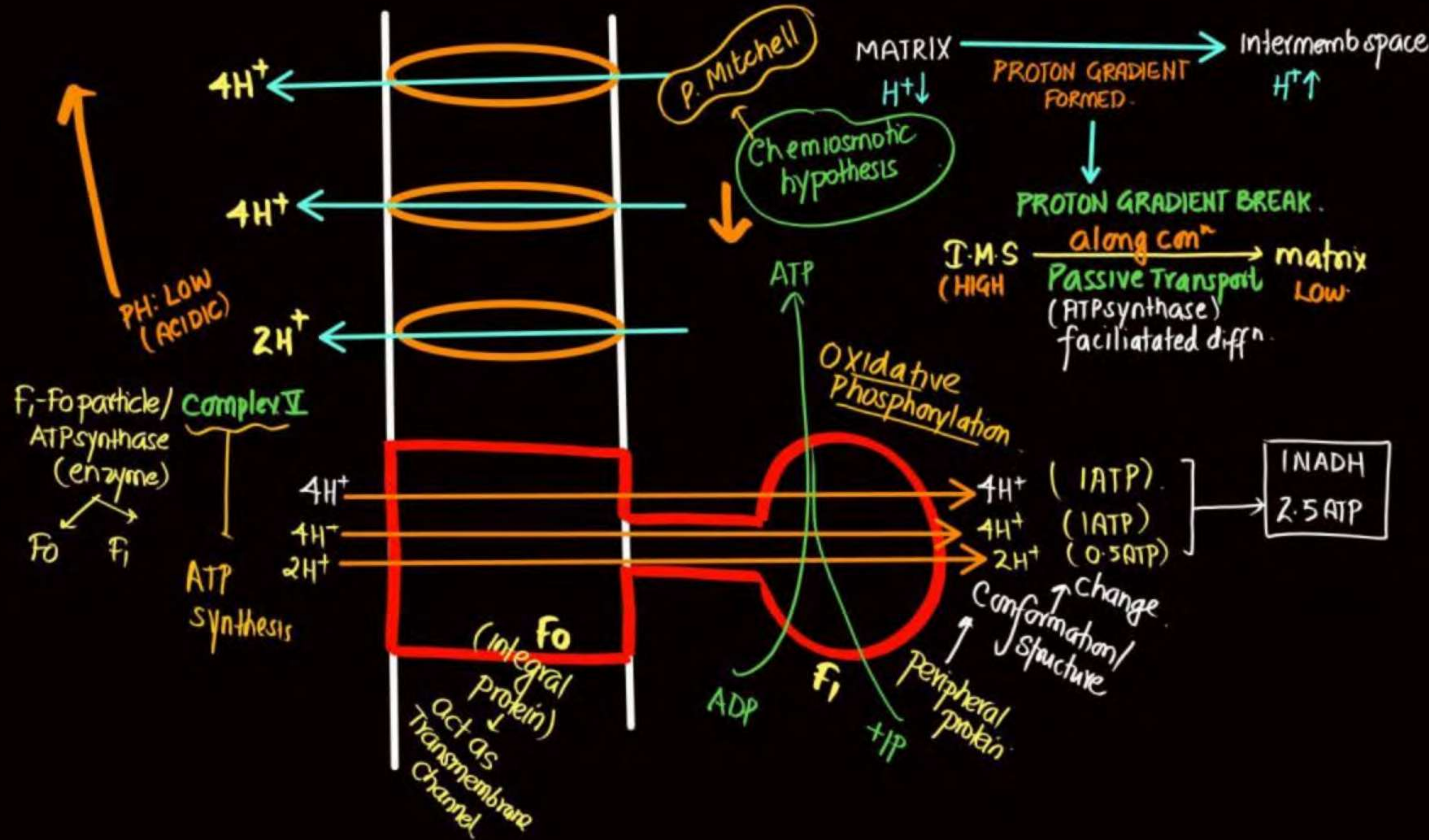
⇒ Cyt c (protein): Mobile e^- carrier
(outer surface of inner membrane).

⇒ Final acceptor of e^-: oxygen.

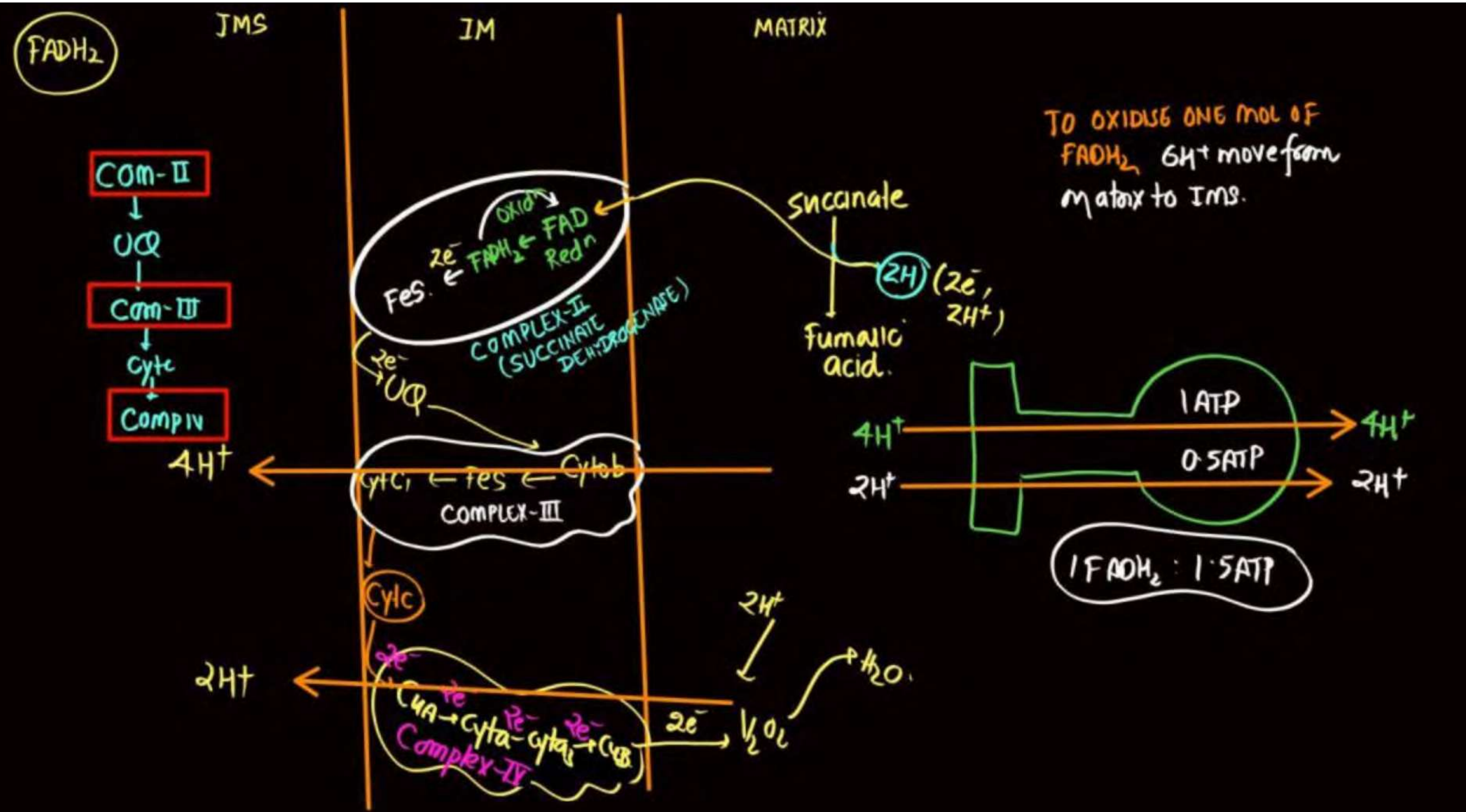
⇒ Complex IV / cytochrome C oxidase

⇒ No. of proton moves from matrix to intermembranous space to oxidise one molecule of NADH

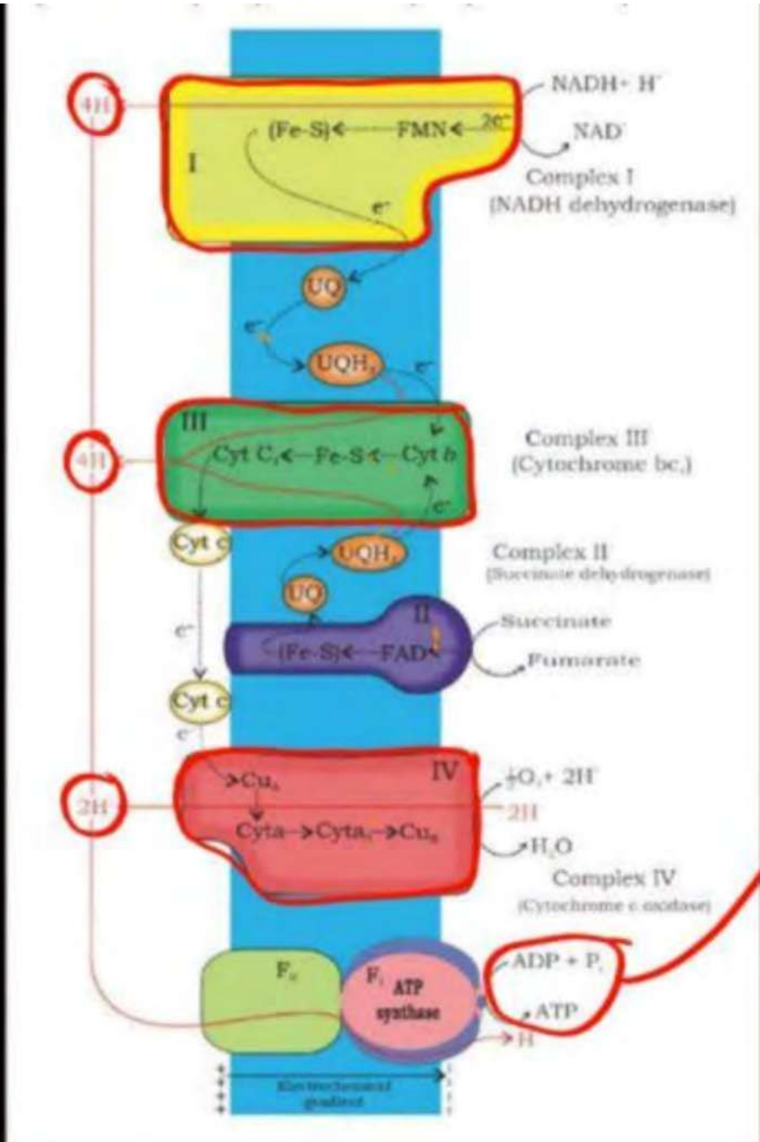
10



P. Mitchell
Chemiosmotic hypothesis
MATRIX
H+↓
PROTON GRADIENT FORMED
Intermemb space
H+↑
PROTON GRADIENT BREAK.
I·M·S (HIGH
along conn
Passive Transport
(ATPsynthase)
faciliatated diffn
matrix LOW
4H+
4H+
2H+
PH: LOW (ACIDIC)
ATP
Oxidative Phosphorylation
Fi-Fo particle/ ATPsynthase (enzyme)
Complex V
Fo Fi
ATP synthesis
4H+
4H+
2H+
4H+ (1ATP)
4H+ (1ATP)
2H+ (0.5ATP)
1NADH 2.5ATP
Change Conformation/ Structure
Fo (integral protein) act as Transmembrane Channel
ADP
Fi
+IP
Peripheral protein



FADH2
IMS
IM
MATRIX
Com-II
UQ
Com-III
Cytc
Comp IV
4H+
2H+
oxidn
2e-
Fes ← FADH2 ← FAD
Redn
COMPLEX-II (SUCCINATE DEHYDROGENASE)
succinate
2H (2e-, 2H+)
fumaric acid
2e-
UQ
Cytc1 ← Fes ← Cytob
COMPLEX-III
Cytc
2e-
CuA → Cyta → Cyta3 → CuB
Complex-IV
2e-
1/2 O2
2H+
H2O
TO OXIDISE ONE MOL OF FADH2 6H+ move from Matrix to Ims.
4H+
1 ATP
4H+
2H+
0.5ATP
2H+
1 FADH2 : 1.5ATP



Oxidative phosphorylation

Electrochemical gradient

FERMENTATION

- ★ INCOMPLETE OXID^{N} OF GLUCOSE IN ABSENSE OF O_2. (ANAEROBIC RESP^{N}).
- ★ O_2 absent, NADH ✓
- ★ BUT NADH do not enter ETC
- ★ ETC X. O_2 X.

★ NET GAIN OF ATP: 2

★ PARTIAL BREAKDOWN

ALCOHOLIC FERMENTATION

glucose

ANAEROBIC GLYCOLYSIS (O_2 absent)

$\rightarrow 4-2 \Rightarrow \boxed{2ATP}$

$2NAD^+ \rightarrow 2NADH$. (Red^{N}).

2 PYRUVATE

1st step: PYRUVATE DECARBOXYLASE, Mg^{+2}

$2\ CH_3CHO + 2CO_2$

2nd step: ALCOHOL DEHYDROGENASE, ZN^{+2}

2 NADH oxidised → $2NAD^+$

$2\ C_2H_5OH$

LACTATE FERM^n

★ NO PRODUCTION OF CO_2.

O_2 X
Anaerobic glycolysis

glucose
→ 4-2 → 2ATP
2NAD$^+$ → 2NADH

2 PYRUVATE
↓ 2NADH → 2NAD$^+$ (1 step)
2 Lactic acid

LACTATE DEHYDROGENASE

NET GAIN OF ATP: 2

NOTE:

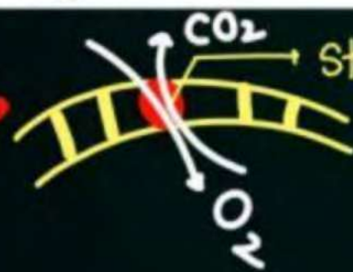
NADH — OXIDISED
- FAST → NAD$^+$ → Aerobic Respn.: O_2 ✓, ETC ✓
- SLOW → NAD$^+$ → Ferm^n: O_2 X, ETC X

ETC
→ NADH
↓ oxid^n.
NAD$^+$

12.1 Do Plants Breathe?

Well, the answer to this question is not quite so direct. Yes, plants require O_2 for respiration to occur and they also give out CO_2. Hence, plants have systems in place that ensure the availability of O_2. Plants, unlike animals, (LUNGS) have no specialised organs for gaseous exchange but they have stomata and lenticels for this purpose.

Leaf → epidermis → (Respiration).

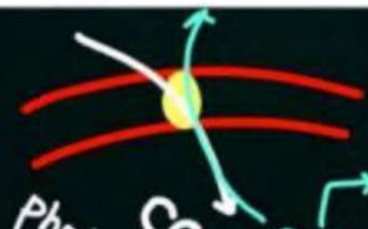


Stomata (main Region!).

Openings: stem. (present)

There are several reasons why plants can get along without respiratory organs. First, each plant part takes care of its own gas-exchange needs. There is very little transport of gases from one plant part to another. Second, plants do not present great demands for gas exchange. Roots, stems and leaves respire at rates far lower than animals do. Only during photosynthesis are large volumes of gases exchanged and, each leaf is well adapted to take care of its own needs during these periods.

each leaf (part)
↓
Stomata present

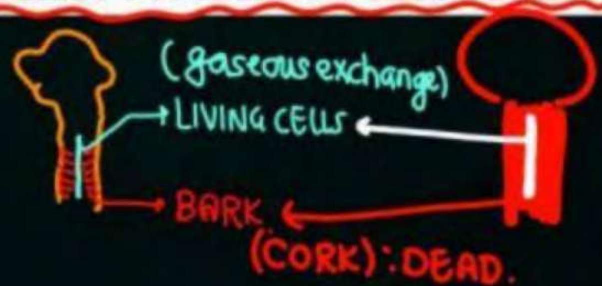


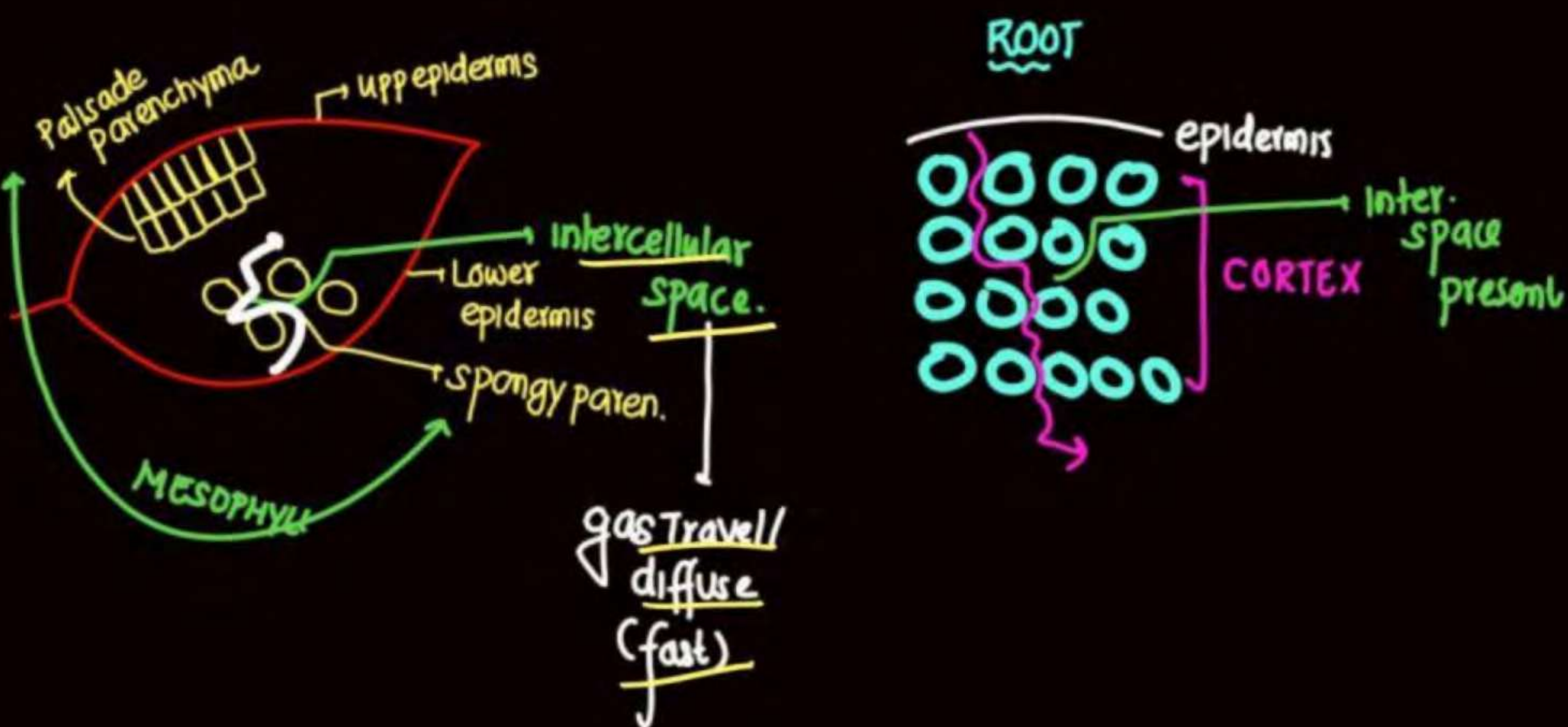
When cells photosynthesise, availability of O_2 is not a problem in these cells since O_2 is released within the cell. Third, the distance that gases must diffuse even in large, bulky plants is not great. Each living cell in a plant is located quite close to the surface of the plant. 'This is true for leaves', you may ask, 'but what about thick, woody stems and roots?' In stems, the 'living' cells are organised in thin layers inside and beneath the bark. They also have openings called lenticels. The cells in the interior are dead and provide only mechanical support. Thus, most cells of a plant have at least a part of their surface in contact with air. This is also facilitated by the loose packing of parenchyma cells in leaves, stems and roots, which provide an interconnected network of air spaces.

most of cell in TREE (DEAD).

Stem (openings) gaseous exchange.

mesophyll cell.




Palisade parenchyma
upp epidermis
intercellular space.
Lower epidermis
spongy paren.
MESOPHYLL
gas Travell/ diffuse (fast)
ROOT
epidermis
inter. space present
CORTEX

The complete combustion of glucose, which produces CO_2 and H_2O as end products, yields energy most of which is given out as heat.

$$C_6H_{12}O_6 + 6O_2 \longrightarrow 6CO_2 + 6H_2O + \text{Energy}$$

38 ATP

Heat loss.

If this energy is to be useful to the cell, it should be able to utilise it to synthesise other molecules that the cell requires. The strategy that the plant cell uses is to catabolise the glucose molecule in such a way that not all the liberated energy goes out as heat. The key is to oxidise glucose not in one step but in several small steps enabling some steps to be just large enough such that the energy released can be coupled to ATP synthesis. How this is done is, essentially, the story of respiration.

During the process of respiration, oxygen is utilised, and carbon dioxide, water and energy are released as products. The combustion reaction requires oxygen. But some cells live where oxygen may or may not be available. *Can you think of such situations (and organisms) where O_2 is not available?* There are sufficient reasons to believe that the first cells on this planet lived in an atmosphere that lacked oxygen. Even among present-day living organisms, we know of several that are adapted to anaerobic conditions. (yeast) Some of these organisms are $\boxed{\text{facultative anaerobes}}$, while in others the requirement for anaerobic condition is obligate. In any case, all living organisms retain the enzymatic machinery to partially oxidise glucose without the help of oxygen. This breakdown of glucose to pyruvic acid is called **glycolysis.**

fermentation
Bactena,
yeast.

NORMALLY LIVE IN PRESENSE OF OXYGEN BUT IF O_2 IS not available the they can live as anaerobe

Obligate anaerobe
(only in absense of O_2: SURVIVE)

$CO_2 + H_2S \xrightarrow[\text{Non-oxygenic Photosynthesis}]{\text{Bacteria}}$ O_2 was not present

12.3 FERMENTATION

alcoholic fermN.

In fermentation, say by yeast, the incomplete oxidation of glucose is achieved under anaerobic conditions by sets of reactions where pyruvic acid is converted to CO_2 and ethanol. The enzymes, pyruvic acid decarboxylase and alcohol dehydrogenase catalyse these reactions. Other organisms like some bacteria produce lactic acid from pyruvic acid. The steps involved are shown in Figure 12.2. In animal cells also, like muscles during exercise, when oxygen is inadequate for cellular respiration pyruvic acid is reduced to lactic acid by lactate dehydrogenase. The reducing agent is $NADH+H^+$ which is reoxidised to $\boxed{NAD^+}$ in both the processes.

LACTATE FERMN.

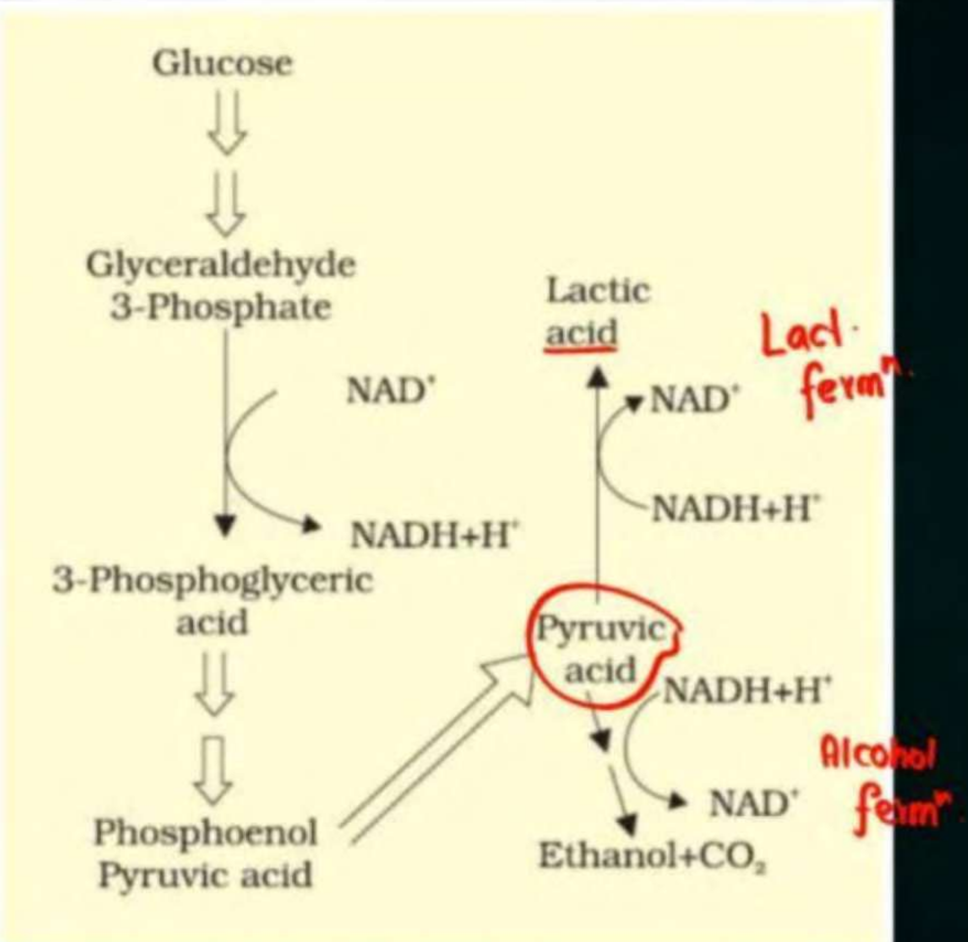


Figure 12.2 Major pathways of anaerobic respiration

In both lactic acid and alcohol fermentation not much energy is released; less than seven per cent of the energy in glucose is released and not all of it is trapped as high energy bonds of ATP. Also, the processes are hazardous – either acid or alcohol is produced. What is the (2) net ATPs that is synthesised (calculate how many ATP are synthesised and deduct the number of ATP utilised during glycolysis) when one molecule of glucose is fermented to alcohol or lactic acid?

2 ATP

4
\-
2

$\rightarrow$ 2 ATP

Yeasts poison themselves to death when the concentration of alcohol reaches about 13 per cent. ***What then would be the maximum concentration of alcohol in beverages that are naturally fermented?*** How do you think alcoholic beverages of alcohol content greater than this concentration are obtained?

13%

distillation process.

What then is the process by which organisms can carry out complete oxidation of glucose and extract the energy stored to synthesise a larger number of ATP molecules needed for cellular metabolism? In eukaryotes these steps take place within the mitochondria and this requires O_2. **Aerobic respiration** is the process that leads to a complete oxidation of organic substances in the presence of oxygen, and releases CO_2, water and a large amount of energy present in the substrate. This type of respiration is most common in higher organisms. We will look at these processes in the next section.

Aerobic Resp^n.
LR, KC, ETC.

glucose

$\boxed{686 \text{ Kcalorie}}$

$$\text{glucose} + 6O_2 \longrightarrow 6CO_2 + 6H_2O + \boxed{686 \text{ Kcal}}$$

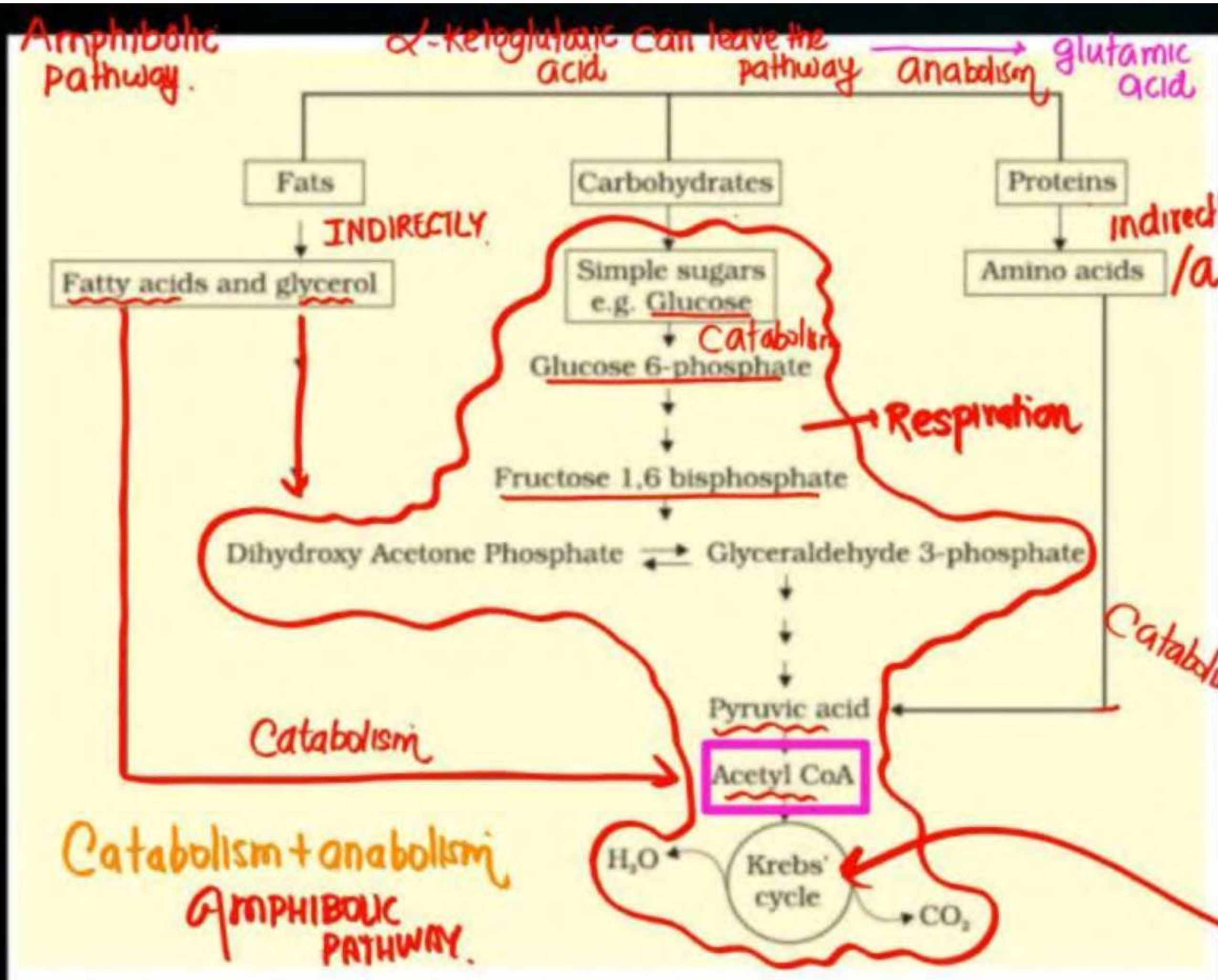


Figure 12.6 Interrelationship among metabolic pathways showing respiration mediated breakdown of different organic molecules to CO_2 and H_2O

⇒ fatty acid can enter in Resp^n

⇒ Acetyl CoA leave Respiration

↓ anabolism

Fatty acid

⇒ SUBSTRATE CAN ENTER / EXIT THE RESP^N.

PROTEIN

↓ PROTEASE

amino acid (glutamic acid)

deamination

$-NH_2$

α-ketoglutaric acid

enter into Respiratory pathway. (Krebcycle)

12.7 Respiratory Quotient

Let us now look at another aspect of respiration. As you know, during aerobic respiration, O_2 is consumed and CO_2 is released. The ratio of the volume of CO_2 evolved to the volume of O_2 consumed in respiration is called the **respiratory quotient** (RQ) or respiratory ratio.

$$RQ = \frac{\text{volume of } CO_2 \text{ evolved}}{\text{volume of } O_2 \text{ consumed}}$$

The respiratory quotient depends upon the type of respiratory substrate used during respiration.

When carbohydrates are used as substrate and are completely oxidised, the RQ will be 1, because equal amounts of CO_2 and O_2 are evolved and consumed, respectively, as shown in the equation below :

$$C_6H_{12}O_6 + 6O_2 \longrightarrow 6CO_2 + 6H_2O + \text{Energy} \quad 686\,\text{kcal}$$

glucose

carbohydrate

$$RQ = \frac{6CO_2}{6O_2} = 1.0$$

$$C \longrightarrow F \longrightarrow P$$

(common Respiratory Substrate)

When fats are used in respiration, the RQ is less than 1. Calculations for a fatty acid, tripalmitin, if used as a substrate is shown:

$$\underset{\text{Tripalmitin}}{2(C_{51}H_{98}O_6)} + 145O_2 \longrightarrow 102CO_2 + 98H_2O + \text{energy}$$

$$RQ = \frac{102CO_2}{145O_2} = 0.7$$

$2C_2H_5OH + 2CO_2$

Anaerobic Resp^n. $\Rightarrow \frac{2CO_2}{0} = \infty$

When proteins are respiratory substrates the ratio would be about 0.9.

Organic acid : More than 1

What is important to recognise is that in living organisms respiratory substrates are often more than one; pure proteins or fats are never used as respiratory substrates.

Perianth

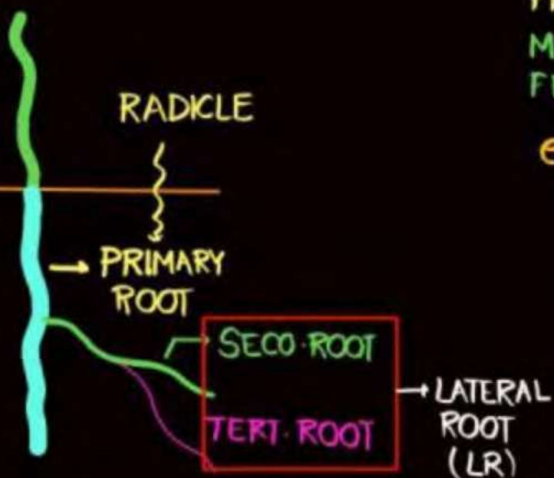
Tepal

6

SOLITARY
FLOWER
(inflorescence)

ROOT

TAP ROOT



⇒ PR + $\boxed{SR + TR}$ → LR

PR → MAIN ROOT (LONG LIVED)

most of DICOT (MUSTARD)

FIBROUS ROOT

PRIMAR ROOT : SHORT LIVED.

MANY FINE ROOT ARISE FROM BASE OF STEM.

eg : wheat (monocot)

ADVENTITIOUS ROOT

ARISE FROM ANYWHERE EXCEPT RADICLE

eg : GRASS (M), MONSTERA (M), BANYAN (D) TREE → ARISE (NODE)

ROOT CHANGE : STRUCTURE, SHAPE. PERFORM OTHER FUN^{N}.

⇒ **SUPPORT**

eg : PROP ROOT — vertical Hanging advent. ROOT. Structure arise from node of Branch, provide support to main stem/TRUNK.

eg : Banyan

eg : STILT ROOT — arise from lower Node of stem & enter into soil.

eg : sugarcane, maize.

⇒ **STORAGE ROOT**

⇒ **RESPIRATORY ROOT** — RHIZOPHORA

NEGATIVELY GEOTROPHIC, COMES UPWARD, TO GET O_2 FROM ATMOSPHERE (Pneumatophore)

Function of Root

- Absorption of water and mineral from soil (main)
- Anchorage to plant parts. (STORAGE ROOT) TAP ROOT
- Stored food material
  - CARROT, TURNIP : FOOD STORED
  - SWEET POTATO : ADVEN. ROOT
- Synthesis of plant growth regulators. (AUXIN ETC)

ADVENTITIOUS ROOT

Monocot

Monocot

Dicot

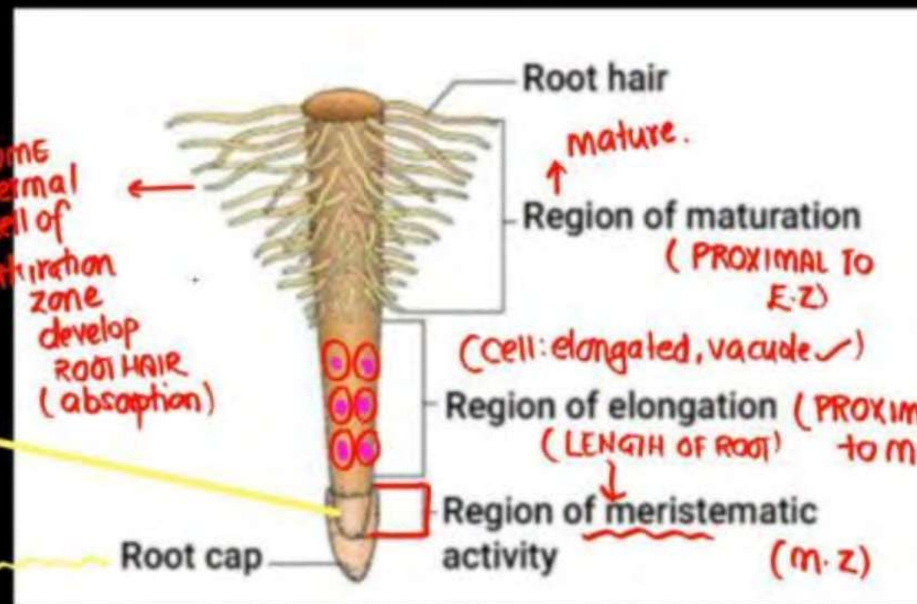
Origin __________

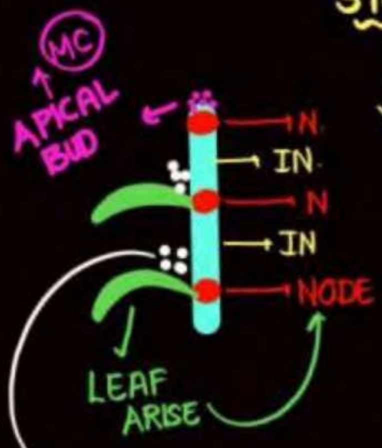
Region of Root

⇒ Cells
- actively divide
- small (vacuole X)
- THIN WALL
- dense protoplasm

⇒ Thimble like protect soft ROOT TIP / APEX.
CREATE EASY PASSAGE FOR ROOT INTO SOIL

some epidermal cell of maturation zone develop ROOT HAIR (absorption)





AXILLARY BUD → FORM BRANCH
(AXIL REGION) MC

MC: MERISTEMATIC CELL.

STEM
- → Plumule
- → aescending part, above soilsurface

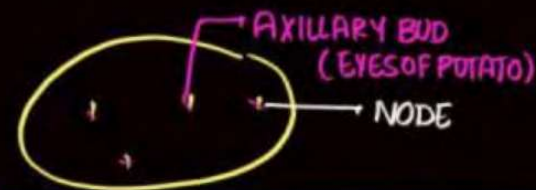
- young → green
- old → (BROWN / WOODY).

modif^n of stem

① Phylloclade
(STEM: GREEN, PHOTOSYNTHESIS),
ARID REGION
(WATER LESS)
LEAVES → SPINES
MINIMISE H_2O LOSS
- Flat → Opuntia
- cylindrical → Euphorbia

② STEM TENDRIL
$\boxed{\text{AXILLARY BUD}}$
↓
MODIFY
↓
THN, SPIRALY COILED STRUCT.
(CLIMBING, SUPPORT)
eg: GOURDS (Cucumber, Pumpkin, Watermelon) & Grapewine

③ STEM THORN
AXILLARY BUD → MODIFY INTO HARD, WOODY, POINTED
PROTECTION (BROWSING ANIMAL)



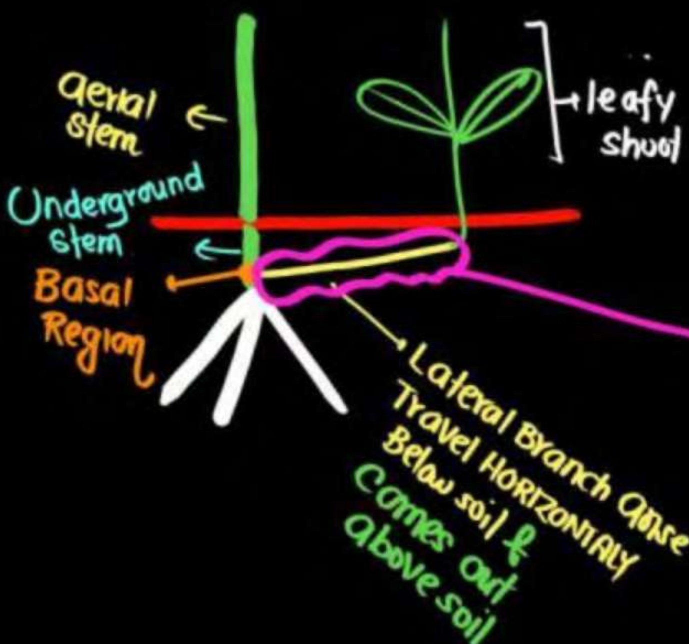
UNDERGROUND STEM.

(TUBER) POTATO,
GINGER, TURMERIC → Rhizome (Stem HORIZONTAL)
COLOCASIA, Amorphophallus → CORM. (STEM VERTICAL)
→ STORE FOOD.
Use during Unfavourable Condn. (Perennation)

vegetative PROPOGATION/ REPN

Sucker

eg: Chrysanthemum
: Pineapple
Banana



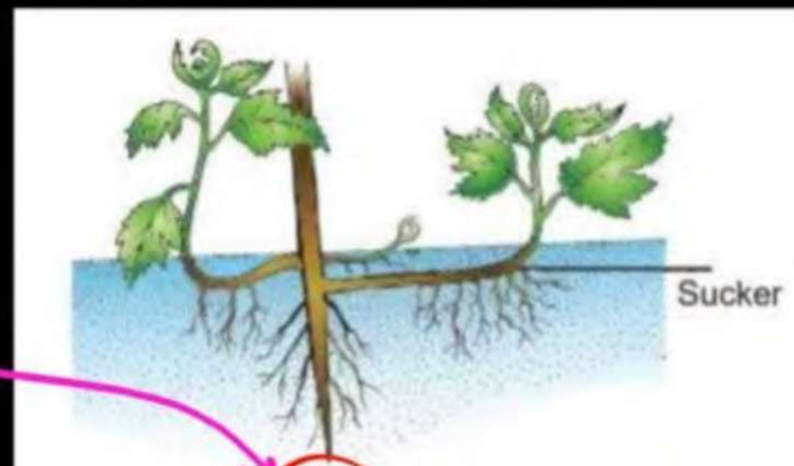
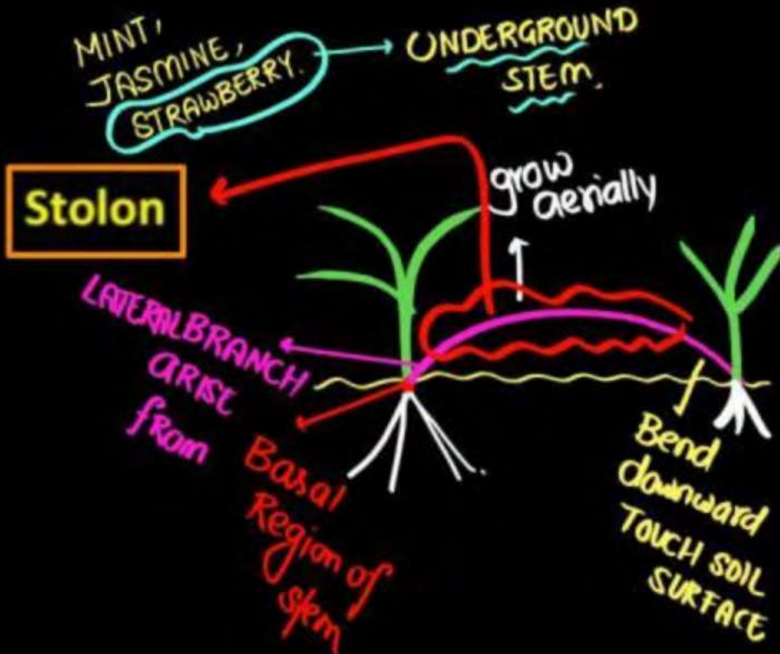
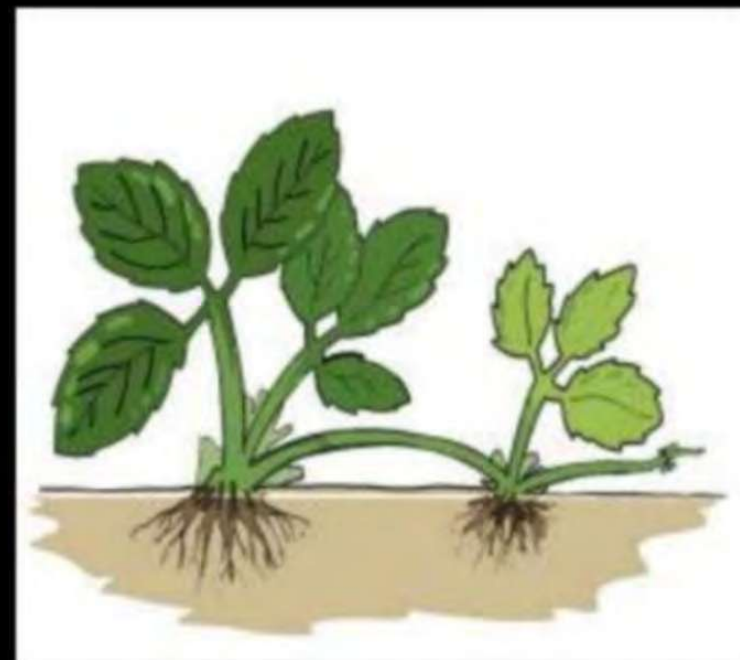
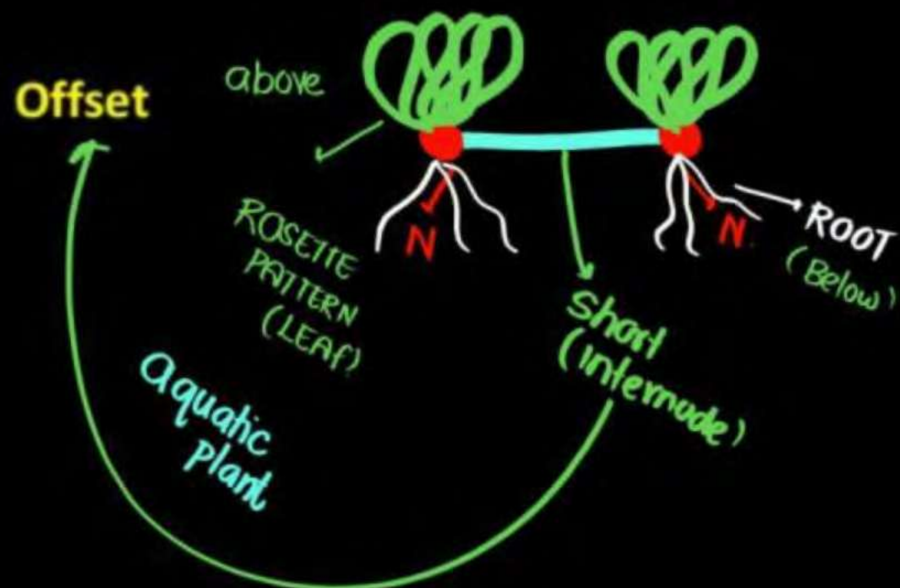


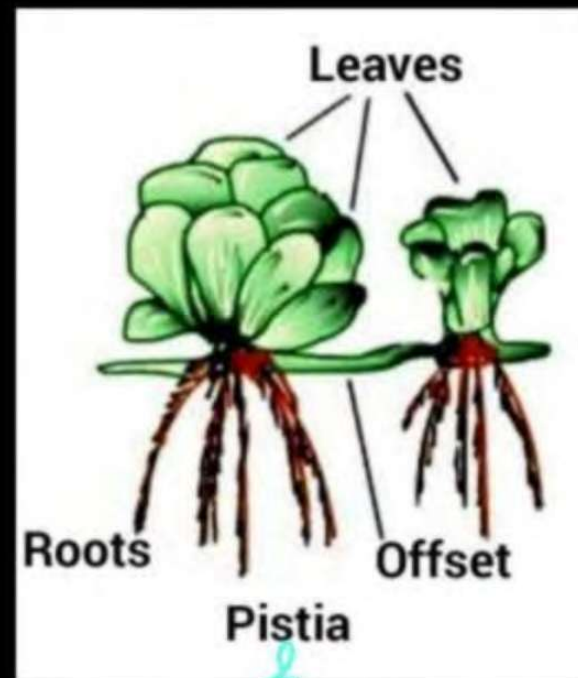
Figure 4b: Sucker - *Chrysanthemum*


MINT,
JASMINE,
STRAWBERRY.
UNDERGROUND
STEM.
Stolon
grow
aerially
LATERAL BRANCH
arise
from
Basal
Region of
stem
Bend
downward
TOUCH SOIL
SURFACE



niche



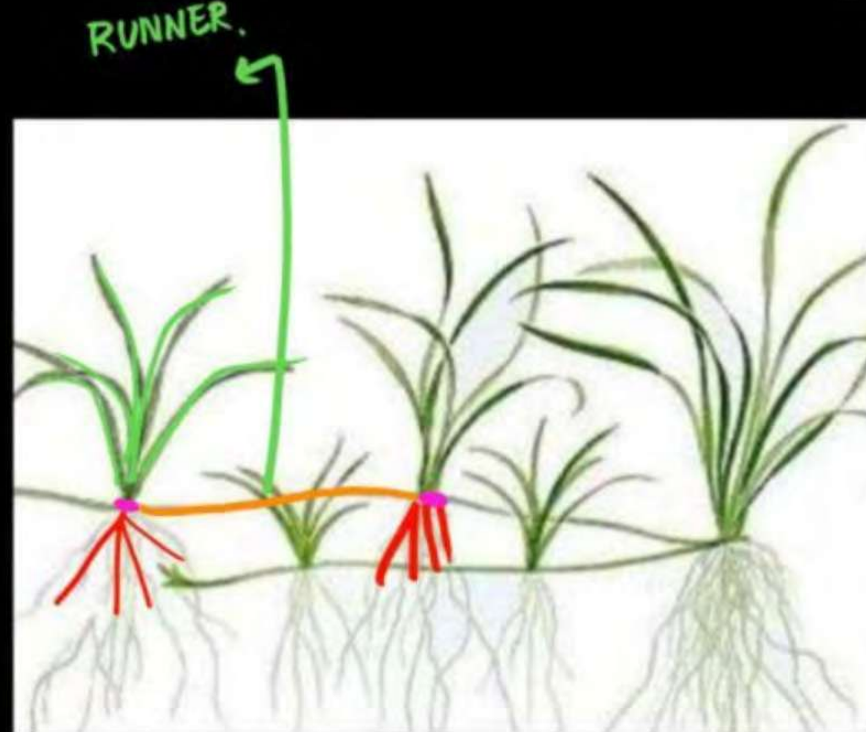


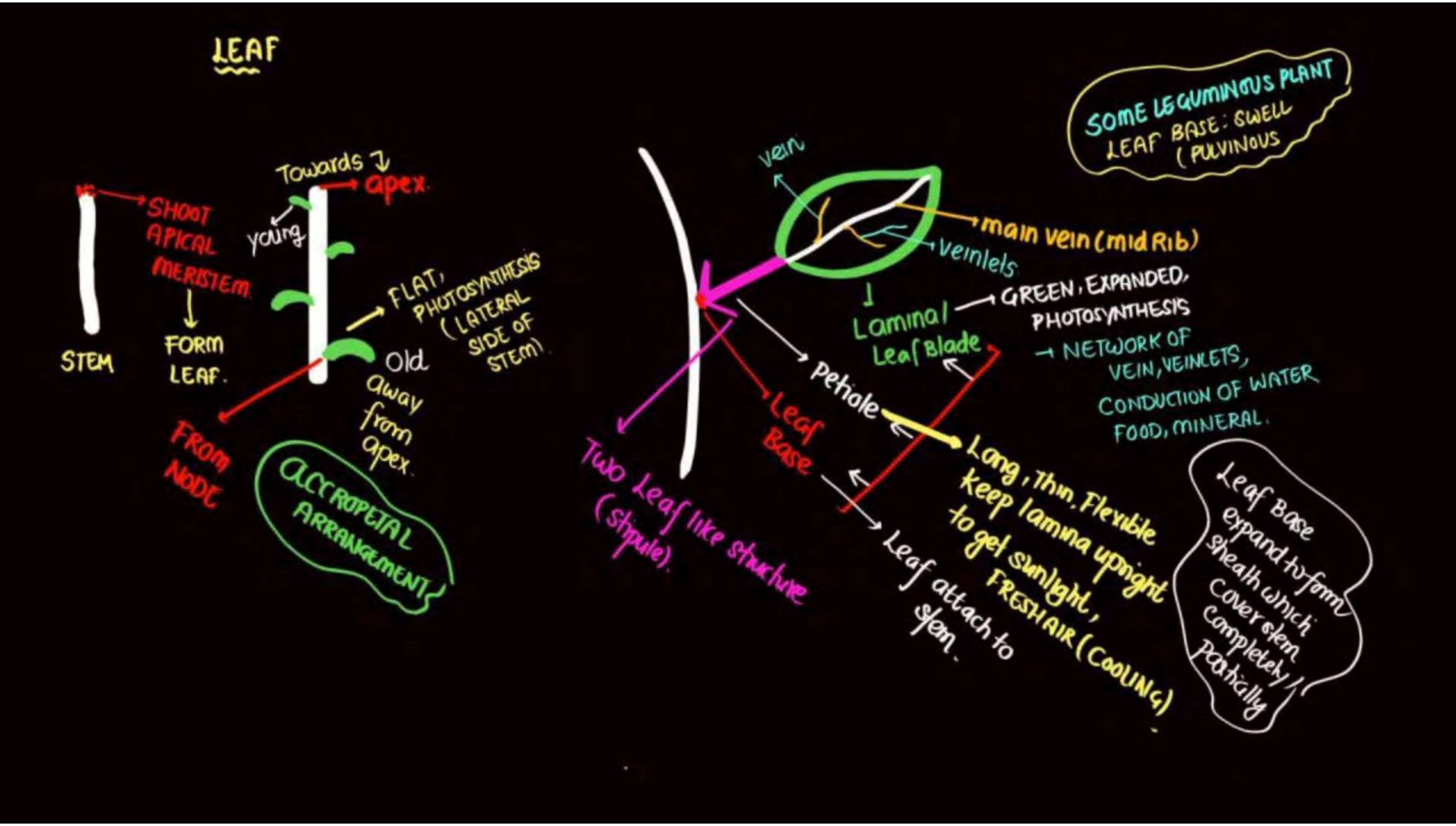
&

Eichhornia

Runner : LONG INTERNODES

GRASS, OXALIS




LEAF
STEM
SHOOT APICAL MERISTEM
FORM LEAF.
FROM NODE
Towards apex.
young
Old
away from apex.
FLAT, PHOTOSYNTHESIS (LATERAL SIDE OF STEM)
ACCROPETAL ARRANGEMENT
vein
main vein (mid Rib)
veinlets
Lamina/ Leaf Blade
GREEN, EXPANDED, PHOTOSYNTHESIS
NETWORK OF VEIN, VEINLETS, CONDUCTION OF WATER FOOD, MINERAL.
SOME LEGUMINOUS PLANT LEAF BASE: SWELL (PULVINOUS
Petiole
Long, Thin, Flexible Keep lamina upright to get sunlight, FRESH AIR (COOLING)
Leaf Base
Leaf attach to stem.
Two Leaf like structure (stipule).
Leaf Base expand to form sheath which cover stem completely/ partially

Venation

⇒ arrangement of vein, veinlets in lamina/leaf.

Reticulate

⇒ Vein, Veinlets FORM NETWORK

most of dicot.

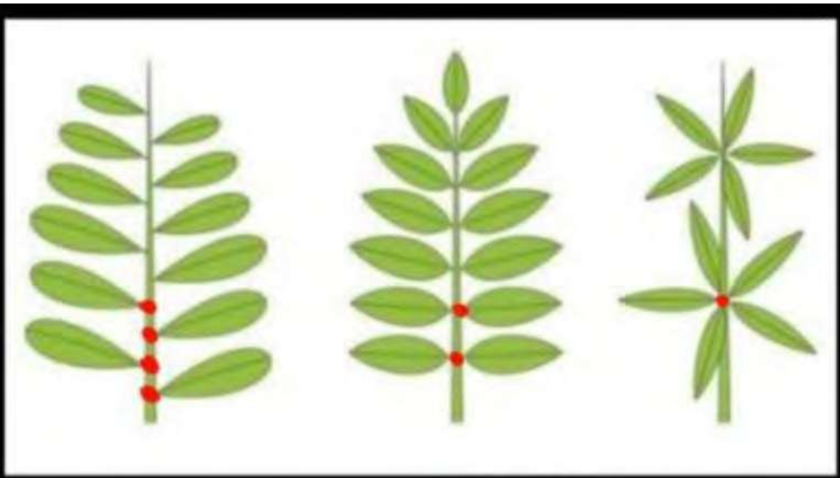
parallel

veins parallel to each other

most of monocot.

Phyllotaxy

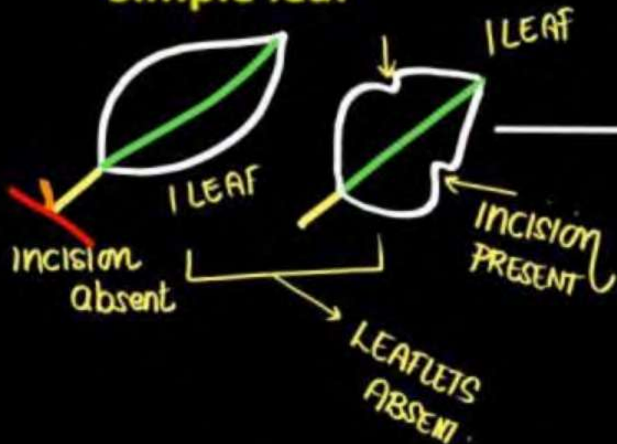
Definition arrangement of leaf on plant.



Alternate	Opposite	Whorled
At one node One leaf. alternate order.	Two leaf at one node	group more than Two leaf
Example : Sunflower	Example : Guava	Example : Alstonia.
Mustard	Calotropis	
China Rose		

Types of Leaf

Simple leaf

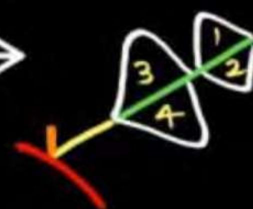


Leaf is entire

Generally incision ___absent___

If ___incision___ present, it doesn't touch the ___mid RIB___

Compound leaf

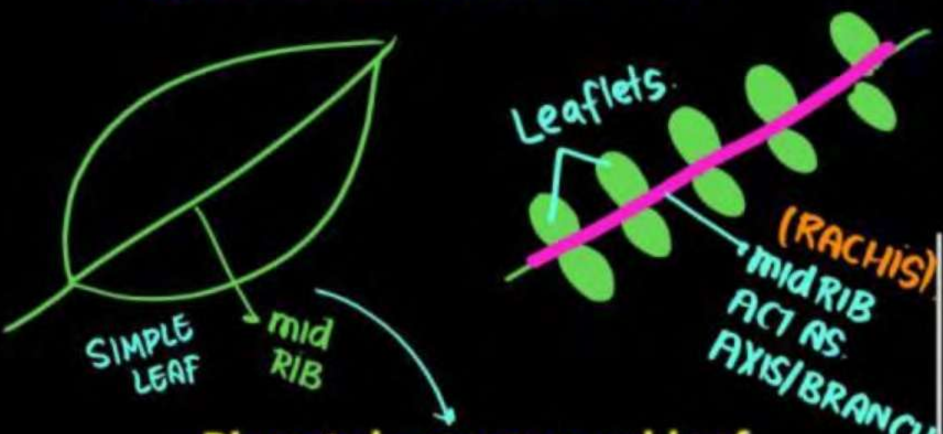


AXILLARY BUD: PETIOLE OF LEAF

Incision ___✓___ & it touches ___mid RIB.___

So leaf divided into ___4 leaflets___

Types of compound leaf

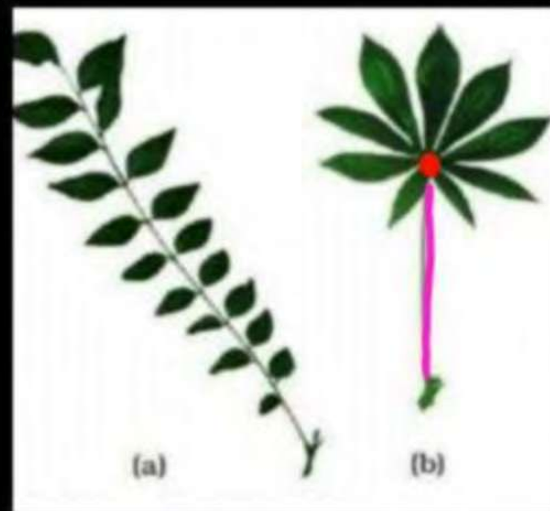


Pinnately compound leaf

No. of leaf lets present on ___Rachis___

which represent the ___mid RIB___

Example : ___Neem.___



Palmately compound leaf

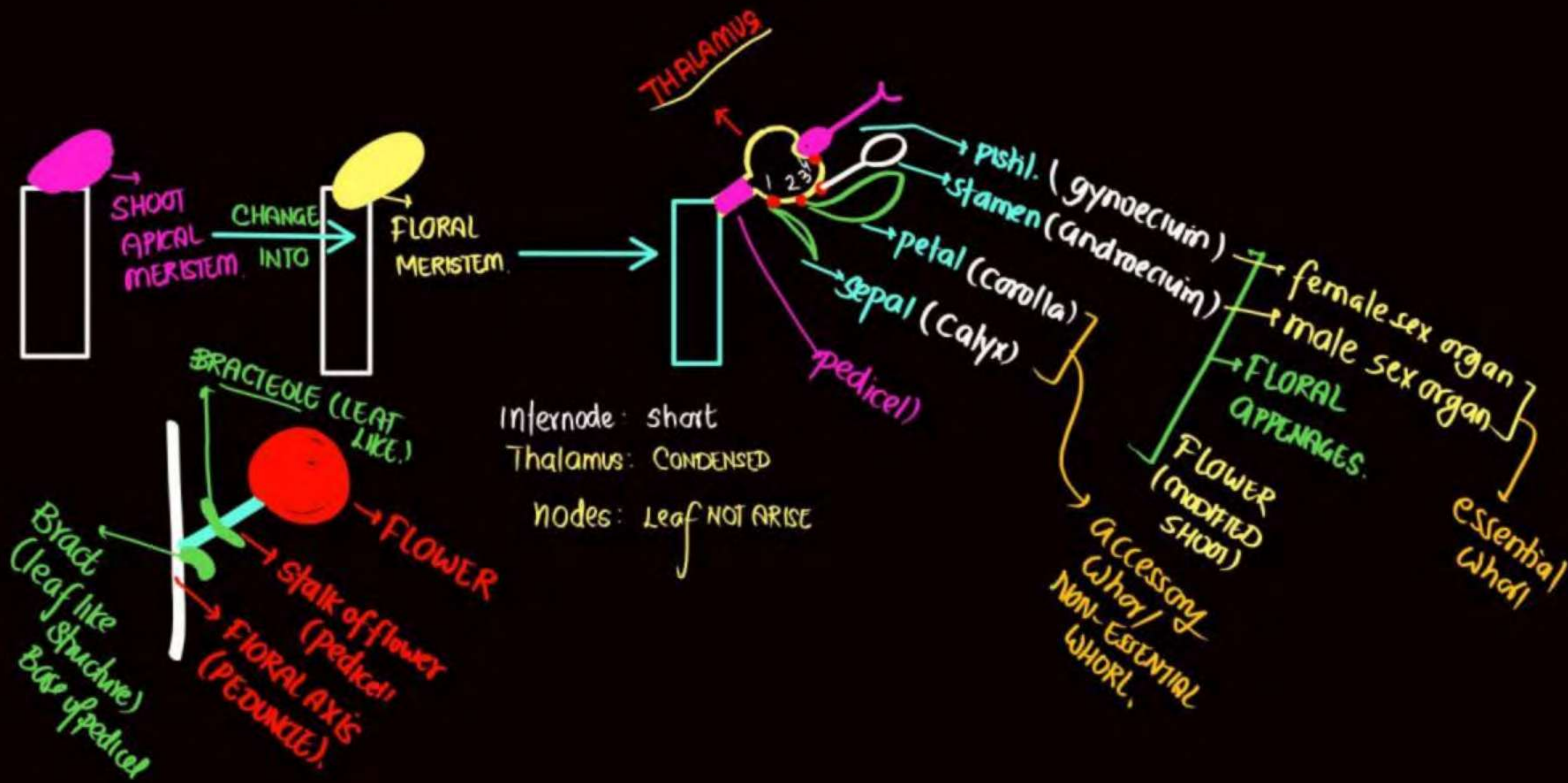
Leaflet present at ___Tip of petiole.___

Example ___Silk. Cotton___

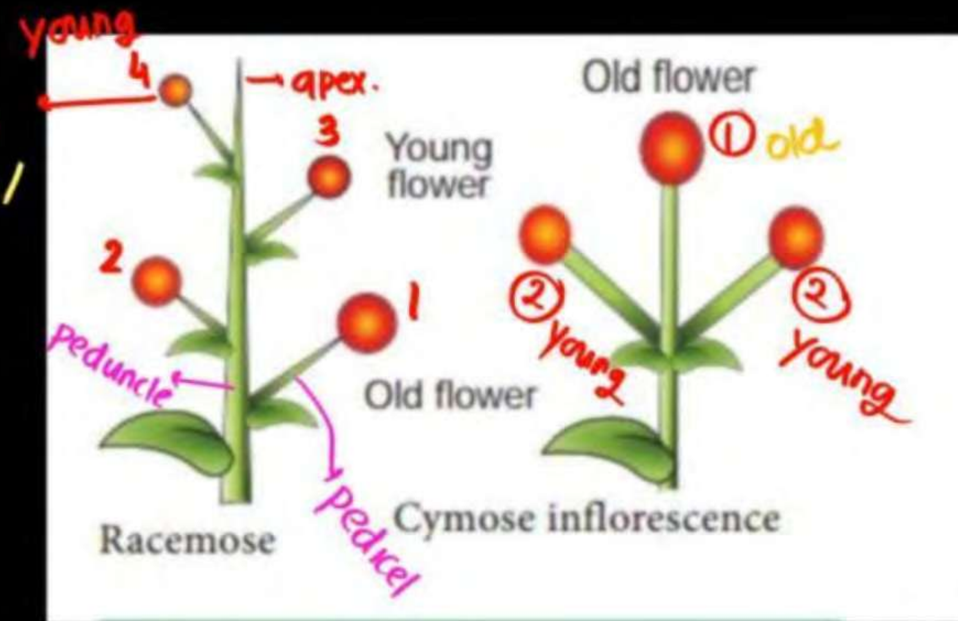
mod^n of leaf

- Leaf Tendril
  - ↓ spirally coiled, support
  - pea
- Leaf spines
  - ↓ spines
  - Cactus
- Leaf food
  - eg onion garlic.
- Phyllode
  - Petiole: expand, green, photosynthesis
  - Leaf/leaflets: short lived
  - eg: Australian acacia
- Insectivores plant
  - Pitcher plant (Nepenthes
  - Venus Fly Trap. (Dionea)
  - TRAP INSECT ↓ KILL.

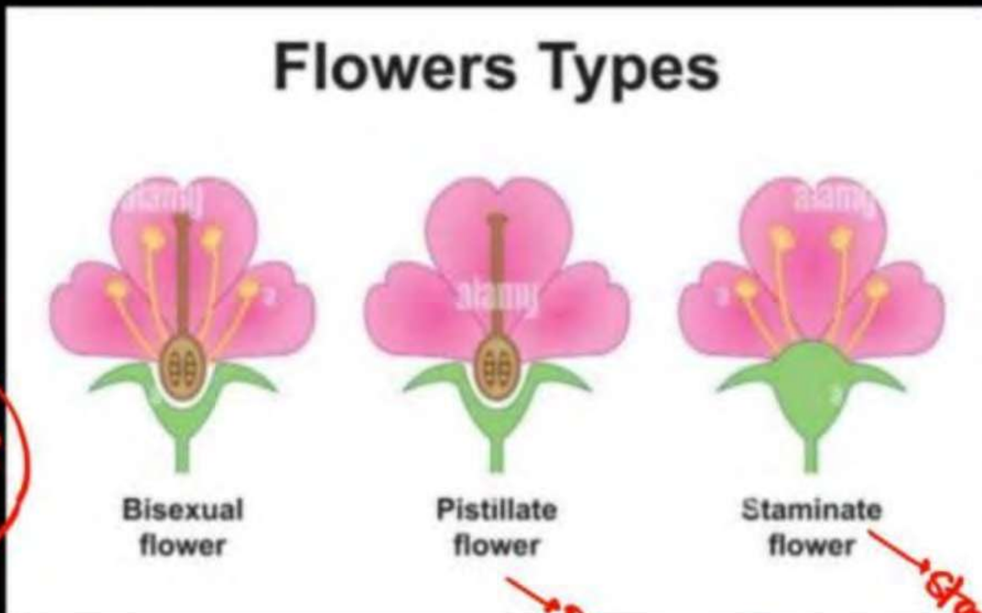
INFLORESCENCE : arrangement of flower on floral axis / peduncle.



	Racemose	Cymose
Growth	of peduncle continuous/ unlimited. /indefinite	peduncle Terminate into flower, Limited/discont^{n}/ definite.
Arrangement of flower	accropetal.	
Old flower	away from apex.	Towards apex
Young flower	Towards apex	away from apex.
Eg	mustard.	Solanum



Flower Types



stament
pistil

→ pistil

→ stamen

Unisexual.

Tetramerous : 4S, 4P

Pentamerous : 5S, 5P

Trimerous: 3S, 3P
(6 TEPALS)

Perianth:

Calyx & corolla
NOT DIFFERENTIATED.

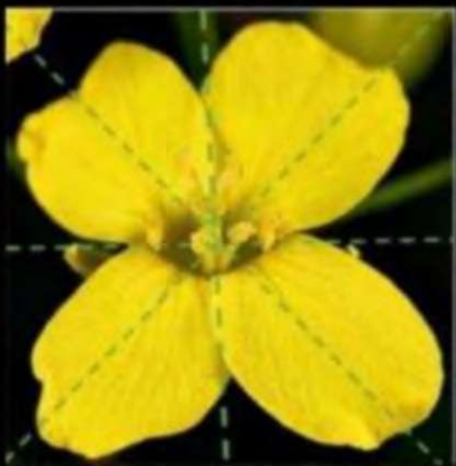
Each UNIT: TEPAL.

6 Tepals → outer: 3
→ inner: 3

arrange in two whorl.

Symmetry of flower

Actinomorphic Flower (Radial symmetry) : Flowers divided into Two equal parts through many Planes. passing Through Centre



Mustard

Datura

Chili

Symmetry of flower

Zygomorphic flower (bilateral symmetry)

=equal part, through one plane

P ea

G ulmohur

B ean

C assia

Symmetry of flower

Asymmetric (irregular) : Not in equal part

Canna

Trimerous, tetramerous, pentamerous flower

Figure 4.17: (a)
Trimerous

Figure 4.17: (b)
Tetramerous

Figure 4.17: (c)
Pentamerous

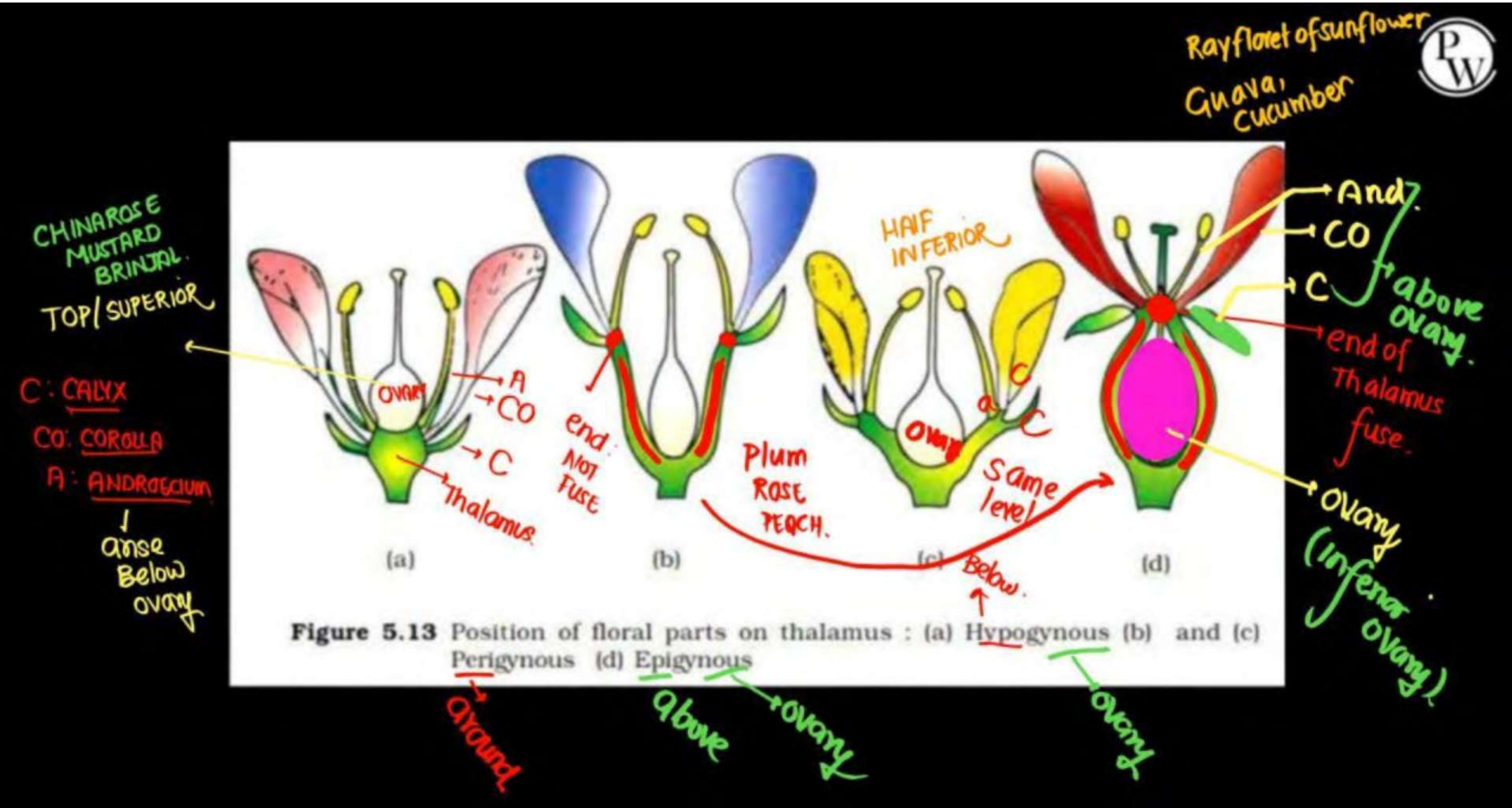
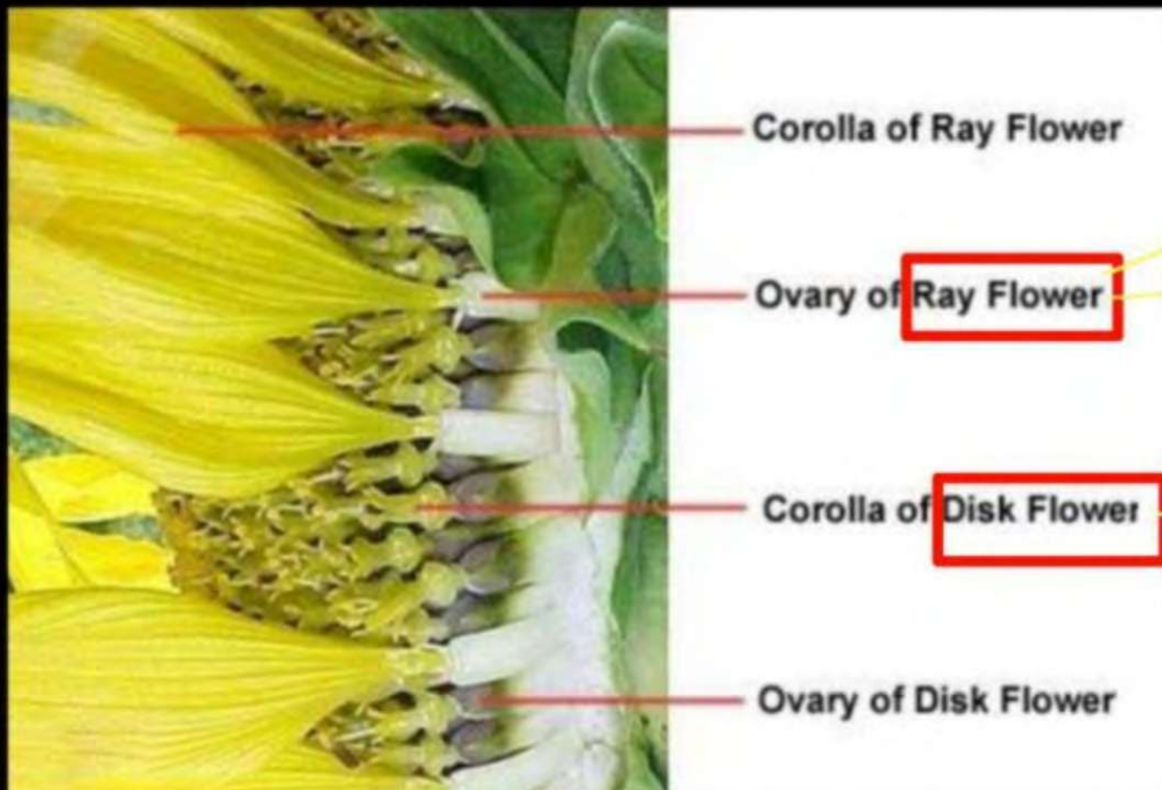


Figure 5.13 Position of floral parts on thalamus : (a) Hypogynous (b) and (c) Perigynous (d) Epigynous

around
above
ovary
ovary



Ray floret → Zygomorphic

Periphery

Disc Floret → Actino-morphic

Centre

: UNIT: SEPAL.

Calyx : Outermost whorl. → PROTECT FLOWER IN BUDSTAGE.

USUALLY GREEN.

Gamosepalous

(K)

K(5)

Sepals fused

Polysepalous

K

K 5

Sepals free.

2^{nd} whorl. ← **Corolla** : Large, BRIGHTLY COLOURED, ATTRACT INSECT (POLLINATION).

Gamopetalous

(C)

$C_{(5)}$

Petals fused

Polypetalous

C

C_5.

Petals free.

Shape of corolla

Tubular

Bell

Funnel

Wheel

Aestivation ⇒ arrang of sepals (in same whorl)
of petals (" " ")

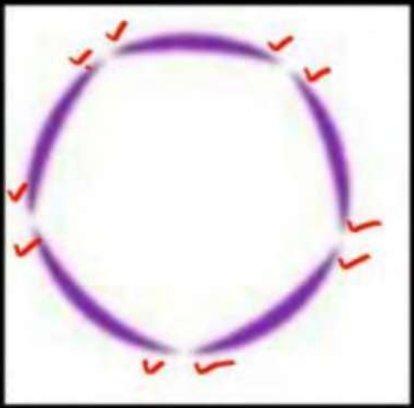
Definition ______________________

1. Valvate

Sepals in a whorl/petals in a whorl almost Touch eachother

but no overlapping

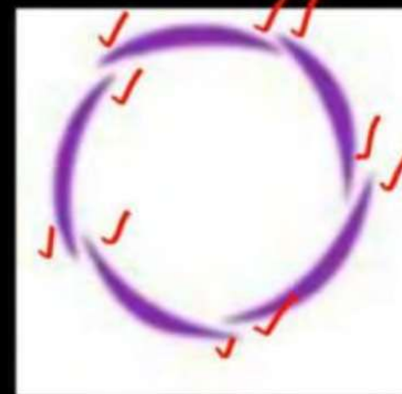
Example Calotropis



2. Twisted

If one margin of member overlap with. margin of other memb.

But in particular. direction



Example

China Rose

Lady finger

Cotton.

3. Imbricate

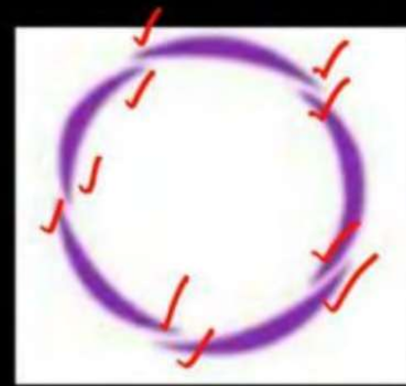
If one margin of member overlap with other

But not in particular direction

Example

C Cassia

G Gulmohur



Gulmohur & Cassia

4. Vaxillary/papilionaceous

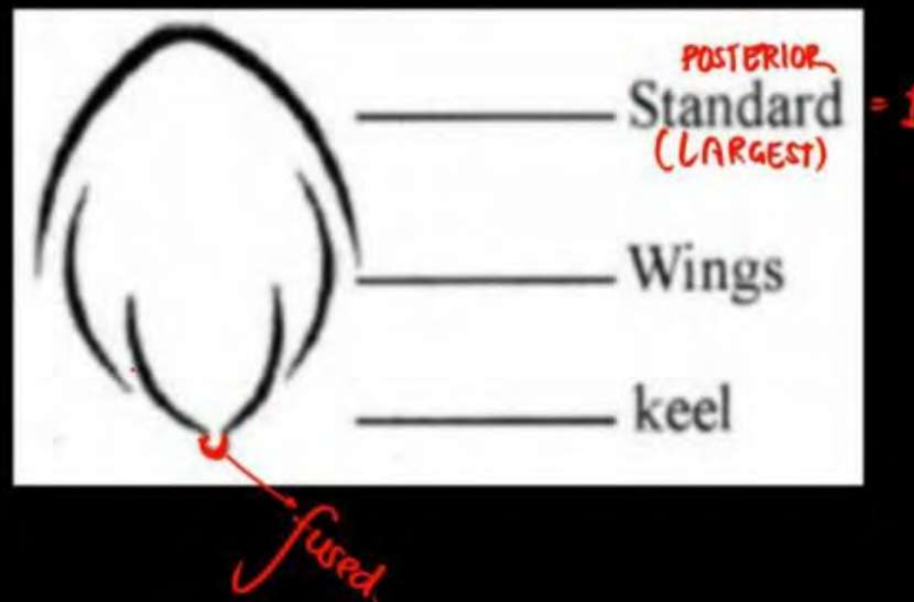
Example

Posterior petal Standard : 1

Lateral petal wings : 2

Anterior petal keel 2 (Smallest)

eg : pea,
· Bean



$C_{1+2+(2)}$

Androecium : 3rd whorl

Whorl 3rd.

Member Stamen.

Stamen parts anther & filament

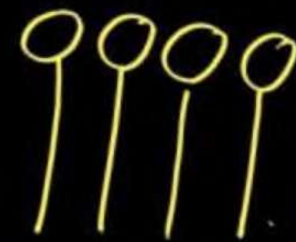
Each anther Two lobe

Each lobe has Two pollen sac

In pollen sac Pollen mother cell present which produced pollen grain

Sterile stamen Staminode

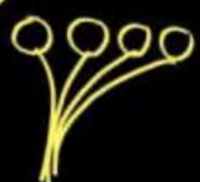
If stamen are free polyandrous.



Androecium

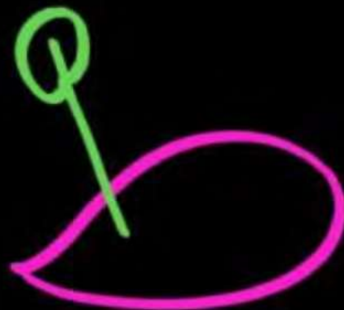
If stamen are united with the help of filament Called adelphous.

Types of Adelphous (Cohesion) $\boxed{S+S}$ → same लोग.

Monoadelphous	Diadelphous	Polyadelphous
one BUNDLE	(9) (1)	
	 TWO BUNDLE	
	$A_{(9)+1}$ ← Fused (Filament)	
Eg. China Rose	Eg. Pea	Eg. Citrus.

(DIFFERENT लोग).

Adhesion of stamen



1. Epipetalous : STAMEN + PETAL

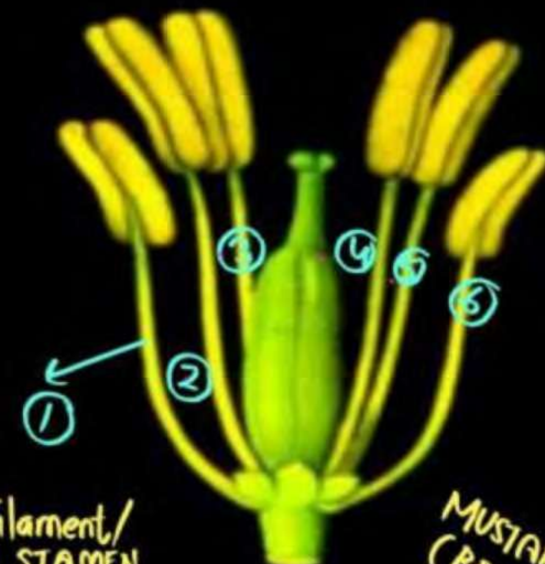
Example : Solanaceae
Tomato, BRINJAL

2. Epiphyllous/epitepalous

Example : Stamen + Perianth/Tepal
eg: Liliaceae

Variation in length of filament

Example Salvia and mustard



outer
1 & 6 : short filament/ STAMEN.

2 3 4 5 : Long filament/ Stamen.

inner → Tetradynamous

MUSTARD (BRASSICACEAE)

Gynoecium 4th whorl → unit: pistil.

Apocarpous FREE

Example :

ROSE

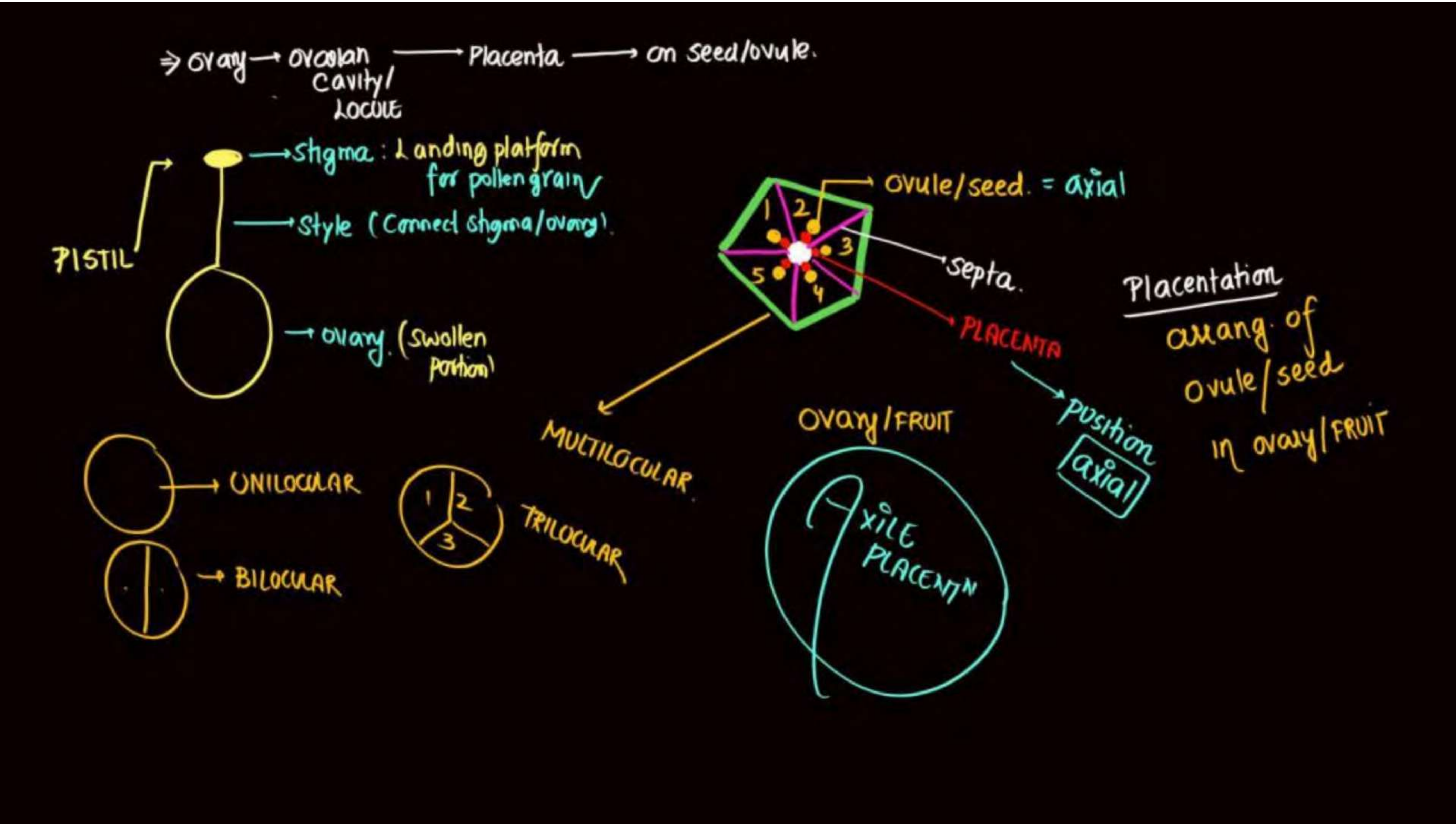
LOTUS

Syncarpous FUSED.

Example :

MUSTARD

TOMATO.

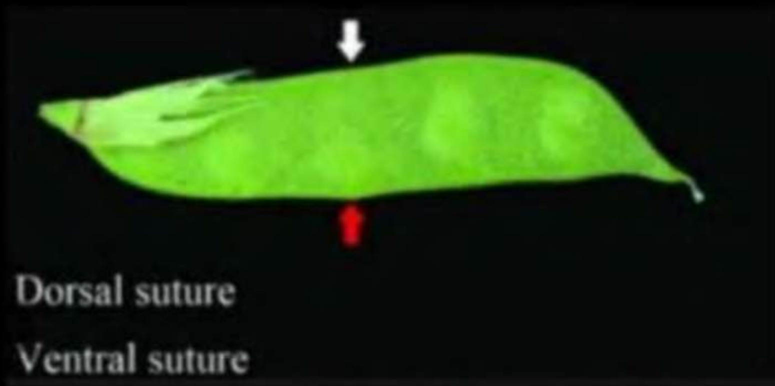

⇒ ovary → ovarian cavity/ LOCULE → Placenta → on seed/ovule.
stigma : Landing platform for pollen grain
Style (Connect stigma/ovary).
PISTIL
ovary. (swollen portion)
UNILOCULAR
BILOCULAR
1 2 3
TRILOCULAR
1 2 3 4 5
ovule/seed. = axial
septa.
PLACENTA
MULTILOCULAR.
position
axial
Ovary/FRUIT
AXILE PLACENTN
Placentation
arrang. of ovule/seed in ovary/FRUIT

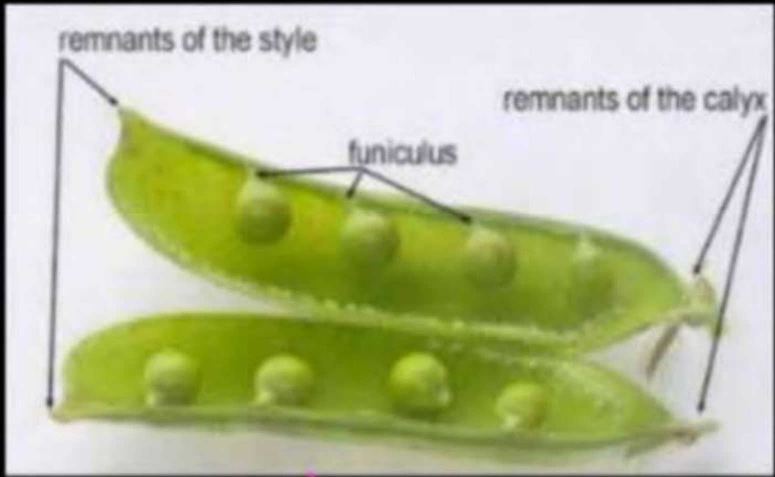
Placentation

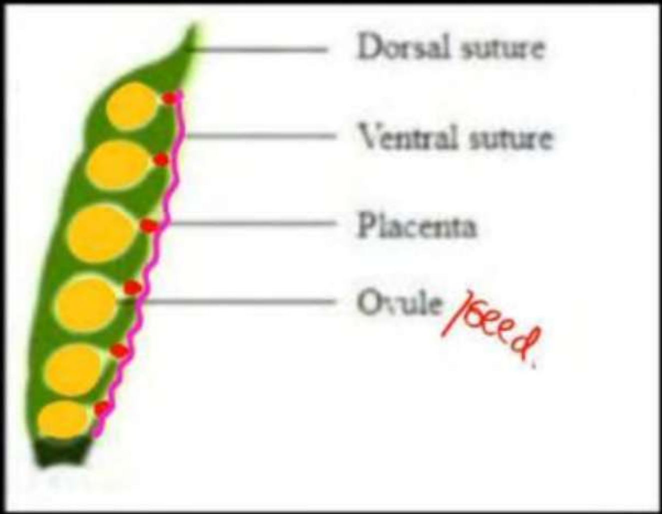
Definition ______________________________

1. Marginal : Placenta on margin, Ventral SUTURE
(ovule) Two Rows.

Example :
pea.







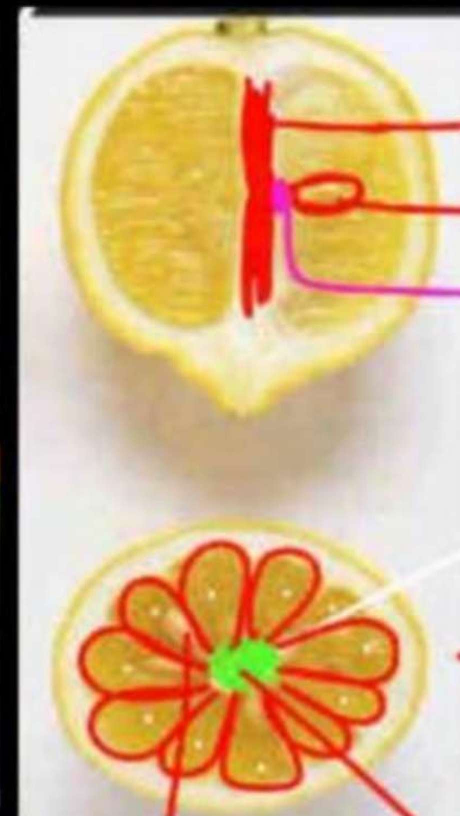
2. Axile

Example :

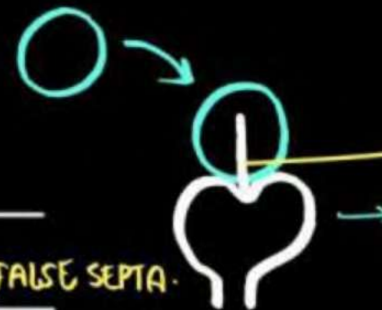
China Rose

Tomato

Lemon.



3. Parietal (outer/peripheral).



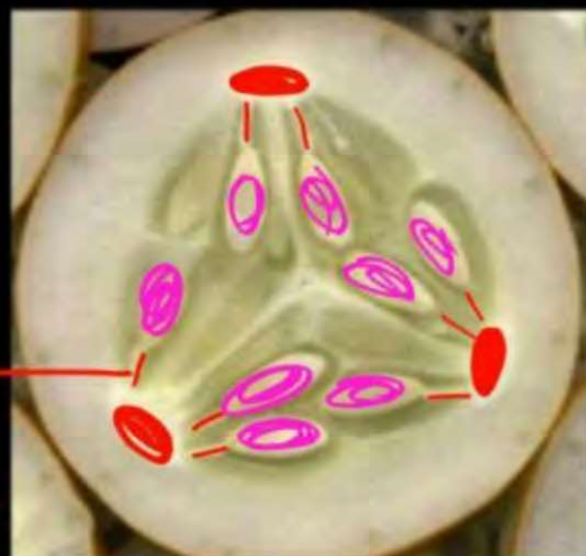
Ovary is one chambered but BECOMES BILOCULAR DUE TO FALSE SEPTA.
(UNILOCULAR)

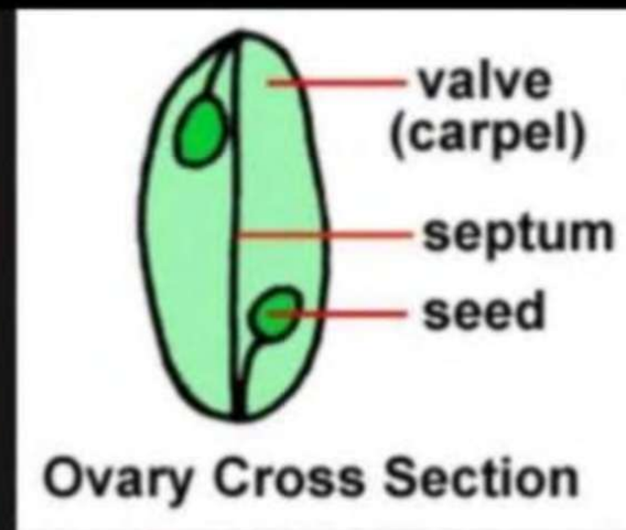
Example :

M USTARD

A RGEMONE.

Placenta (outer/Parietal)





Ovary Cross Section

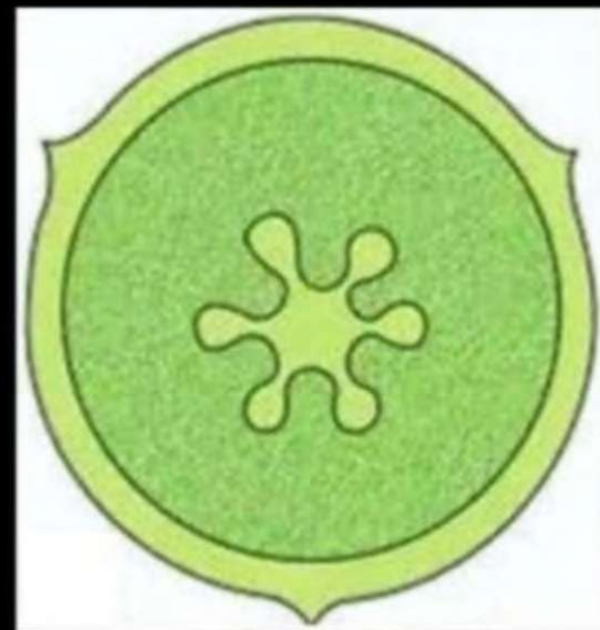
4. Free Central

septa absent
placenta/ovule: centre.

Example :

Primerose

Dianthus



5. Basal

→ Basal.

ovule/placenta in ovary

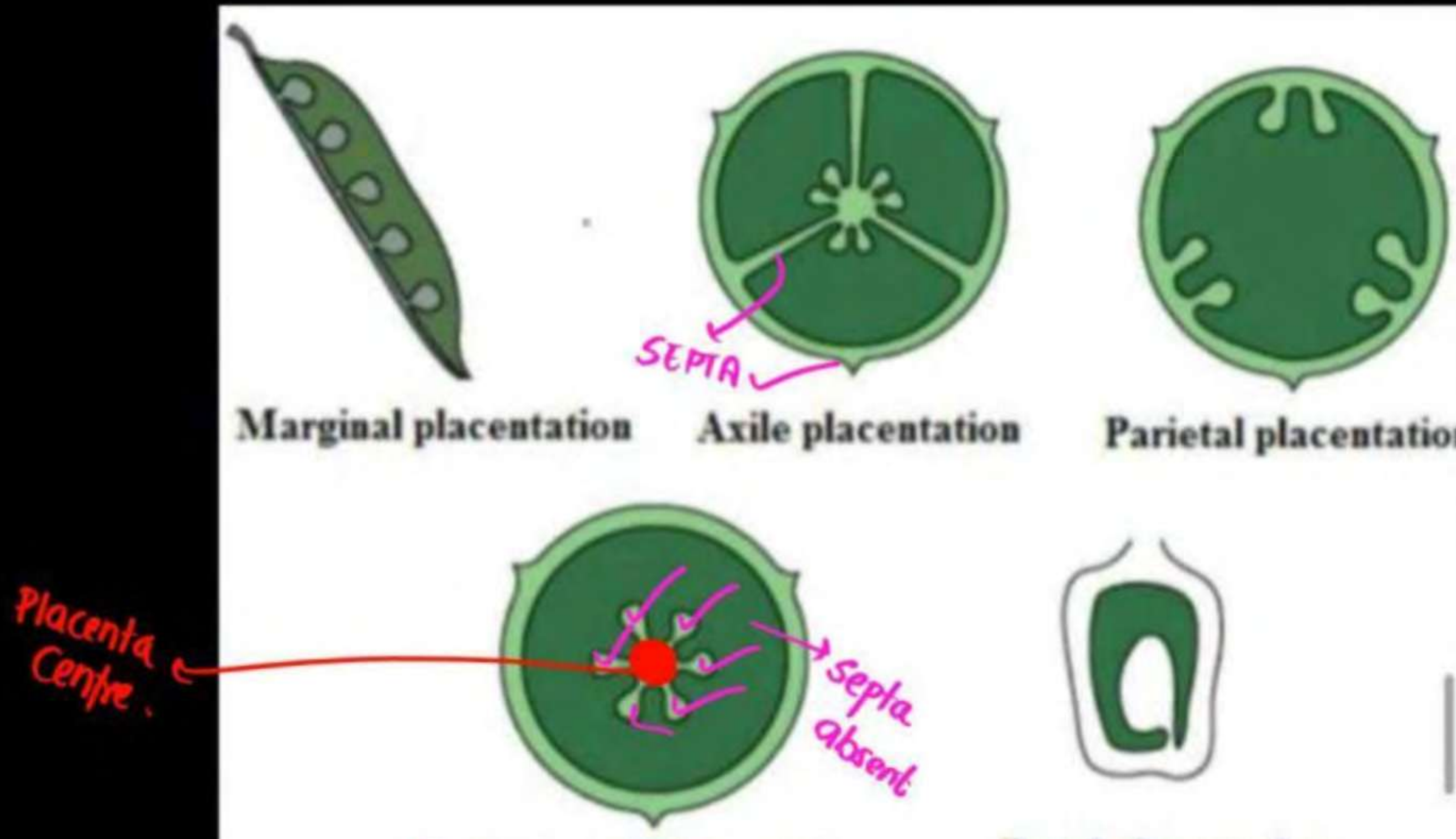
Single ~~ovary~~ ovule.

Advanced Type.

Example :

SUNFLOWER

MARIGOLD

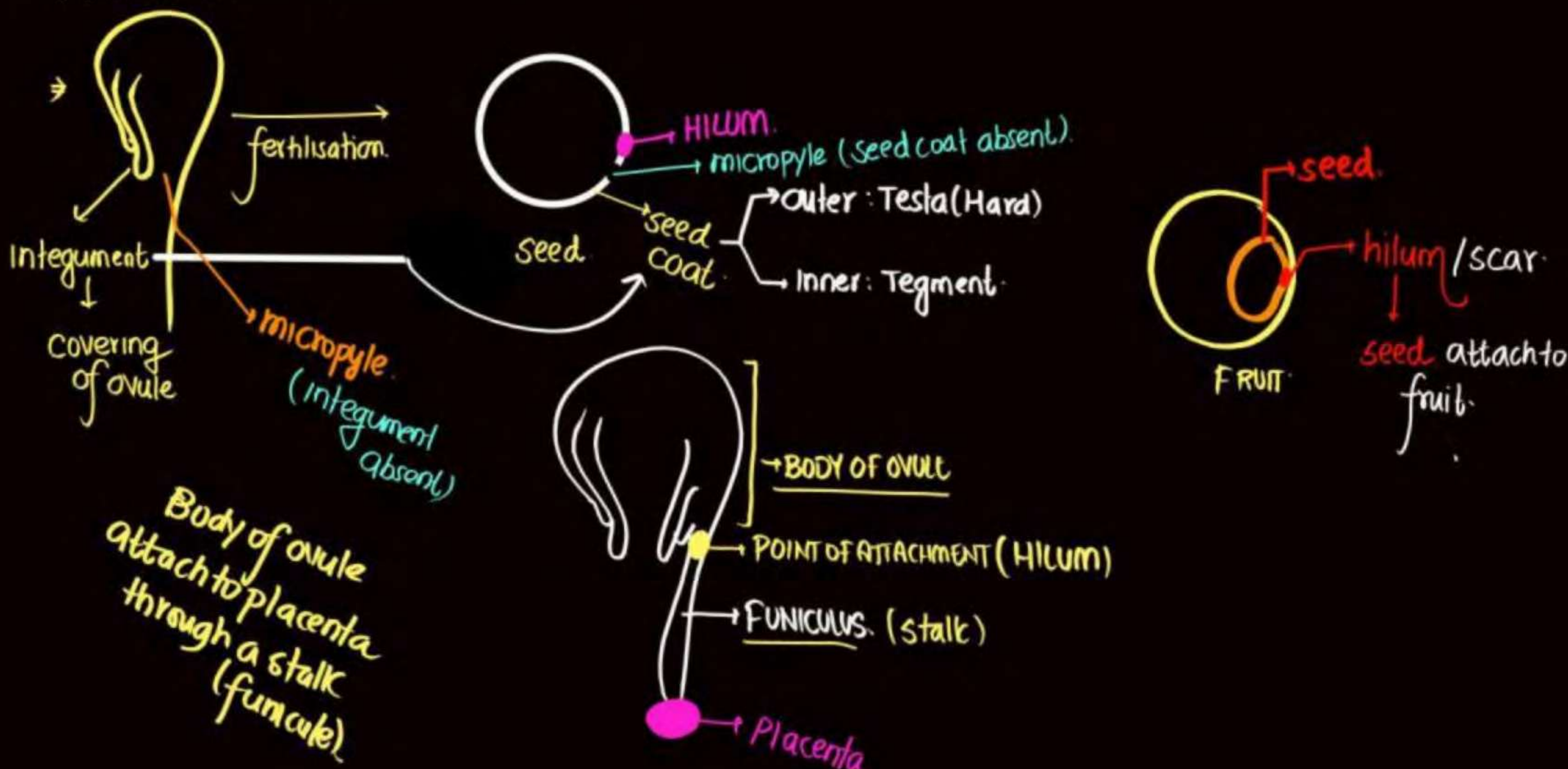


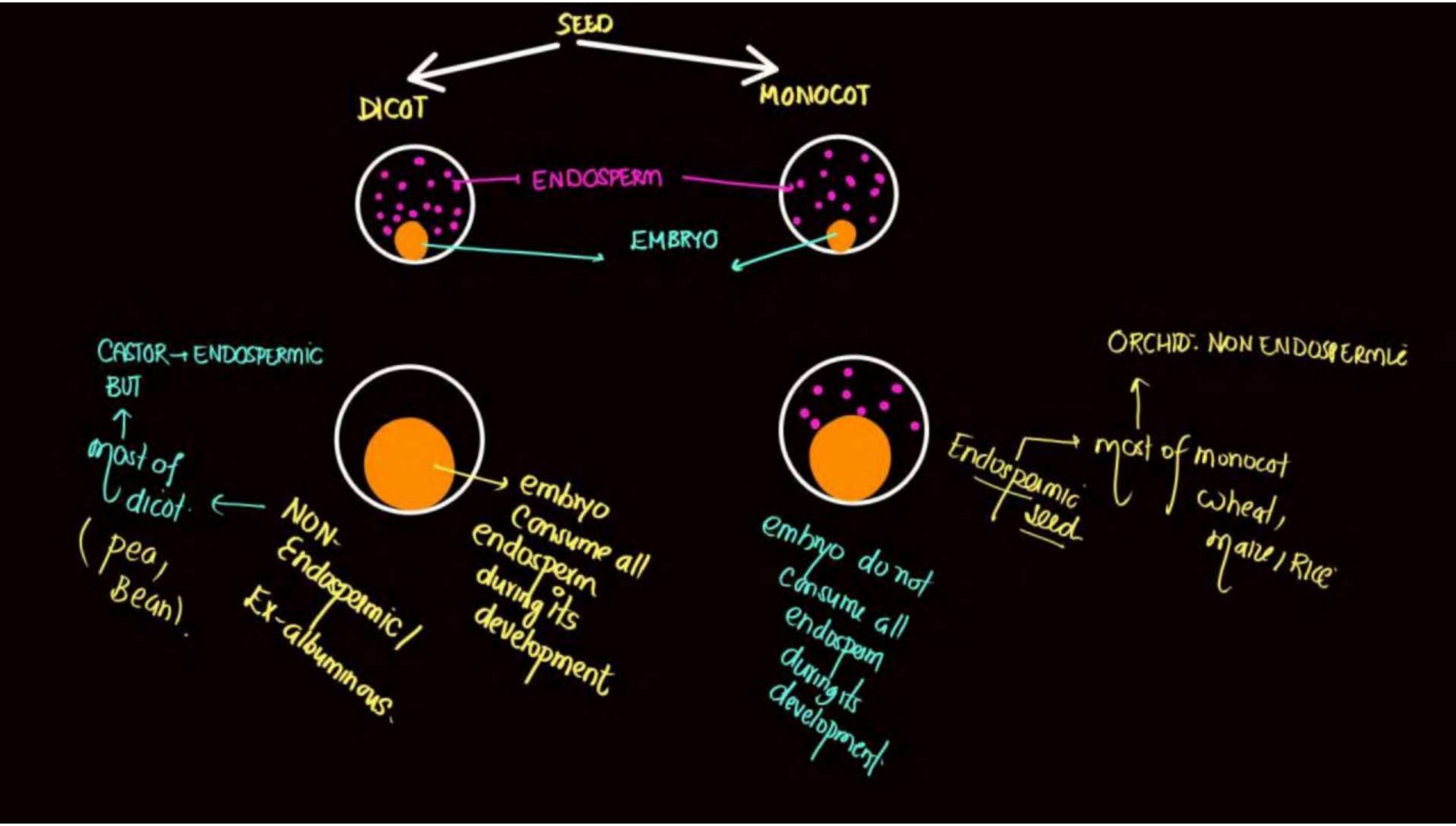
Marginal placentation Axile placentation Parietal placentation

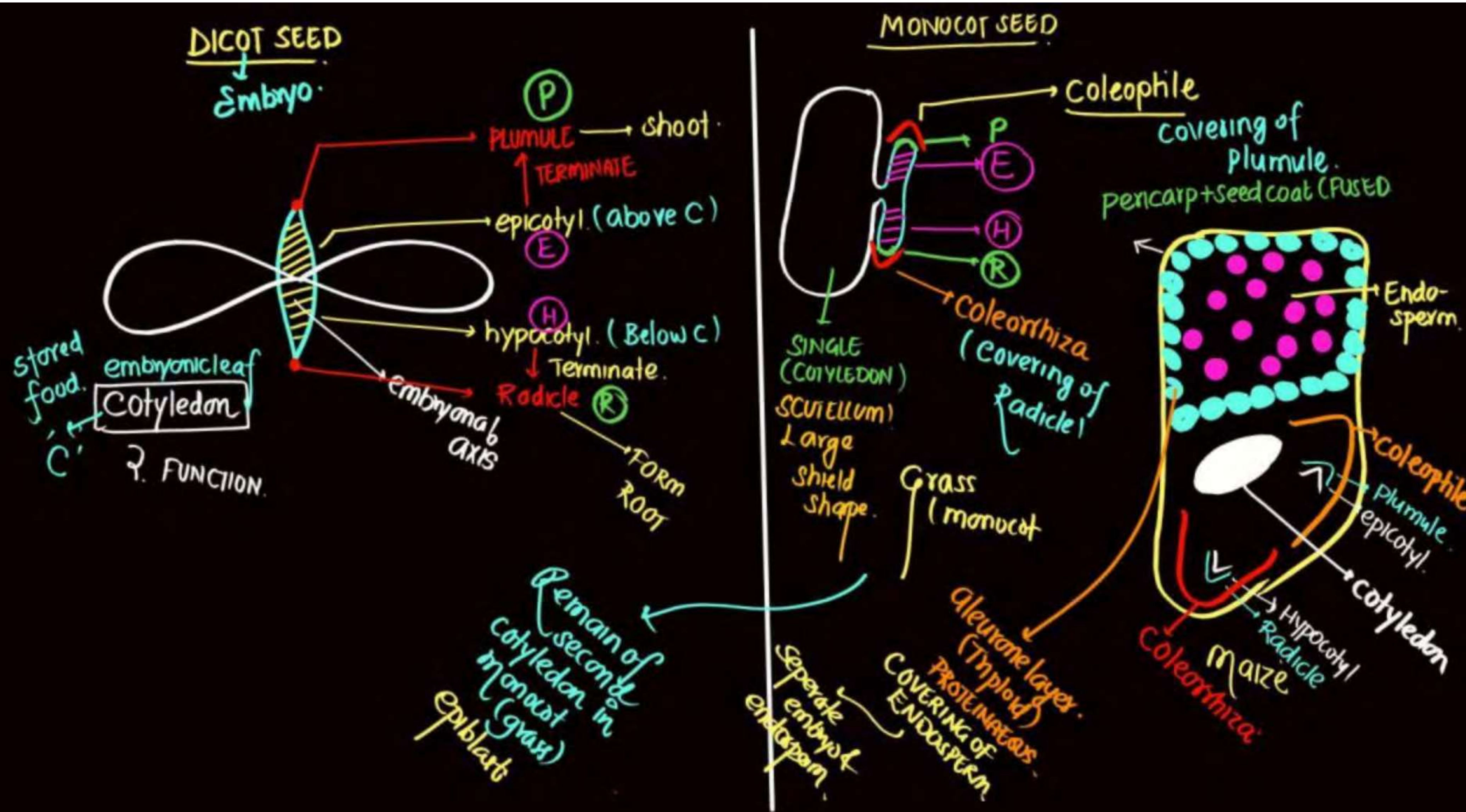
Free central placentation Basal placentation

SEED

⇒ Fertilised ovule: seed.




SEED
DICOT
MONOCOT
ENDOSPERM
EMBRYO
CASTOR → ENDOSPERMIC
BUT
most of dicot
(pea, Bean).
NON-Endospermic / Ex-albuminous.
embryo consume all endosperm during its development
embryo do not consume all endosperm during its development.
Endospermic seed
most of monocot
wheat, maize / RICE
ORCHID: NON ENDOSPERMIC



DICOT SEED
Embryo
P
PLUMULE → shoot
TERMINATE
epicotyl (above C)
E
H
hypocotyl (Below C)
Terminate
Radicle R
FORM ROOT
embryonal axis
stored food
embryonicleaf
Cotyledon
'C'
? FUNCTION
Remain of second cotyledon in monocot (grass)
epiblast
MONOCOT SEED
Coleophile
covering of Plumule.
pericarp+seed coat (FUSED
P
E
H
R
Coleorrhiza (covering of Radicle)
SINGLE (COTYLEDON) SCUTELLUM) Large Shield Shape.
Grass (monocot
Endo-sperm
Coleoptile
Plumule
epicotyl
cotyledon
Hypocotyl
Radicle
Coleorrhiza
Maize
aleurone layers (Triploid)
PROTEINACEOUS COVERING OF ENDOSPERM
Seperate embryo & endosperm.

FRUIT

TRUE
- ⇒ mostly
- ⇒ develop from ovary.

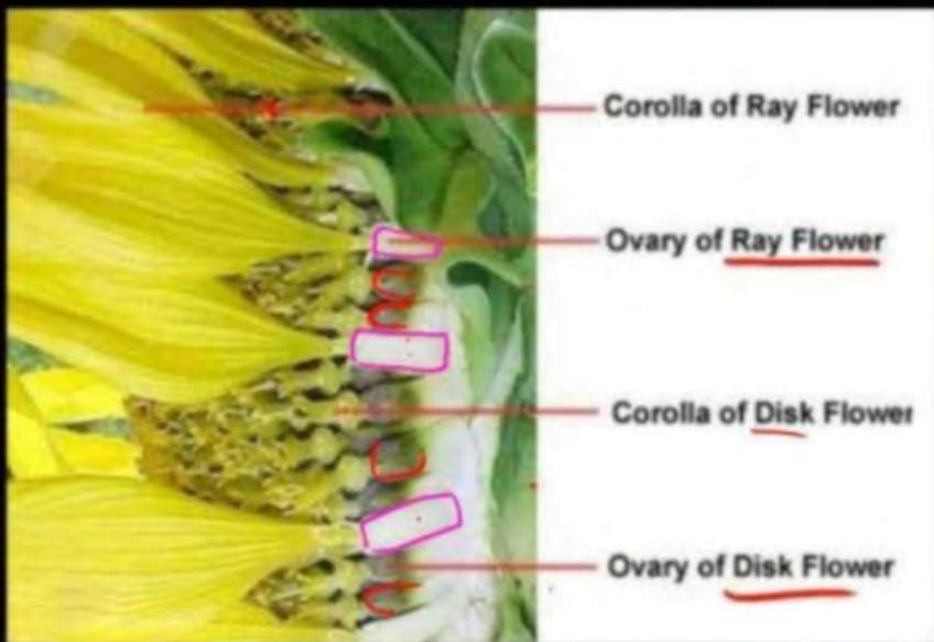
FALSE
- ⇒ other part (Thalamus) contribute in fruit formtn.
- eg: apple, pear, cashew, strawberry.

PARTHENOCARPIC
- without fertilisation
- seedless

SIMPLE FRUIT

dry
- ⇒ pericarp is not divided.
- eg: LITCHI
- ARIL

Fleshy (DRUPE) → one seeded FRUIT
- ⇒ pericarp is divided (SUPERIOR OVARY, MONOCARPELLARY)
- ① Epicarp: outer → covering
- ② mesocarp: middle → fleshy edible part (mango); FIBROUS
- ③ endocarp: inner (stony/hard)
- eg: mango, coconut. → edible part (endosperm)



a) Stamen : ♂ (Unisex)

b) pistil : ♀ (Unisex)

c) stamen & pistil : Bisexual : ⚥

Sunflower (dimorphic).

↓

Two Types of flower

- disc Floret (Centre)
  ↓
  Actinomorphic
  - ★ stamen ✓
  - ★ pistil ✓

  (Bisexual flower)

  ⚥

- Ray Floret (peripheral) / outer
  ↓
  zygomorphic
  - (Unisexual) androecium absent
    ↓
    pistillate Flower

    ♀
  - androecium & gynoecium absent

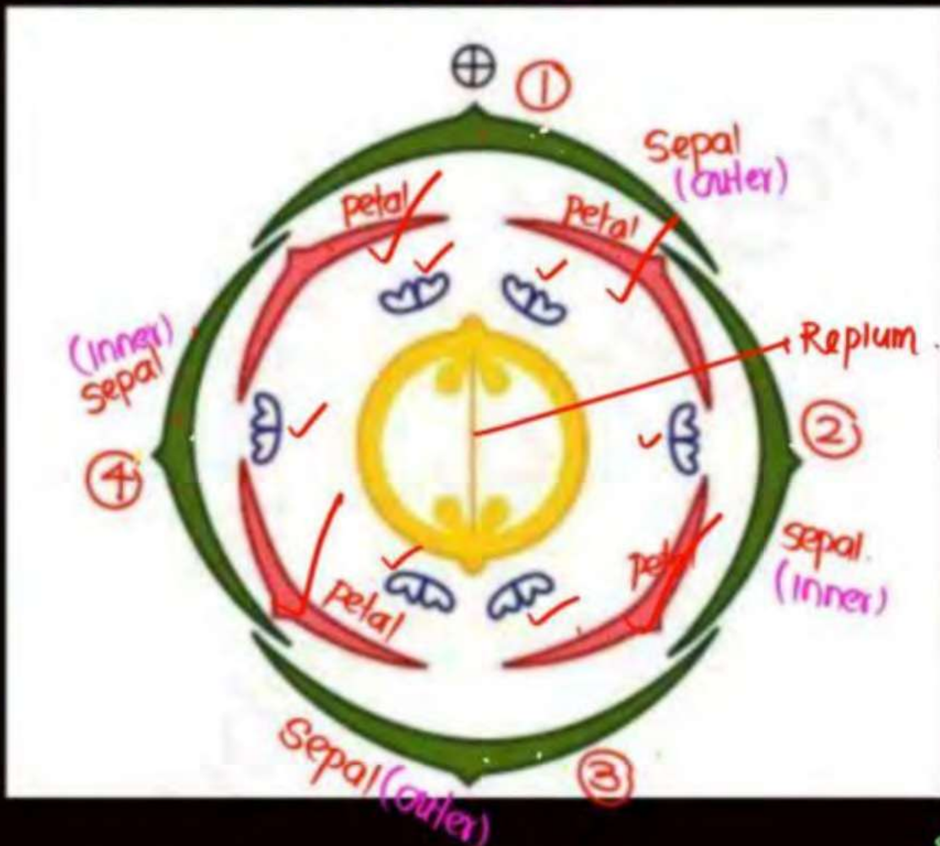
    Neuter flower

    $A_0 G_0$

Character	CRUCIFERAE OR Brassicaceae	Fabaceae	Solanaceae	~~Liliaceae~~	GRAMINAE OR Poaceae	Malvaceae	COMPOSITAE OR Asteraceae
DICOT OR MONOCOT	D	D	D	M solitary/cymose ??	M (advanced) GRASS FAMILY	D COTTON, LADYFINGER, CHINAROSE	D (advanced). SUNFLOWER.
Inflorescence	$\boxed{\text{Racemose}}$	$\boxed{\text{Racemose}}$	Solitary axillary, cymose in Solanum.	Racemose (Umbellate cluster). → ONION	Racemose	Racemose	Racemose.
Symmetry	Act	Zygo	Act	Act	Zy	Act.	disc floret: actinom → Centre. Bisexual Ray Floret: zygomorphic (Pistillate & Neuter Flower)
Bisexual/ Unisexual.	B	B	B	B	B	B.	BISEXUAL. & UNISEXUAL.
OVARY	Superior	S	S	S	S	S	Inferior ovary.

Character	Brassicaceae	Fabaceae	Solanaceae	Liliaceae	Poaceae (grass Family)	Malvaceae	Asteraceae
Flower	Hypog.	Hypo.	Hypo.	Hypo.	Hypo,	Hypogy.	epigynous
Floral appendages	4 (Tetramerous)	5 (Penta)	5 (penta).	3 (Trimerous)	3 (Tri)	5 (penta)	5 (penta)
Seed.	Non-endo	Non-endo	endospermic	Endosp.	Endosp.	Non-endo	Non-endo
ebract/ Bracteate	Ebr	Br	Br	Br	Br	Br	Br.
Placentation	Parietal	Marginal	Axile	Axile	Basal	Axile	Basal.
FRUIT	Siliqua/ Silicula	Legume	Berry (Mostly) Capsule	Capsule (Mostly) Berry	Caryopsis	Capsule	cypsela

Brassicaceae / cruciferae



K.

Calyx: 4 Sepal
- 2 : OUTER
- 2 : INNER

K_{2+2}, imbricate

COROLLA: 4 Petals: valvate C_4.

androecium: 6 stamen A_{2+4}.

- 2 outer, short
- 4 (inner, long)

Gynoecium: Unilocular But Becomes BILOCULAR due to false septa (Replum)

$\underline{G}_{(2)}$ → Bicarpellary, syncarpous ovary (fused)

superior ovary.

Brassicaceae

BISEXUAL.

CALYX

COROLLA

Gynoecium

$$\text{Ebr} \oplus ⚥\ K_{2+2}\ C_4\ A_{2+4}\ \underline{G}_{(2)}$$

BICARPELLARY

SYNCARPOUS OVARY

SUPERIOR OVARY

Bract absent

Achnomorphic

outer inner

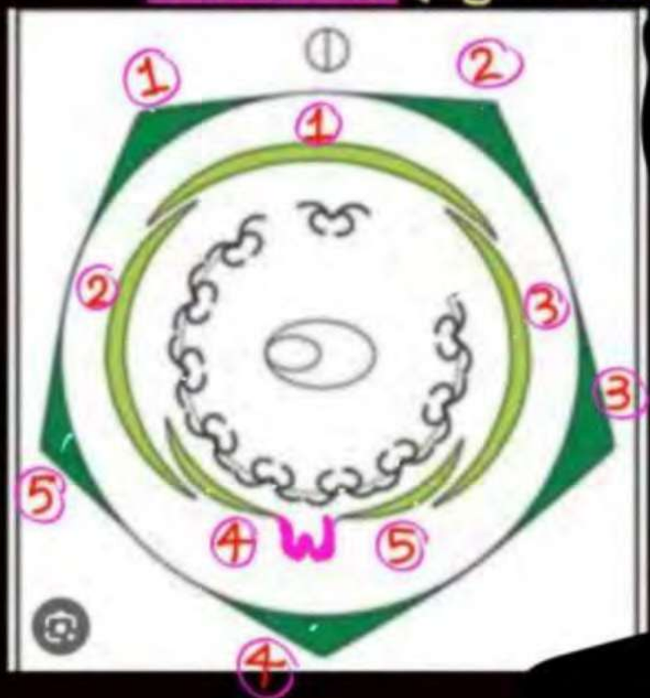
4 petals.

short, inner.

Long, outer.

Cauliflower
Cabbage } Brassica
Mustard
Radish (Raphanus)

Fabaceae (leguminoacene).



Calyx: sepal 5, FUSED, gamosepalous, valvate. $K_{(5)}$

COROLLA: $C_{1+2+(2)}$ vexillary aestivation.

1 → Standard, 2 → wings, (2) → keel.

androecium: $A_{(9)+1}$ ⇒ DIADELPHOUS.

(9) → one BUNDLE FUSED

1 → ONE BUNDLE

Gynoecium: monocarpellary, Unilocular.

$\underline{G_1}$ → sup. ovary

Fabaceae

$\% \; ⚥ \; K_{(5)} \; C_{1+2+(2)} \; A_{(9)+1} \; \underline{G}_1$

Zygomorphic

BISEXUAL

CALYX

5 sepal

gamo-sepalous (FUSED)

STANDARD, POSTERIOR, LARGE

Lateral, 2

anterior, small

9 stamen

FUSED

fused.

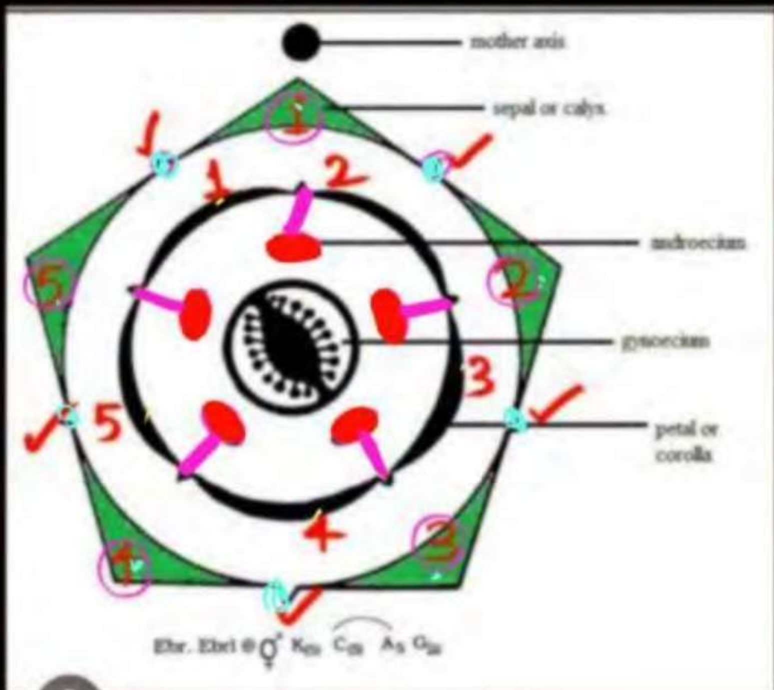
1 stamen

diadelphous

monocarpellary.

SUPERIOR OVARY

Solanaceae



Persistent calyx.

Calyx: 5 sepal, fused, gamosepalous., valvate $K_{(5)}$

Corolla: 5 petal., Fused gamopetalous, valvate, $C_{(5)}$.

androecium: 5 stamen, stamen attach to petal.

$\overset{\frown}{C_{(5)}\ A_5}$ → epipetalous.

Gynoecium: Bicarpellary, Bilocular, syncarpous ovary

$\underline{G}_{(2)}$

→ SUP OVARY.

Solanaceae

epipetalous

$$\oplus\ \text{⚥}\ K_{(5)}\ \overgroup{C_{(5)}\ A_5}\ \underline{G}_{(2)}$$

actinom.

BISEXUAL

Calyx

5 sepal

gamo-sepalous

5 petals

gamopetalous

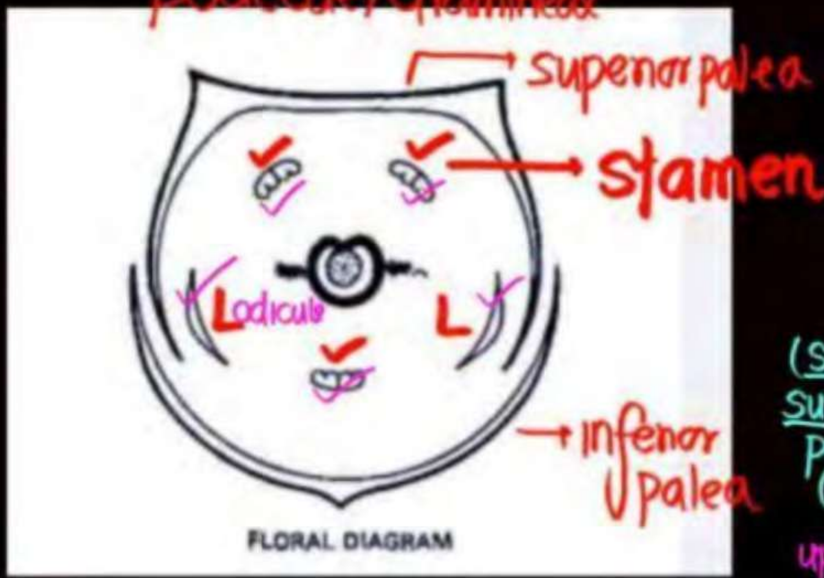
5 stamen

SYNCARPOUS

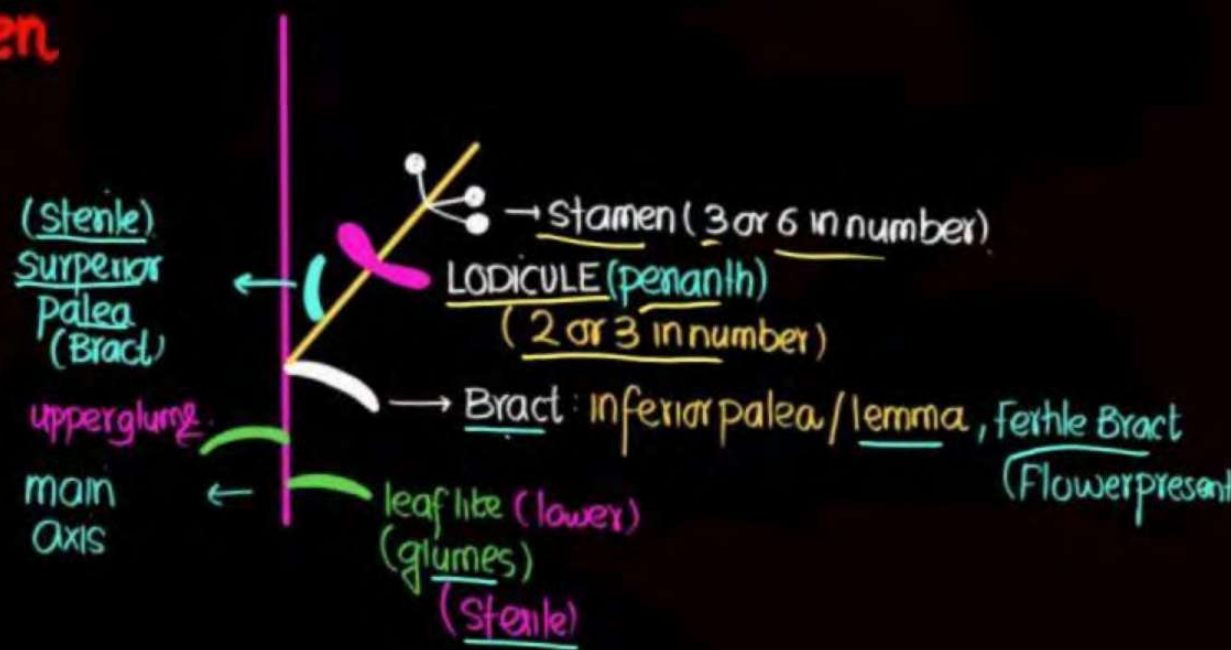
BICARPELLARY,

SUPERIOR OVARY.

Poaceae/Gramineae



Poaceae (Inflorescence)



Gramineae (poaceae)

zygomorphic

penanth Represented By

Br % ⚥ $P_{2 \text{ or } 3 \text{ (lodicules)}}$ $A_{3 \text{ or } 6}$ $\underline{G}_{1}$

moncarpellary/ Unilocular

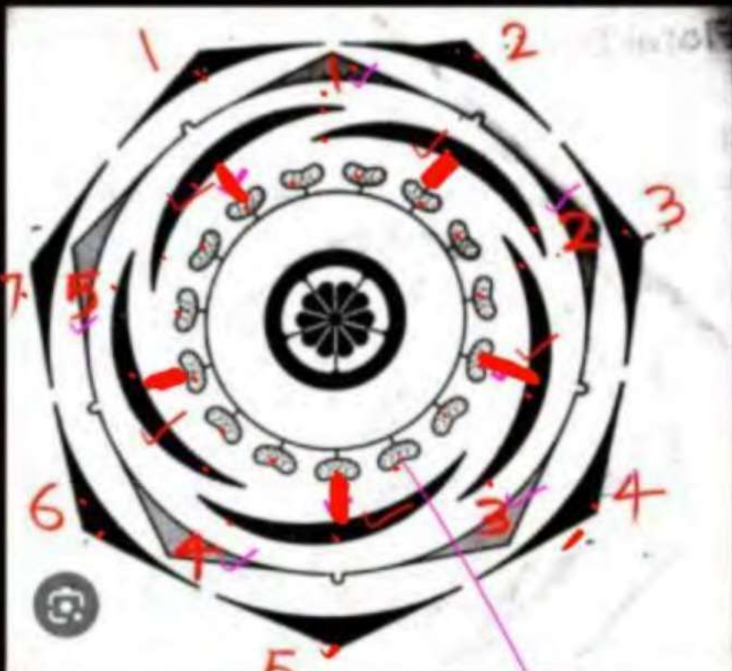
Bract

Bisexual

Stamen

superior ovary

Malvaceae (China Rose (Hibiscus), Cotton, lady finger.



Calyx: Sepals 5, fused, gamosepalous, valvate. $K_{(5)}$

COROLLA: Petals 5, Free, polypetalous, Twisted: C_5

ANDROECIUM: Stamen many, infinite, stamen Fused with help of filament, present in one Bundle. (monoadelphous), MONOTHECOUS ANTHER (TWO POLLEN SAC PRESENT)

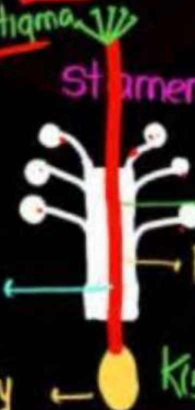
Stamen attach to PETALS: EPIPETALOUS.

Bract

On pedicel leaflike structure (BRCTEOLE)

Collection of Bracteole (Epicalyx)

Epi_{3-9}



pentafid stigma

Staminal Tube.

style

Fusion of filament: a Tube is formed (Staminal Tube)

Epipetalous.

ovary

$K_{(5)}\, C_5\, A_{(\infty)}$

monoadelphous (filament Fused)

stamen

Gynoecium: Multilocular, Multicarpellary, syncarpous ovary. (Fused). many ovules.

Malvaceae

Bisexual

$Br \oplus ⚥ \; Epi_{3-9} \; K_{(5)} \; \overset{\frown}{C_5 \; A_{(\infty)}} \; \underline{G}_{(5-\infty)}$

epipetalous.

Bracteate

Actinomorphic

Epicalyx: Coll^n of Bracteole.

sepals 5

gamosepalous

petal 5.

syncarpous ovary.

SUP OVARY.

MULTICARPELLARY.

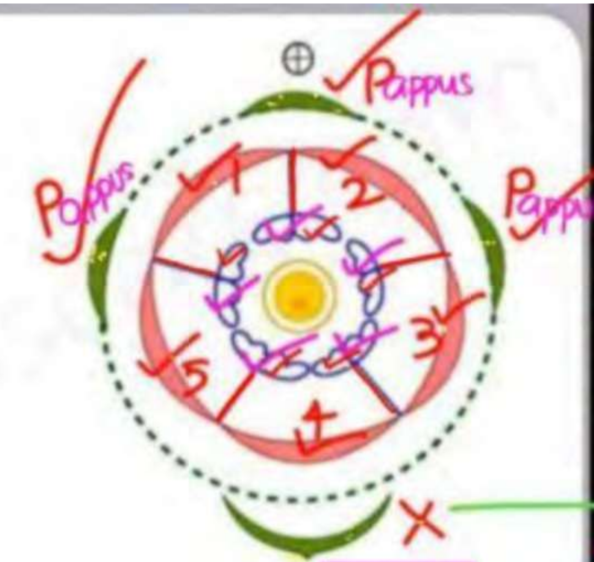
FUSED: ONE BUNDLE: MONOADELPHOUS

many stamen

StaminalTube.

Floral Diagram of Ray floret

Floral formula: Br % ♀ $K_{(2\text{-}3)(pappus)}\ \overset{\frown}{C_{(3\text{-}5)}\ A_0}\ \overline{G}_{(2)}$



Floral Diagram of Disc floret

Floral formula: Br ⊕ ⚥ $K_{2\text{-}3\,(pappus)}\ \overset{\frown}{C_{(5)}\ A_5}\ \overline{G}_{(2)}$

Collection of Bract

Asteraceae / Compositae (sunflower), marigold.
↓
Helianthus annus.

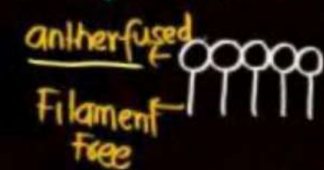
$\boxed{\text{DISC FLORET}}$ ⚥

Actinomorphic ⊕, Bisexual

Calyx: modify into Pappus: K pappus.

Corolla: 5 petals, Fused, gamopetalous, valvale

$C_{(5)}$

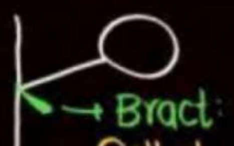


Androecium: stamen 5, Fused with help of anther (SYNGENIOUS)

Stamen attach to petals: Epipetalous.

$K_{pappus}\ \overset{\frown}{C_{(5)}\ A_{(5)}}$

Gynoecium: Unilocular, Bicarpellary, syncarpous ovary, inferior ovary.



Collection
↓
INVOLUCRE

→ Calyx modify into Hair like structure pappus (Helps in fruit dispersal)

Asteraceae/compositae

Disc Floret

Bracteate

Bisexual.

epipetalous.

inferior ovary.

syncarpous

Bicarpellary.

$$Br \oplus ⚥ K_{pappus}\ \overset{\frown}{C_{(5)}\ A_{(5)}}\ G_{(\bar{2})}$$

actinomorphic

Calyx modify into Hair like stucture.

Corolla

5 petals

Fused petal

stamen 5

Fused (anther) Syngenisius

Asteraceae/Compositae (Ray Floret)

zygomorphic %

- pistil present, stamen absent (Pistillate Flower), Unisexual: ♀, $A_0 \underline{G}_{(2)}$
- pistile stamen absent (Neuter Flower): $A_0 G_0$

Bracteate zygomorphic stamen & pistil absent calyx modify into hair stamen absent Neuter flower.

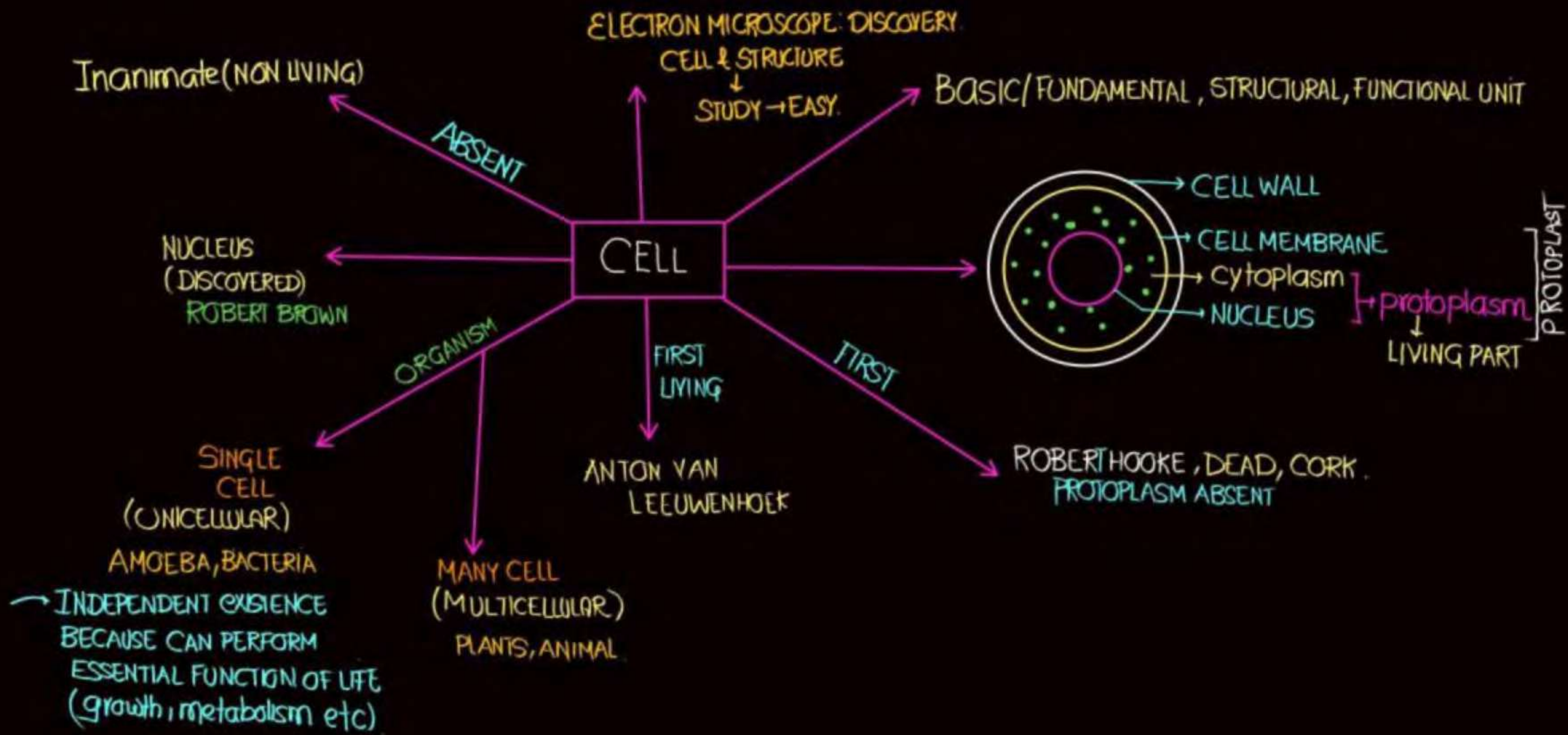
$$Br \; \% \; ♀ / \text{Neuter} \; K_{pappus} \; C_{(5)} \; A_0 \; \overline{G}_{(2)} \text{ or } O$$

inferior ovary.

Unisexual (pistilate)

fused. petal 5

Bicarpellary syncarpous (pistillate)



CELL
ELECTRON MICROSCOPE: DISCOVERY
CELL & STRUCTURE
STUDY → EASY
Inanimate (NON LIVING)
ABSENT
Basic/ FUNDAMENTAL, STRUCTURAL, FUNCTIONAL UNIT
CELL WALL
CELL MEMBRANE
cytoplasm
NUCLEUS
protoplasm
LIVING PART
PROTOPLAST
NUCLEUS
(DISCOVERED)
ROBERT BROWN
ORGANISM
FIRST
LIVING
FIRST
ROBERT HOOKE, DEAD, CORK.
PROTOPLASM ABSENT
SINGLE
CELL
(UNICELLULAR)
AMOEBA, BACTERIA
→ INDEPENDENT EXISTENCE
BECAUSE CAN PERFORM
ESSENTIAL FUNCTION OF LIFE
(growth, metabolism etc)
MANY CELL
(MULTICELLULAR)
PLANTS, ANIMAL
ANTON VAN
LEEUWENHOEK

CELL THEORY

FORMULATED BY

MATTHIAS SCHLEIDEN, 1838
GERMAN BOTANIST

STUDY: ALL PLANTS

COMPOSED OF CELLS
WHICH FORMS TISSUE

DRAWBACK

DIDN'T EXPLAIN

"HOW NEW CELLS WERE FORMED"

BUT

1855, RUDOIF VIRCHOW:

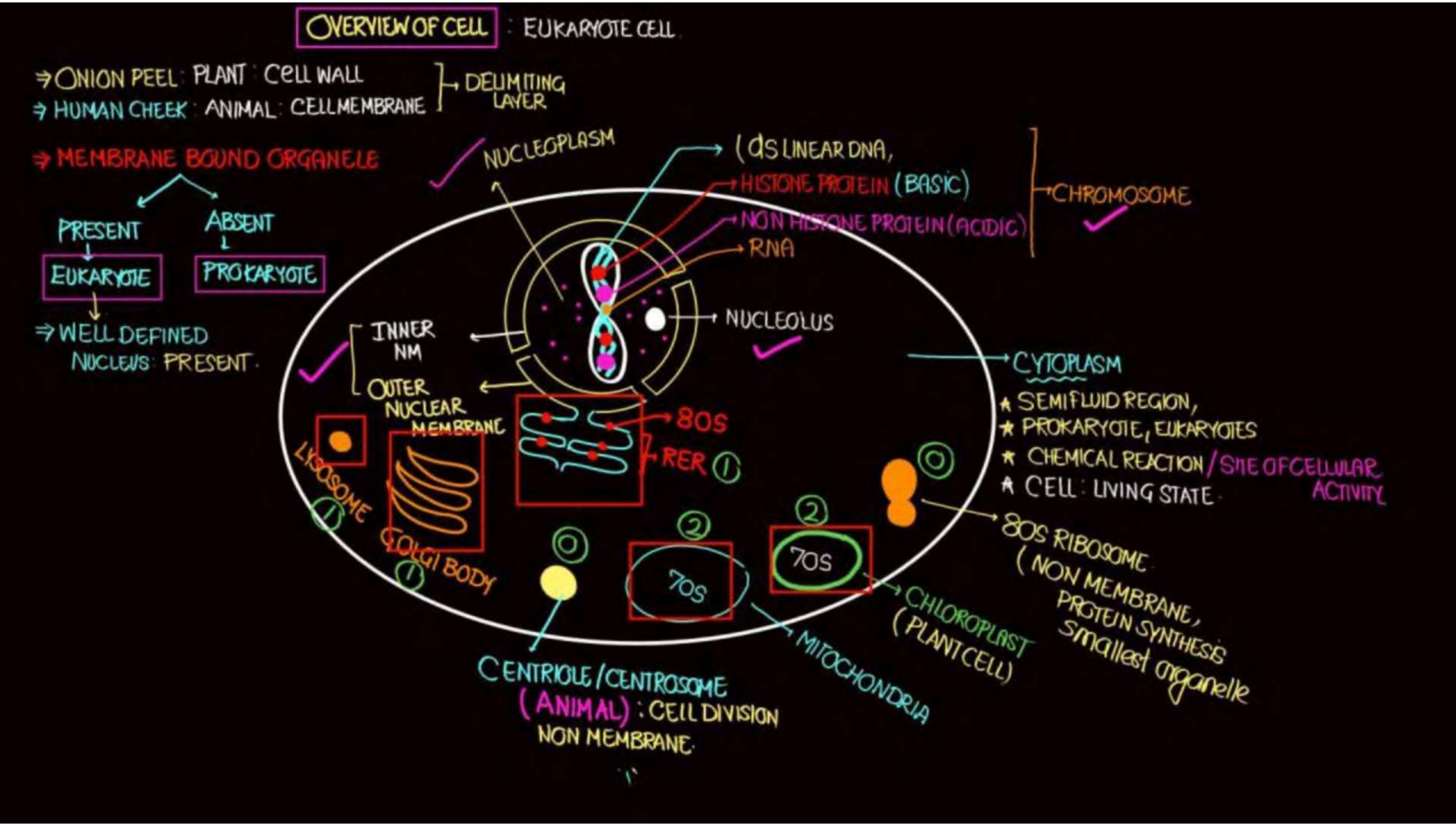
THEODORE SCHWANN, 1839
BRITISCH ZOOLOGIST

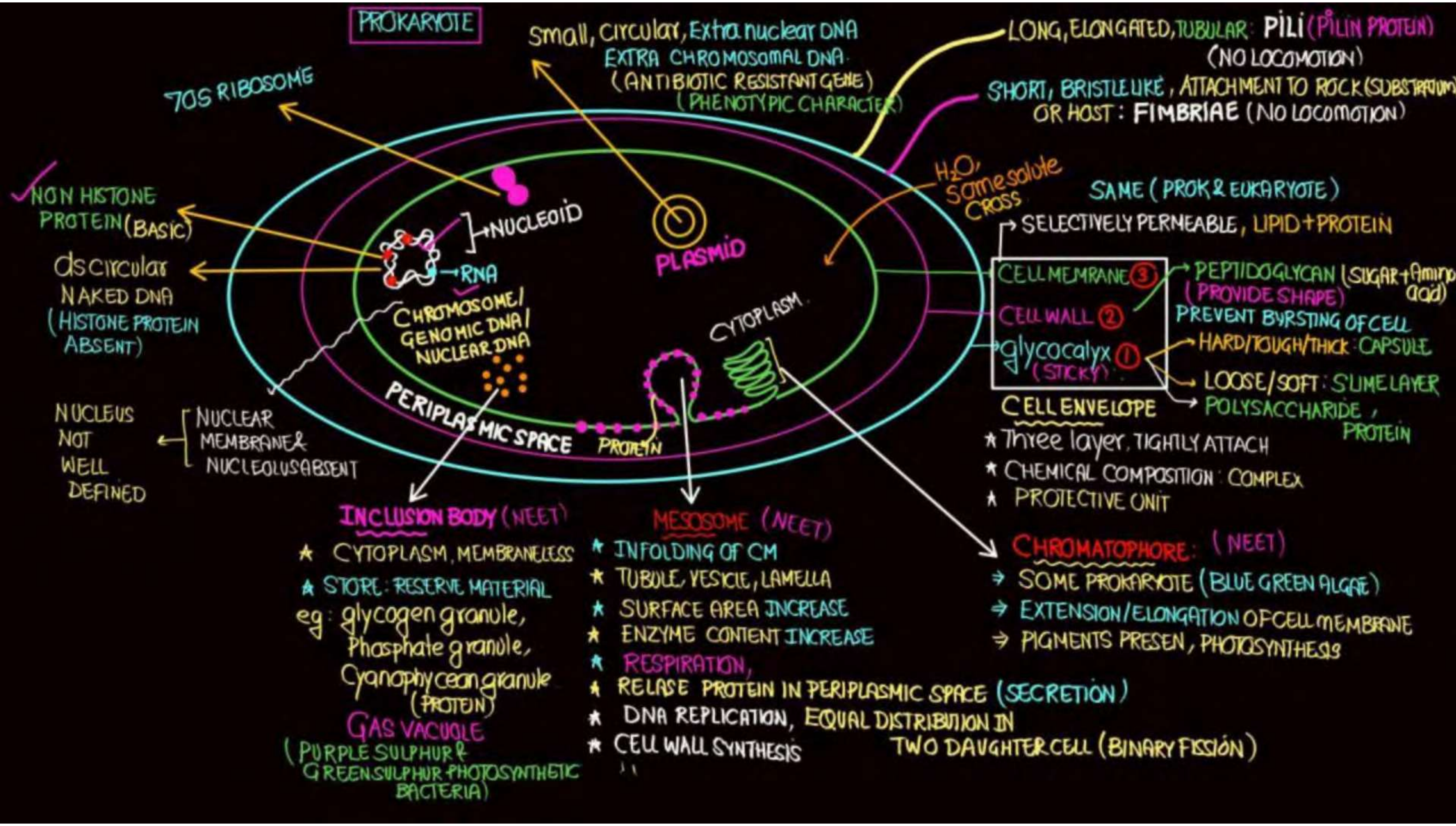
- ★ STUDY: ANIMAL CELL ⟶ COVERED BY THIN LAYER
  PLASMA MEMBRANE
- ★ STUDY: PLANT CELL ⟶ CELL WALL PRESENSE:
  UNIQUE CHARACTER
- ★ HYPOTHESIS: PLANTS & ANIMALS ↓ COMPOSED ↓ CELL & ITS PRODUCT (TISSUE)

① NEW CELL ARISE BY DIVISION OF PRE EXISTING CELL (NEET)

Omnis cellula e cellula

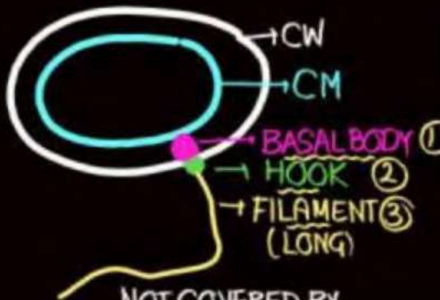
② ALL LIVING ORGANISM: COMPOSED: CELL & PRODUCT OF CELL


OVERVIEW OF CELL : EUKARYOTE CELL
⇒ ONION PEEL : PLANT : CELL WALL
⇒ HUMAN CHEEK : ANIMAL : CELLMEMBRANE
DELIMITING LAYER
⇒ MEMBRANE BOUND ORGANELE
PRESENT
ABSENT
EUKARYOTE
PROKARYOTE
⇒ WELL DEFINED NUCLEUS : PRESENT.
NUCLEOPLASM
(ds LINEAR DNA,
HISTONE PROTEIN (BASIC)
NON HISTONE PROTEIN (ACIDIC)
RNA
CHROMOSOME
NUCLEOLUS
INNER NM
OUTER NUCLEAR MEMBRANE
80S
RER ①
LYSOSOME ①
GOLGI BODY ①
⓪
②
70S
②
70S
⓪
CYTOPLASM
★ SEMIFLUID REGION,
★ PROKARYOTE, EUKARYOTES
★ CHEMICAL REACTION / SITE OF CELLULAR ACTIVITY
★ CELL : LIVING STATE.
80S RIBOSOME.
(NON MEMBRANE,
PROTEIN SYNTHESIS
smallest organelle
CHLOROPLAST
(PLANT CELL)
MITOCHONDRIA
CENTRIOLE / CENTROSOME
(ANIMAL) : CELL DIVISION
NON MEMBRANE.


PROKARYOTE
70S RIBOSOME
Small, circular, Extra nuclear DNA
EXTRA CHROMOSOMAL DNA
(ANTIBIOTIC RESISTANT GENE)
(PHENOTYPIC CHARACTER)
PLASMID
LONG, ELONGATED, TUBULAR: PILI (PILIN PROTEIN)
(NO LOCOMOTION)
SHORT, BRISTLE LIKE, ATTACHMENT TO ROCK (SUBSTRATUM) OR HOST: FIMBRIAE (NO LOCOMOTION)
NON HISTONE PROTEIN (BASIC)
ds circular NAKED DNA (HISTONE PROTEIN ABSENT)
NUCLEOID
RNA
CHROMOSOME/ GENOMIC DNA/ NUCLEAR DNA
H_2O, Some solute Cross
SAME (PROK & EUKARYOTE)
SELECTIVELY PERMEABLE, LIPID + PROTEIN
CELL MEMRANE 3
CELL WALL 2
glycocalyx 1 (STICKY)
PEPTIDOGLYCAN (SUGAR + Amino acid)
(PROVIDE SHAPE)
PREVENT BURSTING OF CELL
HARD/TOUGH/THICK: CAPSULE
LOOSE/SOFT: SLIME LAYER
POLYSACCHARIDE, PROTEIN
CELL ENVELOPE
* Three layer, TIGHTLY ATTACH
* CHEMICAL COMPOSITION: COMPLEX
* PROTECTIVE UNIT
CYTOPLASM
PERIPLASMIC SPACE
PROTEIN
NUCLEUS NOT WELL DEFINED
NUCLEAR MEMBRANE & NUCLEOLUS ABSENT
INCLUSION BODY (NEET)
* CYTOPLASM, MEMBRANELESS
* STORE: RESERVE MATERIAL
eg: glycogen granule, Phosphate granule, Cyanophycean granule (PROTEIN)
GAS VACUOLE
(PURPLE SULPHUR & GREEN SULPHUR PHOTOSYNTHETIC BACTERIA)
MESOSOME (NEET)
* INFOLDING OF CM
* TUBULE, VESICLE, LAMELLA
* SURFACE AREA INCREASE
* ENZYME CONTENT INCREASE
* RESPIRATION,
* RELASE PROTEIN IN PERIPLASMIC SPACE (SECRETION)
* DNA REPLICATION, EQUAL DISTRIBUTION IN TWO DAUGHTER CELL (BINARY FISSION)
* CELL WALL SYNTHESIS
CHROMATOPHORE: (NEET)
→ SOME PROKARYOTE (BLUE GREEN ALGAE)
→ EXTENSION/ELONGATION OF CELL MEMBRANE
→ PIGMENTS PRESEN, PHOTOSYNTHESIS

FLAGELLA

EXTENSION OF CELL WALL



NOT COVERED BY CELL MEMBRANE

⇒ NUMBER & DISTRIBUTION: VARY IN BACTERIA

⇒ FLAGELLIN PROTEIN

⇒ LOCOMOTION (MOTILE)

GRAM STAINING

G+ve	G-ve
RETAIN CRYSTAL VIOLET DYE AFTER ALCOHOL WASHING	LOSE DYE AFTER WASHING
VIOLET/ PURPLE	PINK

SHAPE OF BACTERIA

4 TYPES

- COCCUS : SPHERICAL ○
- BACILLUS : ROD LIKE ▭
- VIBRIO : COMMA LIKE ❜
- SPIRILUM : SPIRAL {

★ PROKARYOTES

BACTERIA

BLUE GREEN ALGAE

MYCOPLASMA : CELL WALL ABSENT
OR
PPLO (PLEURO PNEUMONIA LIKE ORGANISM)

CATTLE : LUNG : PLEURAL FLUID → ISOLATE ORGANISM → PNEUMONIA

★

	PROK	EUKARY
SIZE:	small	LARGE
MULTIPLY:	FAST	SLOW

POLYRIBOSOME / POLYSOME

→ many RIBOSOME ON SINGLE

messenger RNA (mRNA)

TRANSLATION ↓

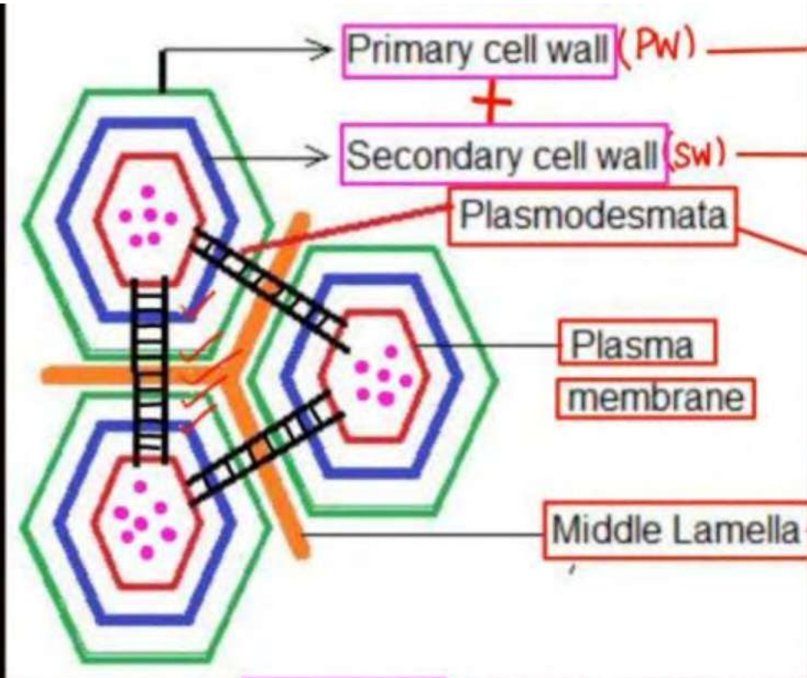
PROTEIN with HELP OF RIBOSOME

	PLANT	ANIMAL CELL
Cell wall	✓	X
PLASTID (CHLOROPLAST)	✓	X
LARGE CENTRAL VACUOLE	✓	X
CENTRIOLE	X	✓

MEMBRANE BOUND ORGANELLE

COMPLEX LOCOMOT STRUCTURE &
CYTOSKELETON (MICROTUBULE, MICROFILAMENT, INTERMEDIATE FILAMENT)

		MEMBRANE BOUND ORGANELLE	COMPLEX LOCOMOT STRUCTURE & CYTOSKELETON
⇒ COMPARTMENTALISATION	PRESENT (EUKARYOTE)	✓	✓
	ABSENT (PROKARYOTE)	X	X.



→ OUTER, YOUNG CELL, THIN, REDUCED/DIMINISHED IN MATURE CELL, CAPABLE OF GROWTH (add^n of cellulose continuously)

→ INNER, MATURE CELL (OLD), THICK (NEAR TO CELL MEMBRANE)

→ CONNECT CYTOPLASM OF TWO CELLS
CELL WALL (PW + SW), MIDDLE LAMELLA CROSS/TRAVERSED BY PLASMODESMATA

→ COMMON LAYER B/W TWO CELL, (CALCIUM PECTATE)

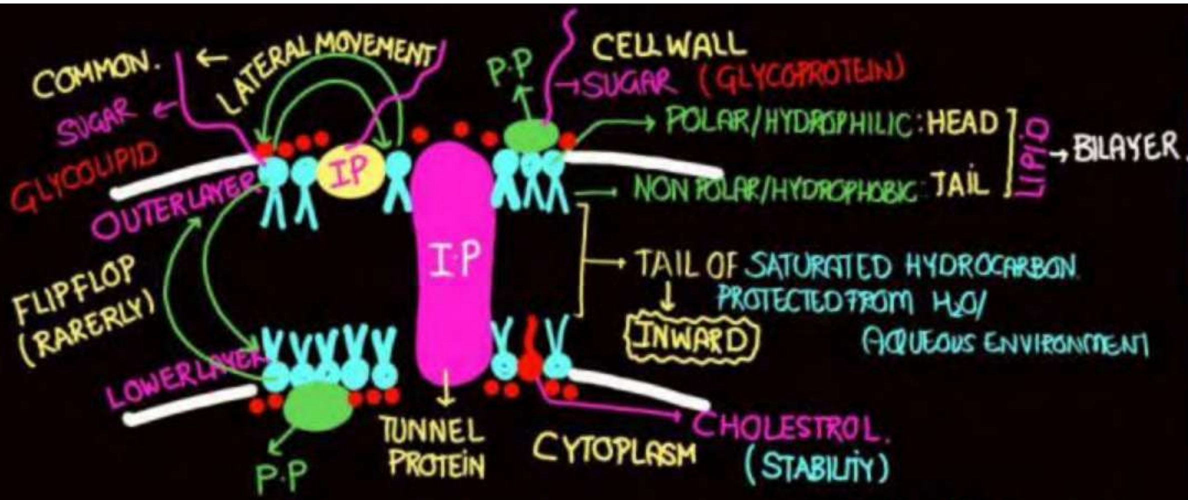
CELL WALL ⇒ PW + SW : DOUBLE LAYER

⇒ RIGID/HARD LAYER, NON-LIVING
⇒ OUTER TO CELL MEMBRANE
⇒ ALGAE: CELLULOSE, GALACTAN, MANNAN, $CaCO_3$ (MINERAL)
⇒ PLANT: CELLULOSE, HEMICELLULOSE, PECTIN, PROTEIN
⇒ FUNGI: CHITIN

FUNCTION

* SHAPE
* PROTEIN PRESENT IN CW PROTECT FROM PATHOGEN/INFECTION
* PROVIDE BARRIER TO UNDESIRABLE MACROMOLECULE (LARGE SIZE)
* CELL TO CELL INTERACTION

CELL MEMBRANE



REMOVE

P.P: PERIPHERAL PROTEIN, EASY

I.P: INTEGRAL PROTEIN, DIFFICULT

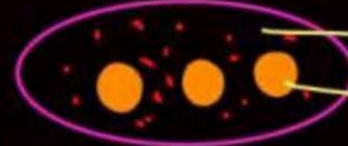
TOTALY BURIED (2 LAYER) — PARTIALLY BURIED (1 LAYER)

COMMON LIPID: PHOSPHOLIPID

SINGER & NICOLSON. 1972

FULID MOSAIC MODEL (QUASI/ SEMIFLUID)

- LIPID → FLUID → UNSATURATED FATTY ACID
- PROTEIN → SOLID
- PROTEIN → LATERAL MOVEMENT OF PROTEIN CONFIRM FLUID NATURE OF CELL MEMBRANE



→ CHEMICAL STUDY: HUMAN RBC: CELL MEMBRANE (LIPID + PROTEIN)

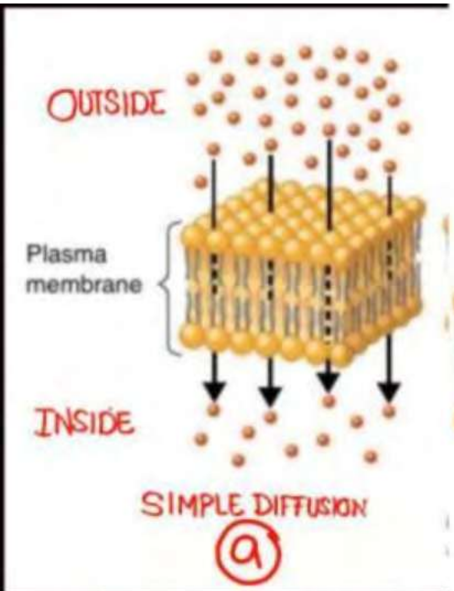
→ BIOCHEMICAL STUDY

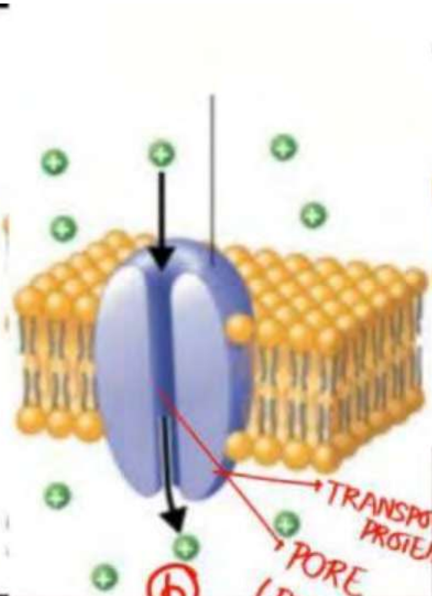
Membrane: Carbohydrate also present

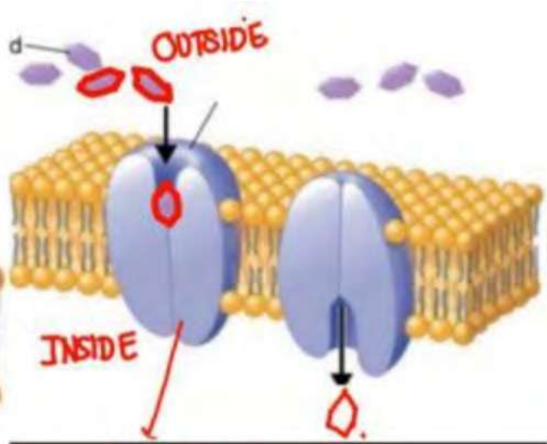
RBC. Membrane: 52% P, 40% L → THIS RATIO VARY IN DIFFERENT CELL MEMBRANE

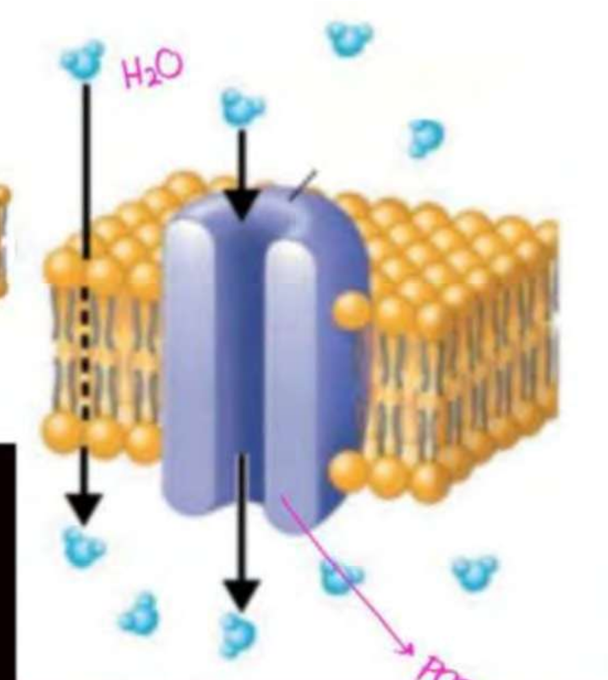
↓

Main FUNCTⁿ (TRANPORT)









eg. NEUTRAL / LIPID SOLUBLE CAN PASS
⇒ NO CARRIER PROTEIN
⇒ HIGH TO LOW CON^n
⇒ NO ENERGY (PASSIVE MOVEMENT)

(PORINS PROTEIN / CHANNEL PROTEIN)
POLAR / HYDROPHILIC
MOVE THROUGH MEMBRANE
DIFFICULT.

TRANSPORT PROTEIN (CARRIER PROTEIN ↓ INTEGRAL PROTEIN)
c

FACILIATATED DIFFUSION
HIGH → LOW CON^n
NO ENERGY, (PASSIVE MOVEMENT)

PORINS

WATER
HIGH CON^n ⟶ LOW CON^n
MOVE THROUGH SELECTIVELY PERMEABLE / CELL MEMBRANE (OSMOSIS).

Active TRANSPORT

⇒ LOW → HIGH CONⁿ (SOME MOLECULES/ IONS

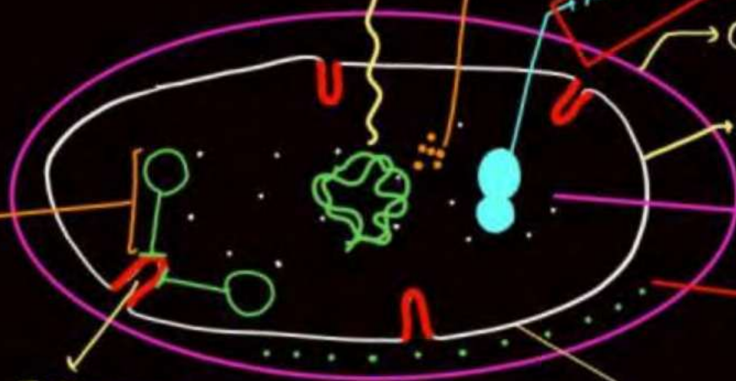
⇒ AGAINST CONCENTRATION

⇒ ATP / ENERGY

⇒ CARRIER PROTEIN

eg. $Na^+ K^+$ pump

MITOCHONDRIA



SINGLE ds circular DNA → PROTEIN SYNTHESIS (semi autonomous organelle)

RNA molecules

70S RIBOSOME → PROTEIN SYNTHESIS

OM : PORINS (PROTEIN) ✓ , MORE PERMEABLE , CONTINUOUS → DIFFERENT ENZYMES

IM : X , LESS , DISCONTINUOUS → DIFFERENT ENZYMES

MATRIX — HOMOGENOUS REGION COVERED BY IM. INNER COMPARTMENT

INTERMEMBRANOUS SPACE → OUTER COMPARTMENT

ATP synthase / Oxysome / F1 F0 particle → ATP synthesis (DURING AEROBIC RESPIRATION) (POWER HOUSE OF CELL)

INFOLDING OF IM — CRISTAE ↓ SURFACE AREA INCREASE

ELECTRON TRANSPORT CHAIN (ATP synthesis)

- ⇒ DIVIDE BY BINARY FISSION
- ⇒ CYLINDRICAL / SAUSAGE STRUCTURE
- ⇒ NOT VISIBLE IN MICROSCOPE UNTIL STAIN BY DYE.

- ⇒ SHAPE, SIZE, number VARY IN DIFFERENT CELL
- ⇒ NUMBER : DEPEND : PHYSIOLOGY OF CELL.

PLASTID

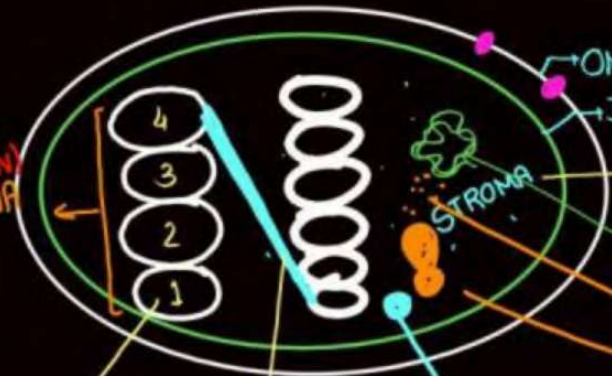
⇒ ALL PLANTS, EUGLENOID: PRESENT
⇒ LARGE ORGANELLE: VISIBLE IN MICROSCOPE
⇒ PIGMENTS PRESENT

PIGMENTS

- CHROMOPLAST
  - ↓ FAT SOLUBLE PIGMENT CAROTENOIDS
  - ⇒ RED, YELLOW, ORANGE BUT NOT GREEN.
  - eg: TOMATO, CARROT
- CHLOROPLAST
- LEUCOPLAST (PIGMENT ABSENT)
  - SHAPE, SIZE, STORED FOOD
  - AMYLOPLAST (STARCH eg: POTATO TUBER)
  - ALEUROPLAST (PROTEIN)
  - ELAIOPLAST (FAT/OIL)

LR + DR ⟶ PHOTOSYNTHESIS

(PILES OF COIN) GRANA



→ OM: PORINS, MORE PERMEABLE
→ IM
STROMA → COVERED BY INNER MEMBRANE

CIRCULAR DNA
RNA
70S RIBOSOME
PROTEIN SYNTHESIS

THYLAKOID (FLAT, MEMBRANOUS, SAC LIKE)
↓
PIGMENT (Chl a, b, carotenoid (carotene + xanthophyll))
↓
absorb light
↓
LIGHT RXN
ATP, NADPH+H (ENERGY)

STROMAL LAMELLA (FLAT, MEMBRANOUS, TUBULE CONNECT TWO GRANA)

ENZYMES (glucose/carbohydrate/ FOOD SYNTHESIS
↓
DARK RXN

Energy utilised in DARK RXN

Semi-autonomous ORGANELLE.

RIBOSOME

⇒ PROTEIN SYNTHESIS, MEMBRANLESS
SMALLEST ORGANELLE, PALADE PARTICLE.

PROK.
↓
RIBONUCLEOPROTEIN ← 70S (RNA+PROTEIN)

30S (small) | 50S (LARGE)

⇒ 16S rRNA
⇒ 21 PROTEIN

⇒ 5S, 23S rRNA
⇒ 34 PROTEIN

EUK
↓
80S

40S | 60S

⇒ 18S rRNA
⇒ 33 P.

⇒ 5S, 28S, 5.8S
⇒ 47P

80 protein

S: Svedbergy UNIT
↓
IS SEDIMENTATION COEFFICIENT (VELOCITY)
HIGH HIGH
(indirect measure
size & density)

Cilia & Flagella

⇒ A [MICROTUBULE) (M.T)
⇒ B

TUBULIN PROTEIN

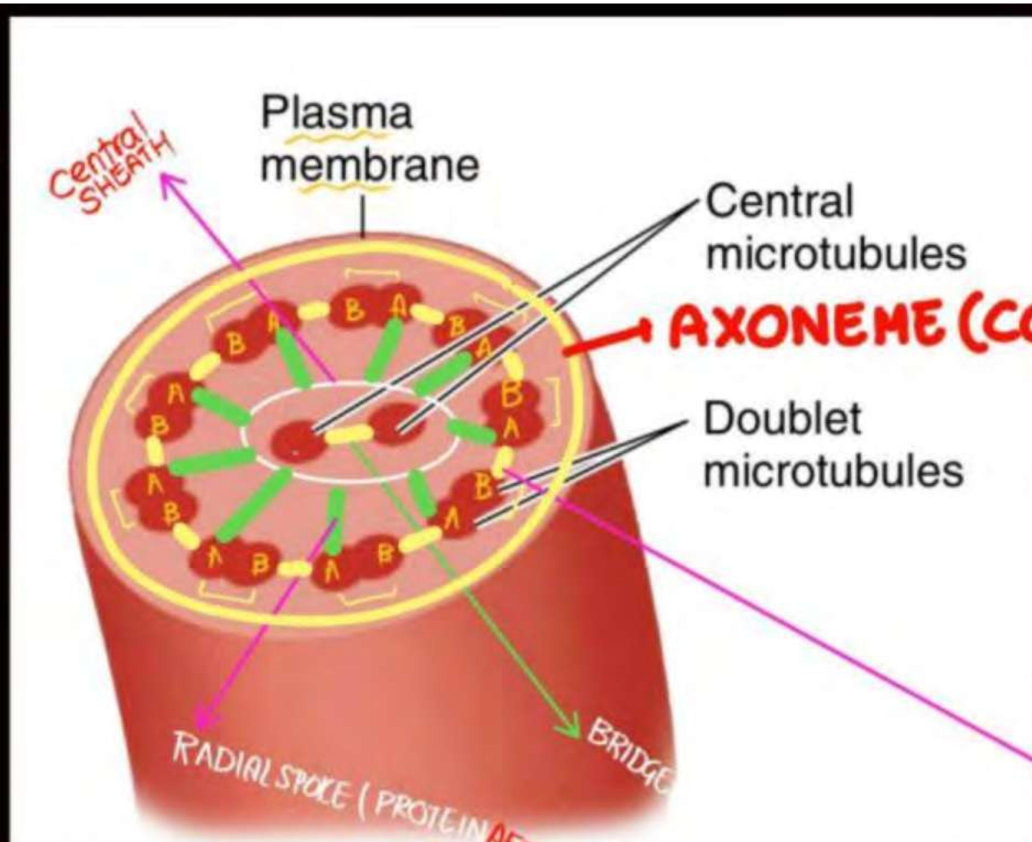
PERIPHERAL MICROTUBULE : (M.T)

⇒ 9 (DOUBLET)

⇒ 1 doublet : 2 M.T → A, B

⇒ 9 X 2 = $\boxed{18\text{ M.T}}$

CENTRE : 2 M.T (pair of M.T)



(Periphery centre.

9 (doublet) + 2

9X2 = 18 + 2

⇒ 20 M.T

⇒ Central M.T connected BY BRIDGE

⇒ Central M.T covered By central SHEATH

⇒ RADIAL SPOKE : 9
arise from one of TWO (A M.T)

⇒ INTERDOUBLET/LINKERS
CONNECT TWO PERIPHERAL DOUBLET.

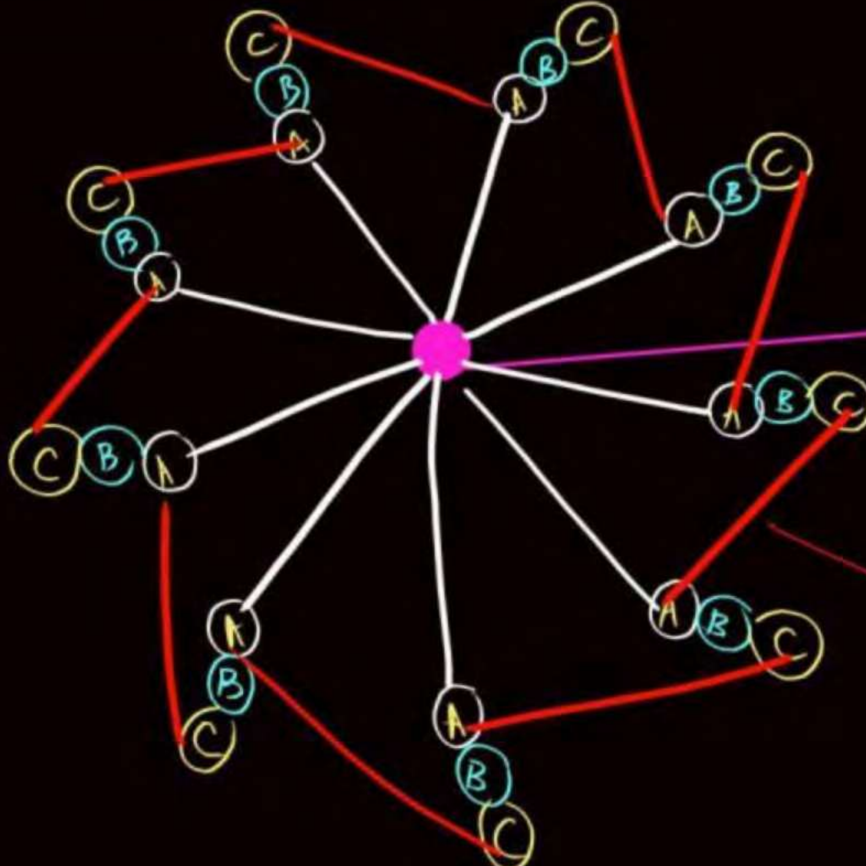
CENTROSOME & CENTRIOLE

Pericentriolar material (protein)

⇒ 1 CENTROSOME: 2 CENTRIOLE (CYLINDRICAL STRUCTURE)

⇒ 90° to each other

⇒ membranless, cartwheel structure



⇒ PERIPHERAL: 9 TRIPLET

⇒ 1 TRIPLET: 3 M.T (A, B, C

⇒ $\boxed{\text{PERIP: } 9 \times 3 \Rightarrow 27 \text{ M.T}}$

CENTRAL HUB: PROTIENAEOUS STRUCTURE

⇒ $\boxed{9(\text{TRIPLET}) + 0}$

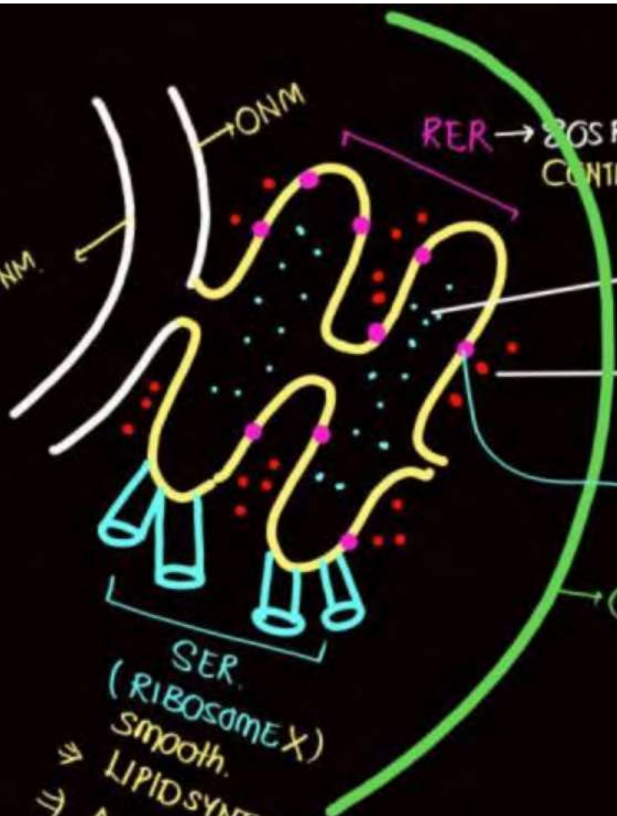
⇒ $9 \times 3 = 27 + 0 \Rightarrow 27$

⇒ 9 RADIAL SPOKE (PROTEIN)

C-A LINKER (PROTEIN)

⇒ Cell division in animal cell

⇒ HELP SPINDLE FIBRE FORMATION



RER → 80S RIBOSOM, PROTEIN SYNTHESIS
CONTINUOUS WITH OUTER NUCLEAR MEMBRANE

INSIDE ER: SPACE: (LUMINAL)

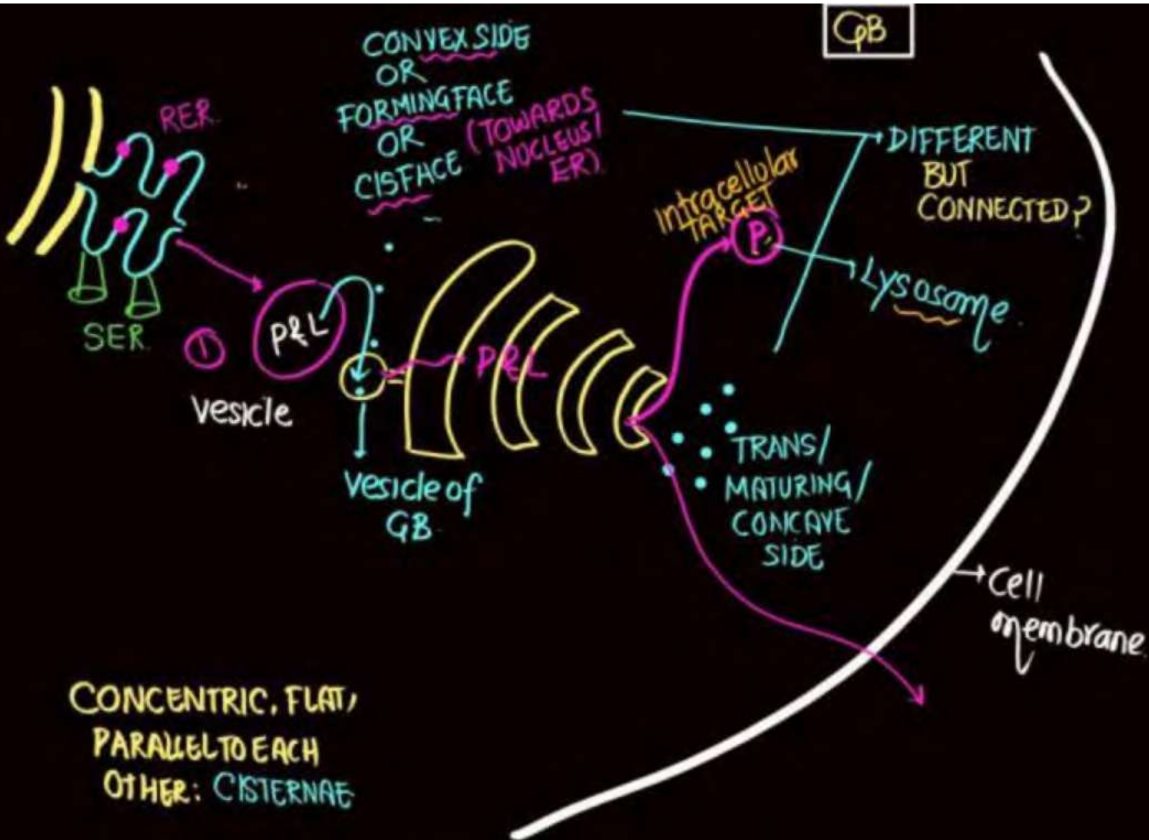
CYTOPLASM: EXTRA LUMINAL.
(OUTSIDE)

PROTEIN SYNTHESIS BY
RER MOVE OUT
SIDE THE CELL
(SECRETION)

SER.
(RIBOSOME X)
smooth.
⇒ LIPID SYNTHESIS
⇒ ANIMAL (STEROID/
LIPID LIKE
HORMONE)
synthesis.

ER

⇒ NETWORK/RETICULUM
OF TINY TUBULAR
STRUCTRE
IN CYTOPLASM



① vesicle come from ER (PROTEIN & LIPID)

② moves to cis side of GB

③ P & L enters into vesicle of GB.

④ P & L moves to cisternae.

P + sugar ⟶ glycoprotein
L + sugar ⟶ glycolipid
(glycosylation of protein & lipid)
modification (cisternae)

⑤ some protein move outside the cell (secretory protein)

⑥ some protein after modification Release inside the cell in form of Lysosome

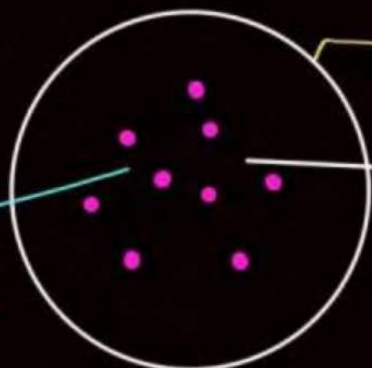
⑦ Lysosome formed due to packaging By G.B. But RER provide protein for synthesis of Lysosome

ENDOMEMBRANE SYSTEM : ER, GB, LYSOSOME, VACUOLE (WORK IN COORDINATION)

NON ENDOMEMBRANE SYSTEM : MITOCHONDRIA, CHLOROPLAST, PEROXISOME (NOT WORK IN COORDINATION)

Lysosome

⇒ formation By G.B



membrane

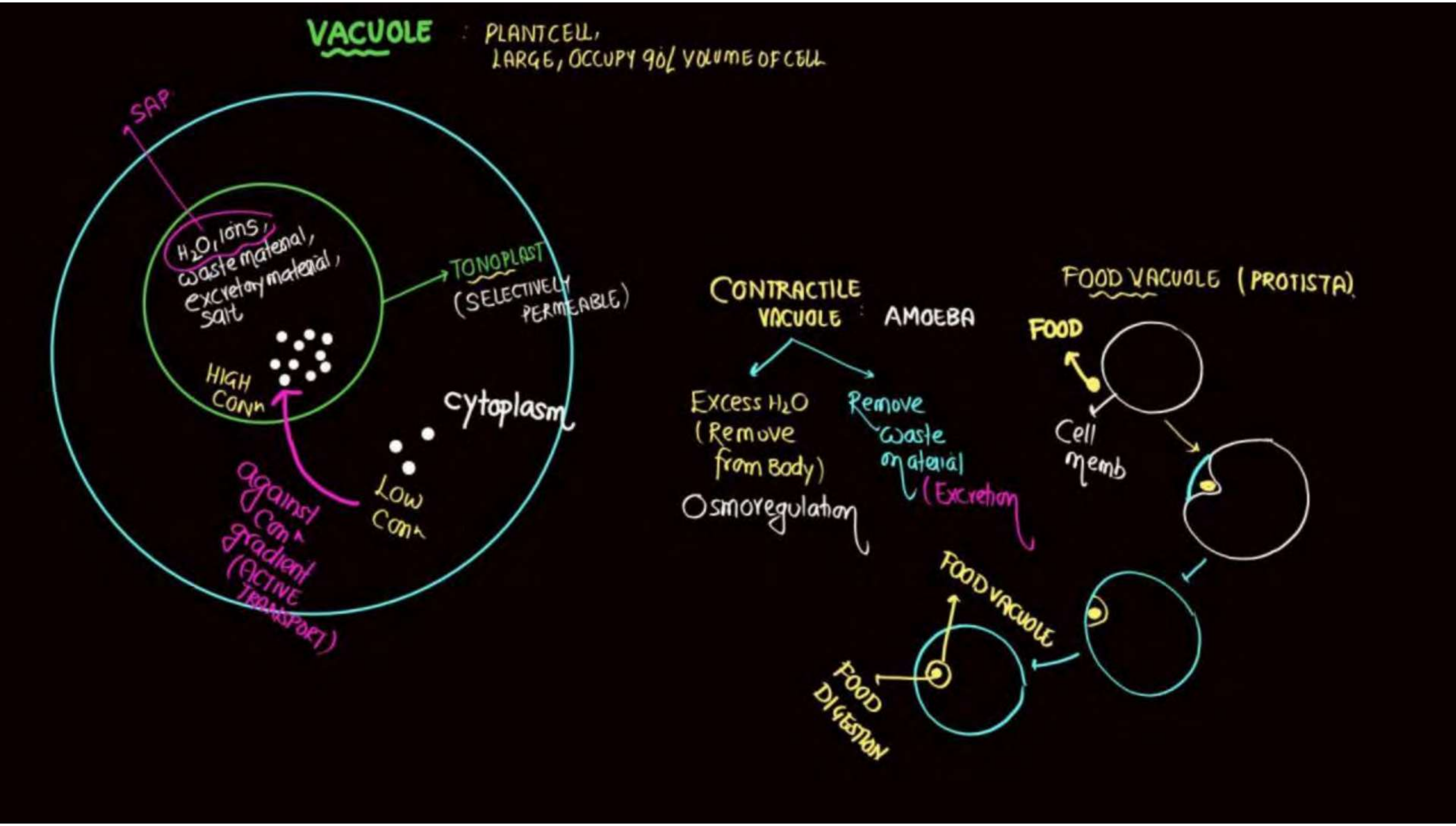
acidic medium

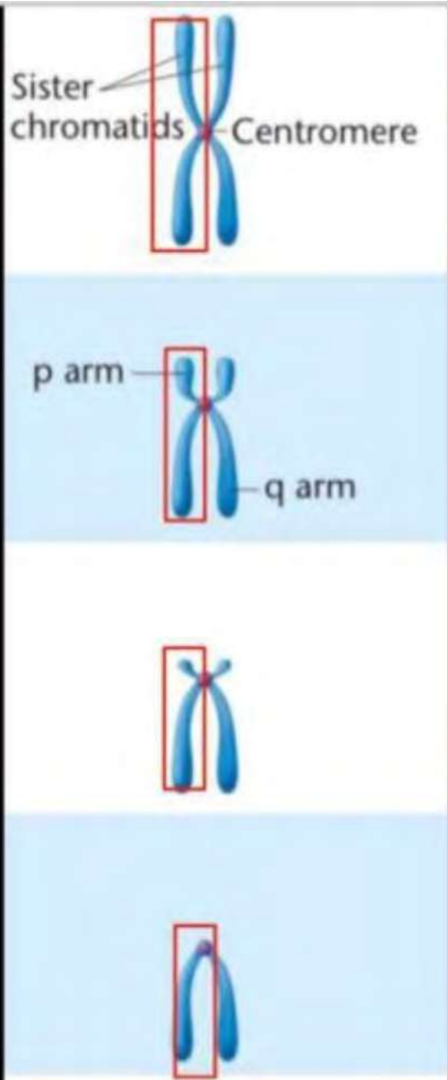
PH: 5.

Carbohydrase
Protease
Lipase
Nuclease

→ DIGESTIVE/ HYDROLYTIC ENZYME → NEED H_2O

FOOD DIGESTION


VACUOLE : PLANT CELL,
LARGE, OCCUPY 90% VOLUME OF CELL
SAP
H_2O, ions, waste material, excretory material, salt
TONOPLAST (SELECTIVELY PERMEABLE)
HIGH Conn
Low Conn
Cytoplasm
against Con gradient (ACTIVE TRANSPORT)
CONTRACTILE VACUOLE : AMOEBA
Excess H_2O (Remove from Body)
Osmoregulation
Remove waste material (Excretion)
FOOD VACUOLE (PROTISTA)
FOOD
Cell memb
FOOD VACUOLE
FOOD DIGESTION



CENTROMERE

TYPE OF CHROMOSOME (ON POSITION OF CENTROMERE).

→ arm
→ arm
CENTRE → EQUAL

METACENTRIC = V

→ short (p)
→ LONG (q)
→ UNEQUAL

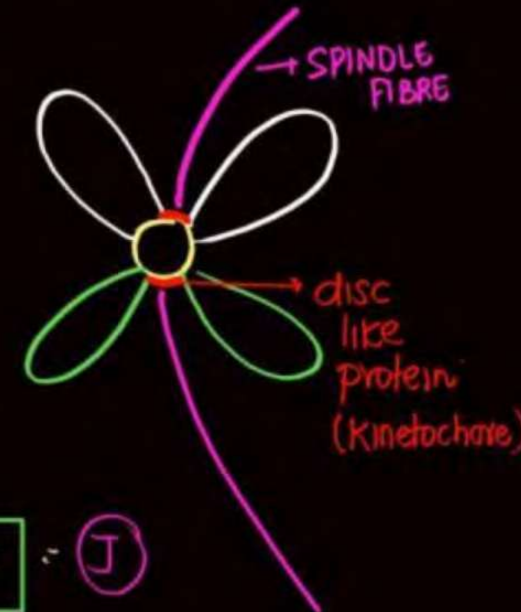
SUB-METACENTRIC = L

→ very short
→ very LONG
→ UNEQUAL (Centromere situated to one end)

Acrocentric = J

→ Centromere Terminal ⇒ I Shape.

TELOCENTRIC

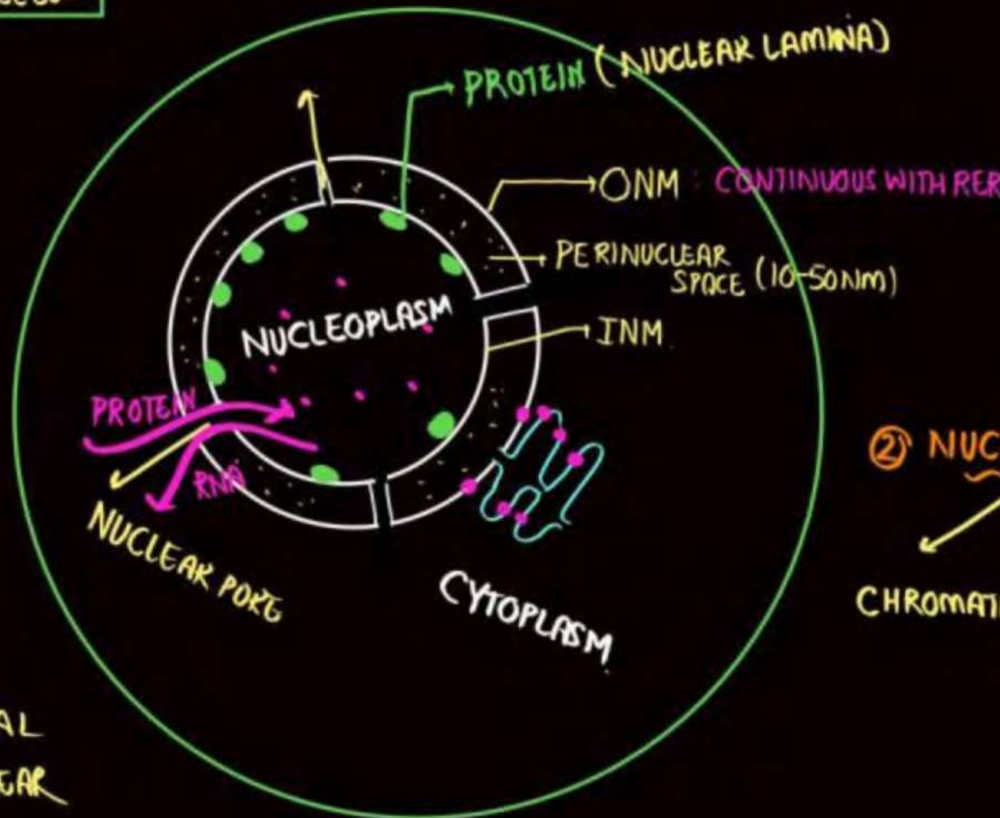


NUCLEUS

⇒ ROBERT BROWN, 1831
⇒ cell : generally : one nucleus
⇒ paramecium : Two nucleus
⇒ Mature sieve Tube, mammalian RBC → NUCLEUS ABSENT
mammalian RBC → LIVING

① NUCLEAR MEMBRANE

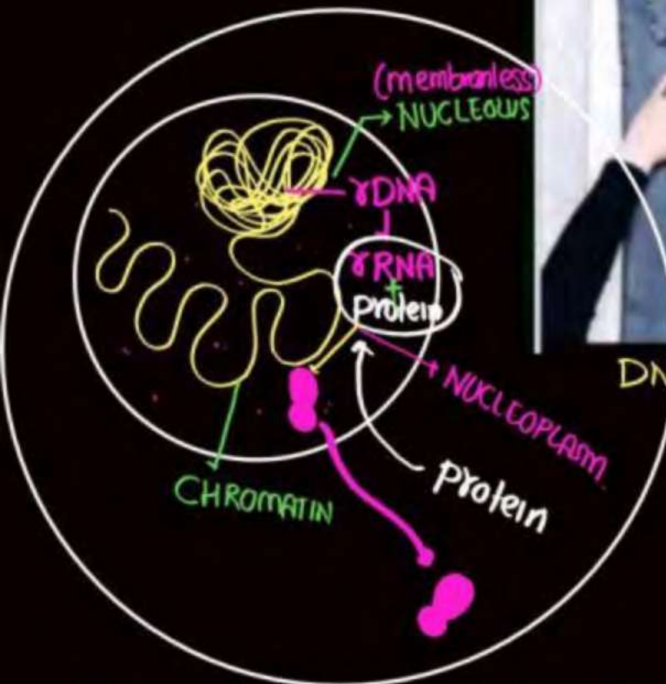
⇒ DOUBLE LAYER
⇒ PERINUCLEAR SPACE/ NM SEPERATE CYTOPLASM & NUCLEOPLASM
⇒ protein & RNA : BIDIRECTIONAL MOVEMENT THROUGH NUCLEAR PORE.



② NUCLEOPLASM

→ CHROMATIN
→ NUCLEOLUS.

③ CHROMATIN:
flemming, stain By Basic DYE



NOTE: NUCLEOLUS: MORE IN NUMBER, LARGE IN SIZE (CELL ACTIVELY INVOLVED PROTEIN SYNTHESIS)

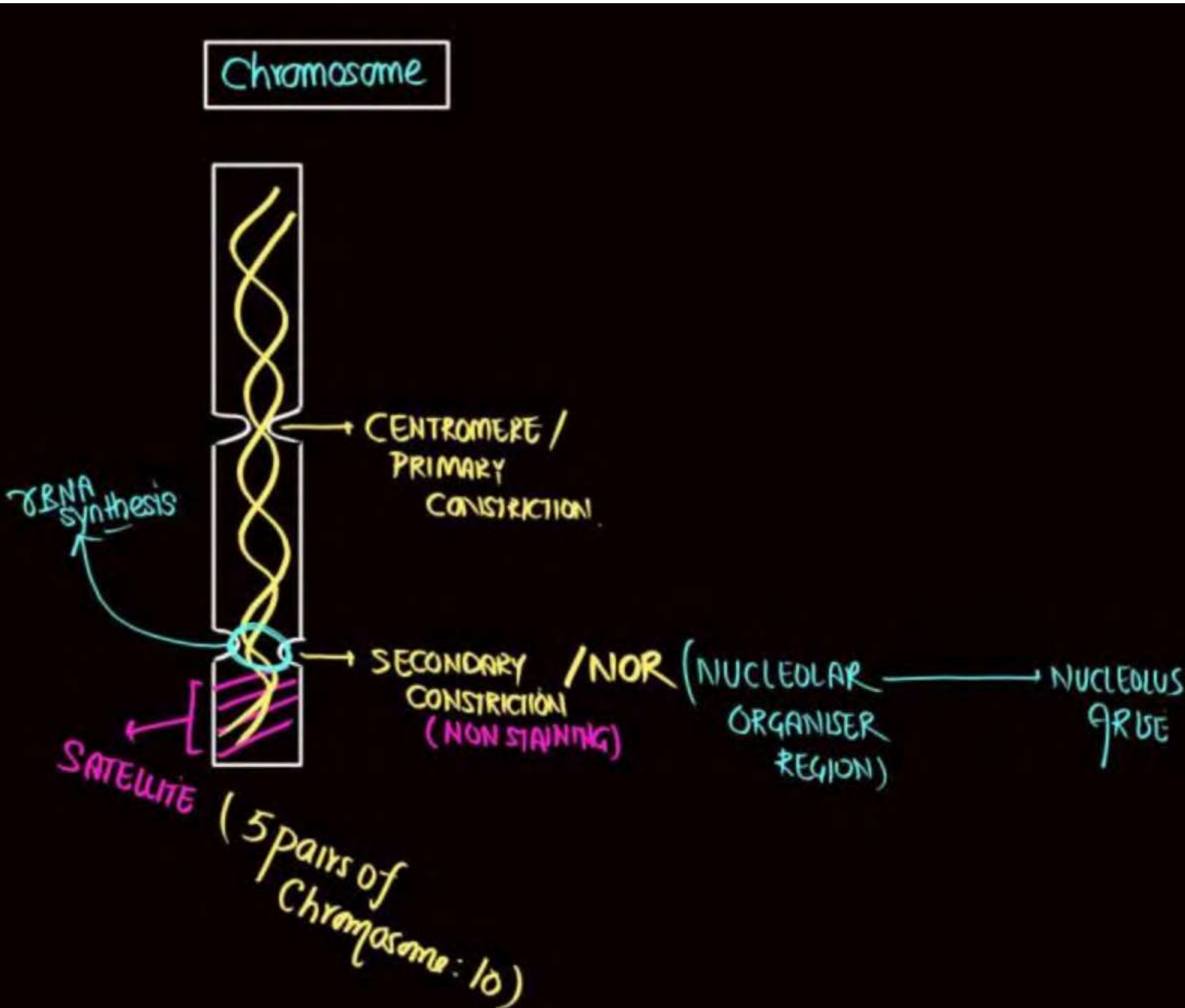
DNA ⟶ $\boxed{\text{Chromatin}}$ ⟶ $\boxed{\text{Chromosome}}$ → DNA, Hist P, Non P, RNA

Chromatin
⇒ LONG
⇒ THIN
⇒ INDISTINCT / DECONDENSED
⇒ INTERPHASE (NON-DIVIDING)
⇒ LOOSE

Chromosome
⇒ SHORT
⇒ THICK
⇒ DISTINCT / CONDENSED
⇒ PRO, META, ANA (DIVIDING PHASE)

me

⇒ Chromatin: collected (NUCLEOLUS)
⇒ No seperation Betw NUCLEOLUS & NUCLEOPLASM Because NUCLEOLUS is MEMBRANELESS.
⇒ NUCLEOUS (γDNA) ⟶ γRNA)
⇒ Protein (cytoplasm) ⟶ NUCLEUS
⇒ γRNA + Protein ⟶ RIBOSOME (NUCLEUS)
⇒ RIBOSOME (NUCLEUS) ⟶ CYTOPLASM


Chromosome
CENTROMERE / PRIMARY CONSTRICTION
rRNA synthesis
SECONDARY CONSTRICTION /NOR (NUCLEOLAR ORGANISER REGION)
(NON STAINING)
NUCLEOLUS ARISE
SATELLITE (5 pairs of Chromosome: 10)

MONERA

- also Found in extreme Habitat/adverse Condition (HOTSPRING, HIGH TEMPERATURE) Snow, desert, deep ocean.
- 100 Bacteria : 1 Handful of soil
- parasite

Sole member Bacteria, Found everywhere, ABUNDANT

Shape

COCCUS : SPHERICAL
BACILLUS : ROD
VIBRIO : COMMA
SPIRAL : SPIRILLUM.

STRUCTURE : SIMPLE
BEHAVIOUR : COMPLEX.

PHOTOAUTOTROPHS → LIGHT ENERGY

NON-OXYGENIC

$CO_2 + H_2S \xrightarrow{\text{LIGHT ENERGY}}$ glucose + S.

inorganic compound : USE

CHEMOAUTOTROPHS → CHEMICAL ENERGY

SOIL

$NH_3 \longrightarrow NO_2^- \longrightarrow NO_3^-$ + Energy

INORGANIC COMPOUND → OXIDATION → CHEMICAL ENERGY RELEASED → UTILISED IN ATP synthesis, Recycling of nutrients.

Extensive metabolic diversity (TYPES OF NUTRITION).

HETROTROPHS (MOSTLY)

- ★ mostly decomposer
- ★ FEED ON DEAD ORGANIC MATTER (SAPROPHYTIC)
- ★ HUMAN WELFARE (AFFAIRS)

eg: MILK $\xrightarrow{\text{LACTOBACILLUS}}$ CURD

eg: ANTIBIOTIC FORMATION

eg: NITROGEN FIXATION.
1. RHIZOBIUM : ROOT OF LEGUMES
2. FRANKIA : ROOT OF NON-LEGUMES (ALNUS, CASUARINA)

PATHOGENIC

- ★ CROPS, PETS, HUMAN, FARM ANIMAL.
- ★ Cholera, Tetanus, Typhoid, CITRUS CANKER.
  (VIBRIO) Clostridium, Salmonella Xanthomonas.

Reproduction

ASEXUAL

Common/Favourable Condition
BINARY FISSION (AMITOSIS)

UNFAVOURABLE CONDITION
SPORE FORMED (ENDOSPORE)

⇛ SORT OF SEXUAL REPRODUCTION
(PRIMITIVE METHOD OF DNA TRANSFER)

eg: CONJUGATION

MYCOPLASMA

* ★ SMALLEST LIVING CELL
* ★ CELL WALL ABSENT, NO DEFINITE SHAPE (PLEOMORPHIC)
* ★ CAN SURVIVE WITHOUT O_2.
* ★ INFECTION IN PLANT & ANIMAL.
* ★ CAN PASS THROUGH BACTERIAL FILTERS.

ARCHAEBACTERIA

MONERA → EUBACTERIA: BACTERIA (TRUE BACTERIA)
MONERA → ARCHAEBACTERIA (PRIMITIVE / ANCIENT BACTERIA)

★ CELL WALL DIFFERENT (PSEUDOMUREIN) ⇝ SURVIVE IN ADVERSE/HARSH/UNFAVOURABLE CONDITION.

HALOPHILES
(EXTREME SALT/ SALINE CONDITION).

THERMOACIDOPHILES (HOT SPRING)
⇛ HIGH TEMP,
⇛ ACIDIC CONDITION

METHANOGENS
⇛ MARSHY AREA.
⇛ CATTLE → STOMACH → RUMEN.
⇛ GOBAR/DUNG → BIOGAS PRODUCED
(CELLULOSE, CH_4 PRODUCING BACTERIA)

CYANOBACTERIA
BLUE GREEN ALGAE

UNICELLULAR, COLONIAL FILAMENTOUS.

FRESH H_2O
MARINE H_2O
TERRESTIAL.

Oxygenic photosynthesis

$CO_2 + H_2O$ ⇝ glucose

Chla, $\underbrace{\text{carotene + xanthophyll}}_{\text{CAROTENOIDS}}$

Excessive growth of BGA IN POLUTED H_2O: WATER BLOOM.

SPIRULINA: FILAMENTOUS, BGA,
RICHEST SOURCE OF PROTEIN,
SPACE FOOD.

NOSTOC, ANABAENA
(FILAMENTOUS BGA)
↓
SPECIAL CELL
(NITROGEN FIXTATION)
HETROCYST)
$N_2 \longrightarrow 2NH_3$.

NOSTOC

→ SPECIAL, LARGE, THICK CELL WALL, ANAEROBIC CONDITION, N_2 FIXT^n

→ PHOTOSYNTHESIS (VEGETATIVE CELL)

PROTISTA

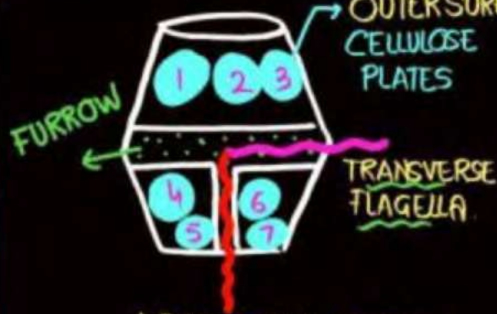
★ UNICELLULAR EUKARYOTES.
★ MEMBERS: MOSTLY AQUATIC
★ MEMBRANE BOUND ORGANELLE PRESENT
★ NUCLEUS PRESENT
★ SHOW CHARACTER OF PLANT, ANIMAL, FUNGI
★ BOUNDARIES NOT WELL DEFINED
★ SOME BIOLOGIST

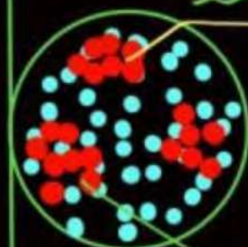
PLANTS ← → PHOTOSYNTHETIC PROTISTAN

★ ASEXUAL (BINARY FISSION)
★ GAMETE/CELL FUSION (FERTILISATION)
↓
ZYGOTE FORMATION
★ SOME HAVE CILIA/ FLAGELLA.

DINOFLAGELLAES

★ MOSTLY MARINE, PHOTOSYNTHETIC,
★ BLUE, BROWN, RED, GREEN, YELLOW
DEPENDS UPON PIGMENT

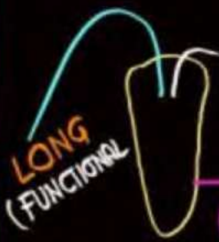




→ RED COLOUR (GONYAULAX: MORE IN NUMBER, FAST REPRODUCTION/ MULTIPLICATION) (PIGMENTS ✓)
RED TIDE

→ TOXIN PRODUCE
↓
HARMFUL FOR FISHES.

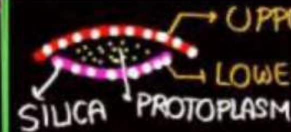
EUGLENOIDS



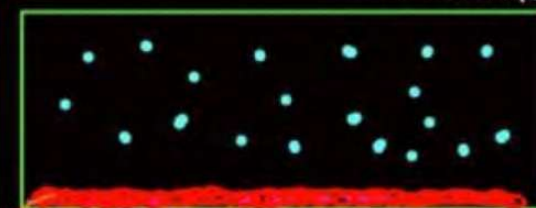
⇒ CELL WALL ABSENT
⇒ BODY FLEXIBLE
⇒ FRESH H_2O (STAGNANT H_2O)
⇒ Chl a, b (Pigments Similar to HIGHER PLANT)
⇒ LIGHT PRESENT: AUTOTROPHS PHOTOSYNTHESIS
⇒ LIGHT ABSENT: FEED ON SMALL ANIMALS, HETROTROPHS.
⇒ TWO MODES OF NUTRITION.

CHRYSOPHYTES

★ DIATOMS & DESMIDS (GOLDEN ALGAE)
★ FRESH H_2O, MARINE H_2O, MOSTLY PHOTOSYNTH.
★ MOVEMENT: ROLE: H_2O CURRENT (PLANKTON) (PASSIVE).
★ MAIN PRODUCER IN OCEAN. (DIATOMS)



→ CELL WALL, THIN, OVERLAPPING, SOAP BOX INDESTRUCTIBLE (NOT DAMAGE)



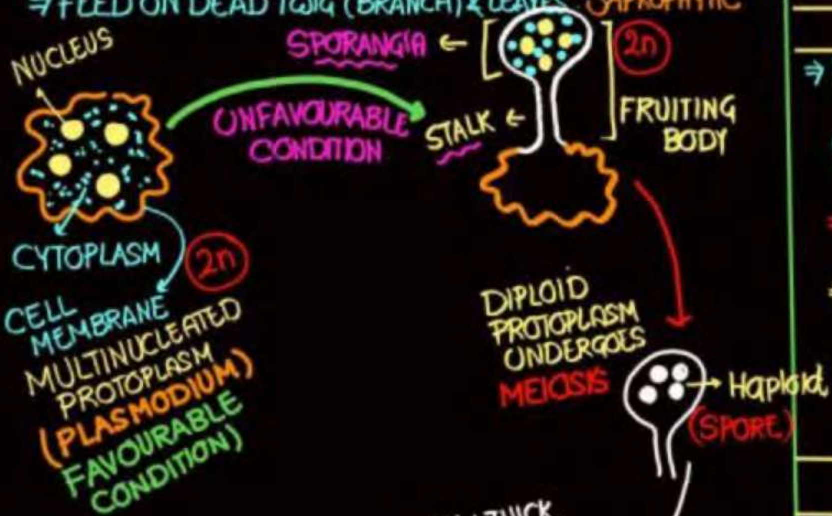
CELL WALL OF DIATOM DEPOSITED AT BOTTOM OF OCEAN, BILLIONS OF YEAR.

→ DIATOMACEOUS EARTH / DIATOMITE

FILTERATION OF OIL & SYRUPS. | GRITTY | POLISHING OF METAL.

SLIME MOULD

⇒ FEED ON DEAD TWIG (BRANCH) & LEAVES : SAPROPHYTIC



⇒ WALL : THICK.
⇒ RESISTANT

⇒ dispersed (air current).

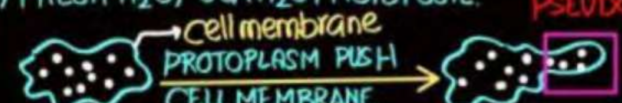
⇒ SPORE COVERED BY TRUE CELLULOSIC WALL.

⇒ SURVIVE FOR MANY YEARS DURING UNFAVOURABLE CONDITION.

PROTOZOA : PRIMITIVE RELATIVE OF ANIMAL , All HETROTROPHS (PREDATOR & PARASITE), CELL WALL ABSENT.

AMOEBOID

⇒ FRESH H_2O, SEA H_2O, MOIST SOIL.



⇒ TEMPORARY / FALSE FEET : LOCOMOTION, FOOD CAPTURE.

⇒ MARINE FORMS COVERED BY SILICA SHELL.

ENTAMOEBA (PARASITE) : DYSENTARY (CONTAMINATED H_2O & FOOD)

FLAGELLATED

⇒ FREE LIVING / PARASITE , FLAGELLA ✓

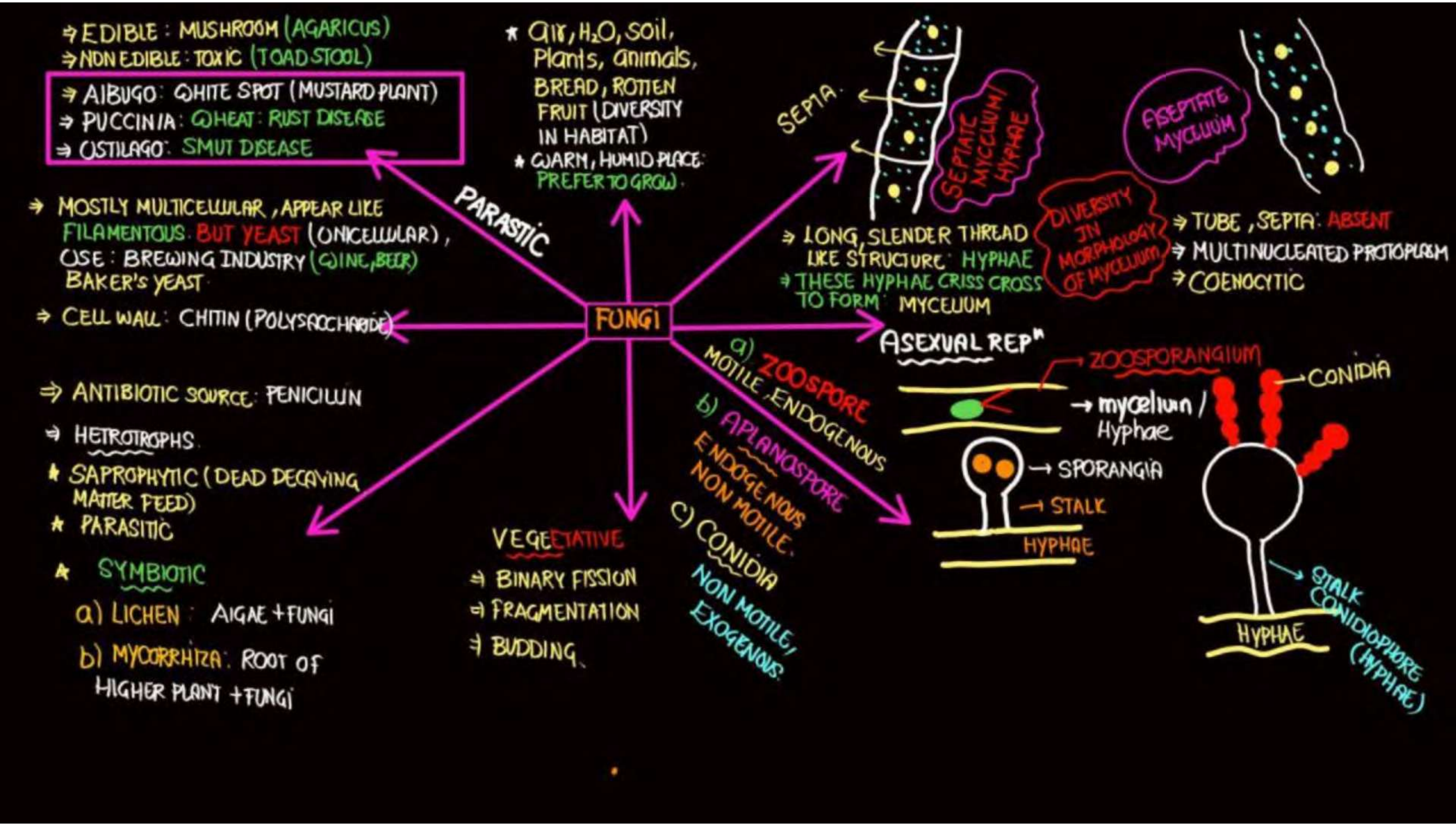
⇒ TRYPANOSOMA (Tse-tse Fly)
↓
BITE HUMAN
↓
RELEASE TRYPANOSOMA
↓
SLEEPING SICKNESS

CILIATED (PARAMECIUM), aquatic

THOUSAND OF CILIA BEAT
↓
H_2O CURRENT PRODUCE
↓
H_2O + FOOD ENTER INTO IT
↓
EXCESS H_2O REMOVE With HELP OF CONTRACTILE VACUOLE (OSMOREGULATION)

SPOROZOAN.

★ PLASMODIUM (NOTORIOUS) ⇒ Malaria
↓
LIFE CYCLE
(infectious spore)
↓
Staggering (Harmful effect on human)



FUNGI
⇒ EDIBLE : MUSHROOM (AGARICUS)
⇒ NON EDIBLE : TOXIC (TOAD STOOL)
⇒ AIBUGO : WHITE SPOT (MUSTARD PLANT)
⇒ PUCCINIA : WHEAT : RUST DISEASE
⇒ USTILAGO : SMUT DISEASE
PARASTIC
⇒ MOSTLY MULTICELLULAR, APPEAR LIKE FILAMENTOUS. BUT YEAST (UNICELLULAR), USE : BREWING INDUSTRY (WINE, BEER) BAKER's YEAST.
⇒ CELL WALL : CHITIN (POLYSACCHARIDE)
⇒ ANTIBIOTIC SOURCE : PENICILLIN
⇒ HETROTROPHS.
* SAPROPHYTIC (DEAD DECAYING MATTER FEED)
* PARASITIC
* SYMBIOTIC
a) LICHEN : ALGAE + FUNGI
b) MYCORRHIZA : ROOT OF HIGHER PLANT + FUNGI
* air, H_2O, soil, Plants, animals, BREAD, ROTTEN FRUIT (DIVERSITY IN HABITAT)
* WARM, HUMID PLACE : PREFER TO GROW.
VEGETATIVE
⇒ BINARY FISSION
⇒ FRAGMENTATION
⇒ BUDDING.
a) ZOOSPORE
MOTILE, ENDOGENOUS
b) APLANOSPORE
ENDOGENOUS
NON MOTILE.
c) CONIDIA
NON MOTILE,
EXOGENOUS
SEPTA
SEPTATE MYCELIUM / HYPHAE
ASEPTATE MYCELIUM
⇒ LONG, SLENDER THREAD LIKE STRUCTURE : HYPHAE
⇒ THESE HYPHAE CRISS CROSS TO FORM : MYCELIUM
DIVERSITY IN MORPHOLOGY OF MYCELIUM
⇒ TUBE, SEPTA : ABSENT
⇒ MULTINUCLEATED PROTOPLASM
⇒ COENOCYTIC
ASEXUAL REP^n
ZOOSPORANGIUM
→ mycelium / Hyphae
→ SPORANGIA
→ STALK
HYPHAE
CONIDIA
STALK
CONIDIOPHORE (HYPHAE)
HYPHAE

PHYCOMYCETES

CLASSIFICATION: FRUITING BODY, SPORE FORMATION, MORPHOLOGY OF MYCELIUM.

⇒ aquatic, Feed on dead decaying (moist, damp placed, parasite obligate (Albugo in MUSTARD.

⇒ ASEPTATE, COENOCYTIC, MYCELIUM.

⇒ ASEXUAL: ZOOSPORE (MOTILE), APLANOSPORE (NON MOTILE)

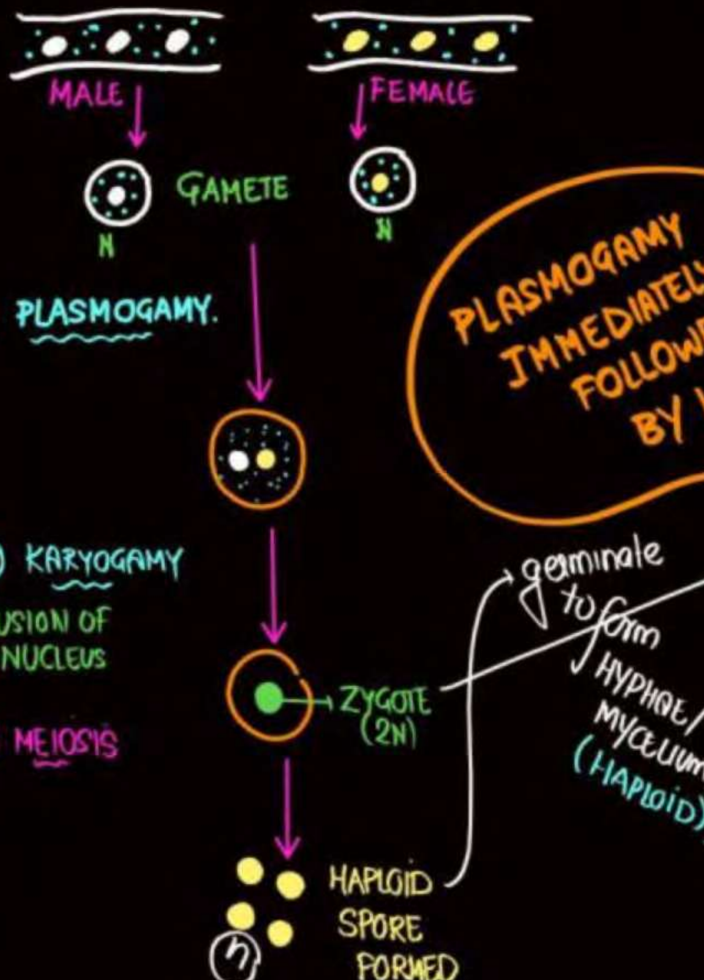
⇒ ISOGAMOUS, (BOTH MALE & FEMALE GAMETE MORPHOLOGICAL SIMILAR) ANISOGAMOUS & OOGAMOUS (DISSIMILAR)

SEXUAL REP^n (3 STEPS)

a) PLASMOGAMY: MIXING OF PROTOPLASM OF TWO CELLS, BUT NOT FUSED NUCLEUS

b) KARYOGAMY

c) MEIOSIS

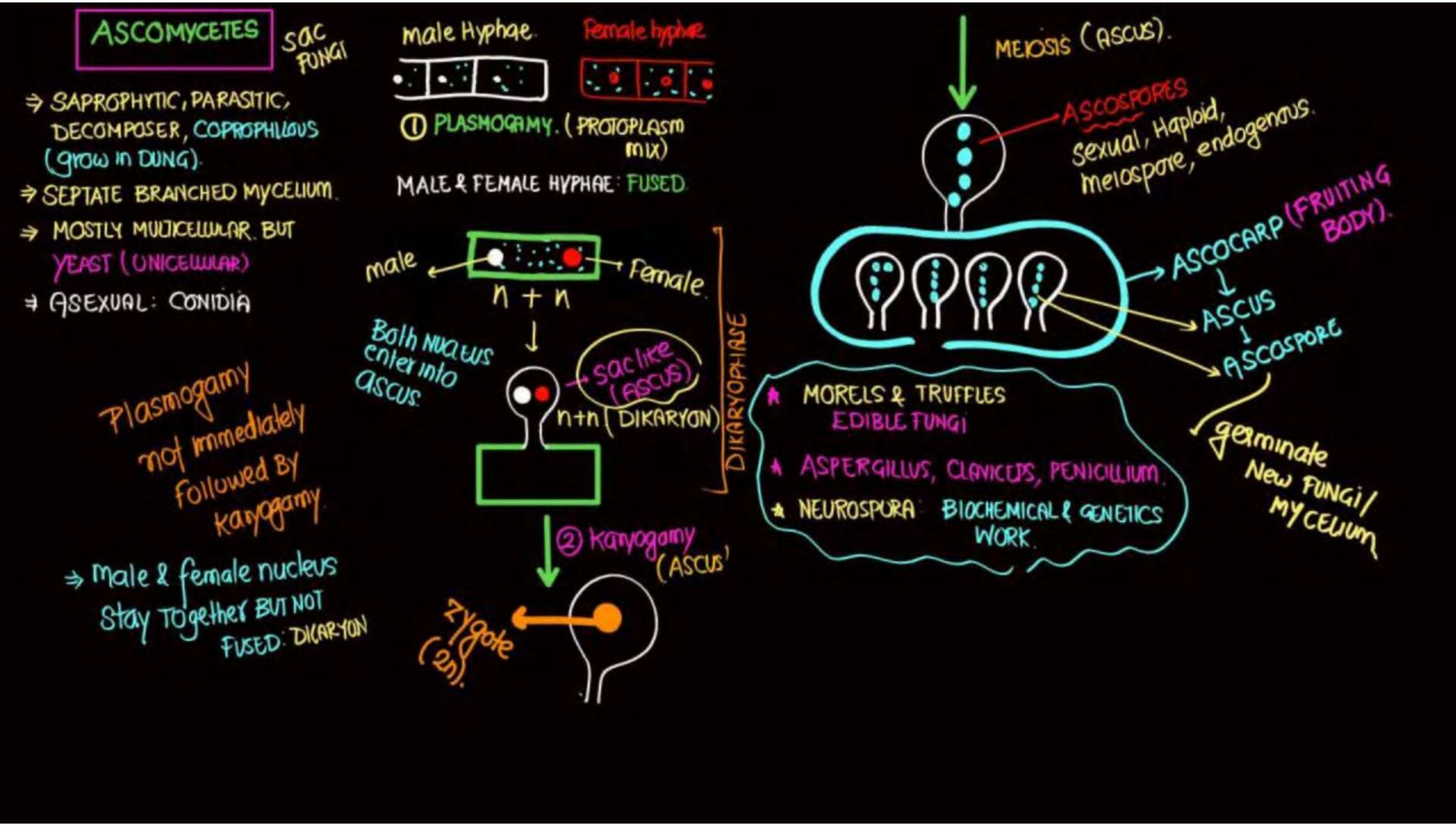


PLASMOGAMY IMMEDIATELY FOLLOWED BY KARYOGAMY

Rhizopus (BREAD MOULD)
MUCOR
ALBUGO

sexual spore: Zygospore (2n) or Oospore (2n)

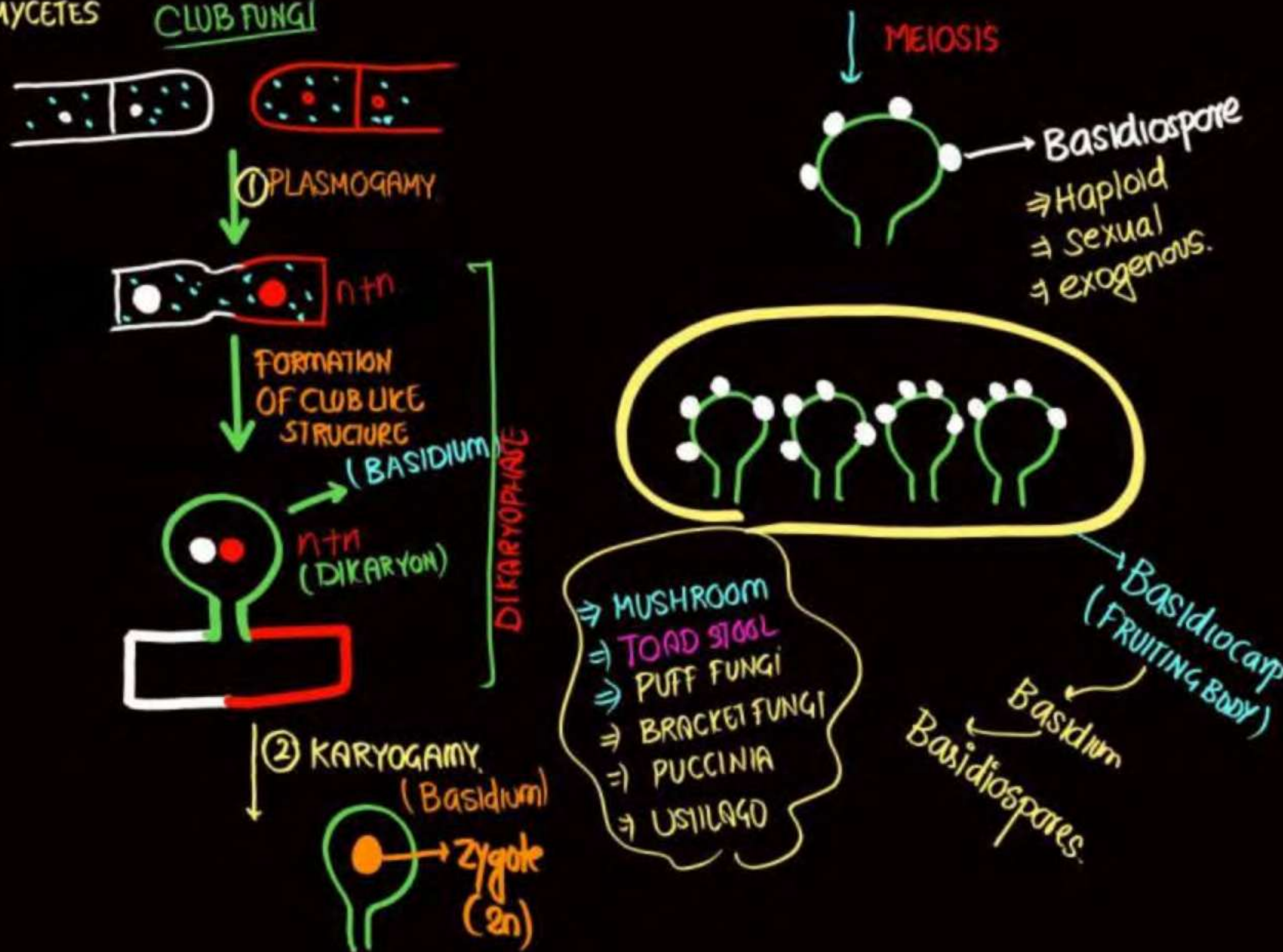
Zoospore Asexual spore


ASCOMYCETES
sac FUNGI
⇒ SAPROPHYTIC, PARASITIC, DECOMPOSER, COPROPHILOUS (grow in DUNG).
⇒ SEPTATE BRANCHED MYCELIUM.
⇒ MOSTLY MULTICELLULAR BUT YEAST (UNICELLULAR)
⇒ ASEXUAL: CONIDIA
Plasmogamy not immediately followed By karyogamy.
⇒ Male & female nucleus stay together BUT NOT FUSED: DIKARYON
male Hyphae.
Female hyphae
① PLASMOGAMY. (PROTOPLASM MIX)
MALE & FEMALE HYPHAE: FUSED
male
Female.
n + n
Both Nucleus enter into ascus
sac like (ASCUS)
n+n (DIKARYON)
DIKARYOPHASE
② karyogamy (ASCUS)
Zygote (2n).
MEIOSIS (ASCUS).
ASCOSPORES
Sexual, Haploid, meiospore, endogenous.
ASCOCARP (FRUITING BODY).
ASCUS
ASCOSPORE
germinate
New FUNGI/ MYCELIUM
★ MORELS & TRUFFLES
EDIBLE FUNGI
★ ASPERGILLUS, CLAVICEPS, PENICILLIUM.
★ NEUROSPORA: BIOCHEMICAL & GENETICS WORK.

BASIDIOMYCETES   CLUB FUNGI

- ★ SEPTATE, BRANCHED MYCELIUM.
- ★ SOIL, LOGS OF WOOD, TREE STUMP, PARASITE (RUST FUNGI & SMUT FUNGI)
- ★ ASEXUAL SPORE : ABSENT
- ★ VEGETATIVE REPRODUCTION BY FRAGMENTATION IS MORE COMMON.
- ★ FUSION OF VEGETATIVE/ SOMATIC MYCELIUM/ HYPHAE (PLASMOGAMY)
- ★ SEX ORGAN : ABSENT

Plasmogamy not immediately followed By Karyogamy.



DE UTROMYCETES

⇒ imperfect fungi

⇒ sexual stage (perfect stage) : ABSENT.

⇒ vegetative / Asexual Rep^n : given one name

⇒ If sexual Rep^n : Reported, that FUNGI SHIFTED TO Ascomycetes / BASIDIOMYCETES.

⇒ MYCELIUM: BRANCHED, SEPTATE

⇒ ASEXUAL: CONIDIA

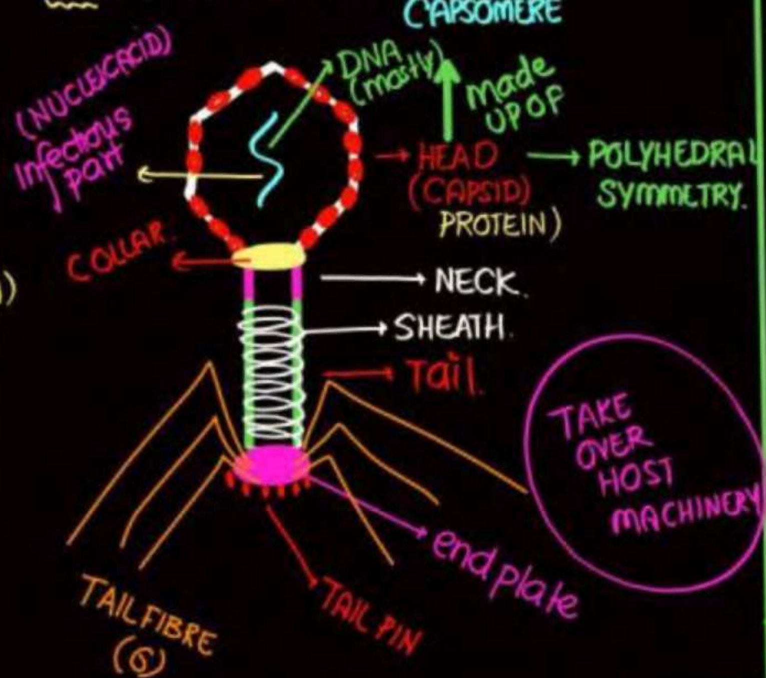
⇒ parasitic, saprophytic BUT mostly decomposer of LITER. (FRESH UNDECOMPOSED PART)

Recycling of NUTRIENT

eg: Alternaria
Colletotrichum
Trichoderma.

⇒ NON-CELLULAR
⇒ LINK B/W LIVING & NON LIVING
⇒ OBLIGATE INTRACELLULAR PARASITE (NEED HOST)
⇒ VENOM/POISONOUS FLUID.
⇒ genetic material/ NUCLEIC ACID (either DNA/RNA)
⇒ BUT NEVER BOTH.
⇒ BACTERIOPHAGE: VIRUS INFECT BACTERIA, DSDNA (mostly)
⇒ NUCLEOPROTEIN: VIRUS.
⇒ Small pox, mumps, herpes, influenza, AIDS. etc.
⇒ CAPSID: HELIX: ARRANGE
HELICAL SYMMETRY (TOBACCO MOSAIC VIRUS.

VIRUS (BACTERIOPHAGE)

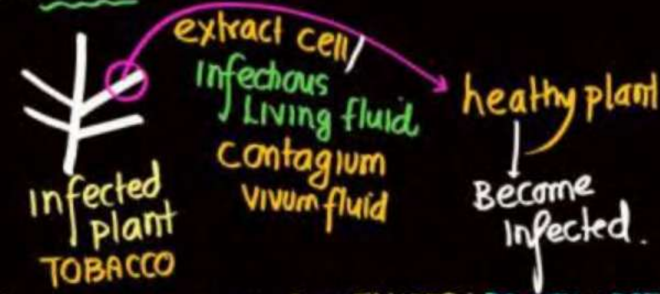


Plant virus: SSRNA
animal virus: SSRNA/dsRNA/dsDNA
Bacteriophage: mostly dsDNA

VIRUS: OUTSIDE THE CELL: INERT/INACTIVE.

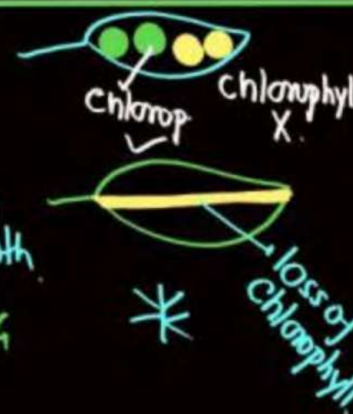
⇒ Ivanowsky: Term VIRUS / POISONOUS FLUID.
TOBACCO MOSAIC DISEASE CAUSED BY TOBACCO MOSAIC VIRUS.
VIRUS CAN CROSS BACTERIAL FILTER.
VIRUS SMALLER THAN BACTERIA.

⇒ BEIJERNEK



⇒ STANLEY: TMV: CRYSTALIZED: PROTEIN PRESENT

a) MOSAIC FORMATION:
b) vein clearing & yellowing
c) Dwarfing & stunted growth.
d) CURLING & ROLLING OF LEAF



⇒ NO PLACE FOR VIRUS, VIROID, PRIONS & LICHEN IN FIVE KINGDOM CLASSIFICATION (WHITTAKER)

VIROID

⇒ Infectious free RNA without PROTEIN COAT

Low molecular weight

⇒ DIOENER.

⇒ smaller than virus

⇒ POTATO SPINDLE TUBER DISEASE IN PLANTS.

PRIONS

⇒ abnormal FOLDED PROTEIN (INFECTIOUS)

⇒ SIZE SIMILA TO VIRUS

⇒ NEURODEGERATIVE DISORDER.

⇒ MAD COW DISEASE / BOWINE SPONGIFORM ENCEPHALOPATHY (CATTLE)

⇒ CREUTZ JACOB DISEASE (HUMAN)

LICHEN

SYMBIOTIC

algae

Phycobiont

5%

Provide FOOD

fungi

mycobiont

95% dominant

SHELTER, absorption HELP.

⇒ polluted area, SO_2 / air pollution LICHEN DO NOT GROW.

⇒ Indicator of air pollution.

Classification

⇒ NEED: FOOD, SHELTER, CLOTHES

⇒ EARLIEST: BASED ON ECONOMIC IMPORTANCE.

BUT

1st classification: Scientific approach (Aristotle)

- Living organism
  - Plants (morphological character)
    - Herbs
    - Shrubs
    - Tree.
  - Animals
    - Anaima (NOT RED)
    - Enaima (Red Blood)

2K : LINNAEUS

PLANTAE : CELL WALL

PLANTS.

⇒ ALGAE	:	Eu, AUTO, MULTICELLULAR BUT CHLORELLA & CHLAMYDOMONAS (UNICELLULAR) (SPIROGYRA).
⇒ BRYO/MOSS	:	E, AUTO, MULTI
⇒ PTER/FERN	:	E, AUTO, MULT
⇒ GYMNO	:	E, AUTO, MULTI
⇒ ANGIO	:	E, AUTO, MULT
⇒ BACTERIA	:	Pro, Hetro (mostly), Unicell
⇒ FUNGI	:	Eu, Hetro, Mostly multi

PRESENSE/ ABSENSE OF CELL WALL.

not sufficient (inadequate)

easy to classify

ANIMALIA : CELL WALL X.

⇒ VERTEBRATES
⇒ INVERTEBRATES
⇒ PROTOZOA (Amoeba, paramecium)

DRAWBACK

* Placed prok & eukaryote in same kingdom.
* AUTOTROPHS (PLANT) & HETROTROPHS (FUNGI) ⟶ SAME KINGDOM: PLANTAE
  CELLULOSE
  CHITIN
  ALTHOUGH DIFFER IN CELL WALL COMPOSITION.
* PLACED MULTICELLULAR (SPIROGYRA) & UNICELLULAR (Chlorella & Chlamydomonas)
* Few can fit either of Two Category
  Euglena ⟶ Cellwall absent (animal character)
  ⟶ Photosynthesis (Plant character)

As time pass : REALISE
CRITERIA INCREASE

- Cell structure
- Cell wall composition
- Habitat
- Reproduction
- evolutionary HISTORY / Phylogeny
- ⇒ NUTRITION

3K
Haeckel

PLANTAE

ANIMALIA

PROTISTA: Chlorella, Chlamydomonas & protozoa (Amoeba, paramecium)

Placed Together

UNICELLULAR EUKARYOTES

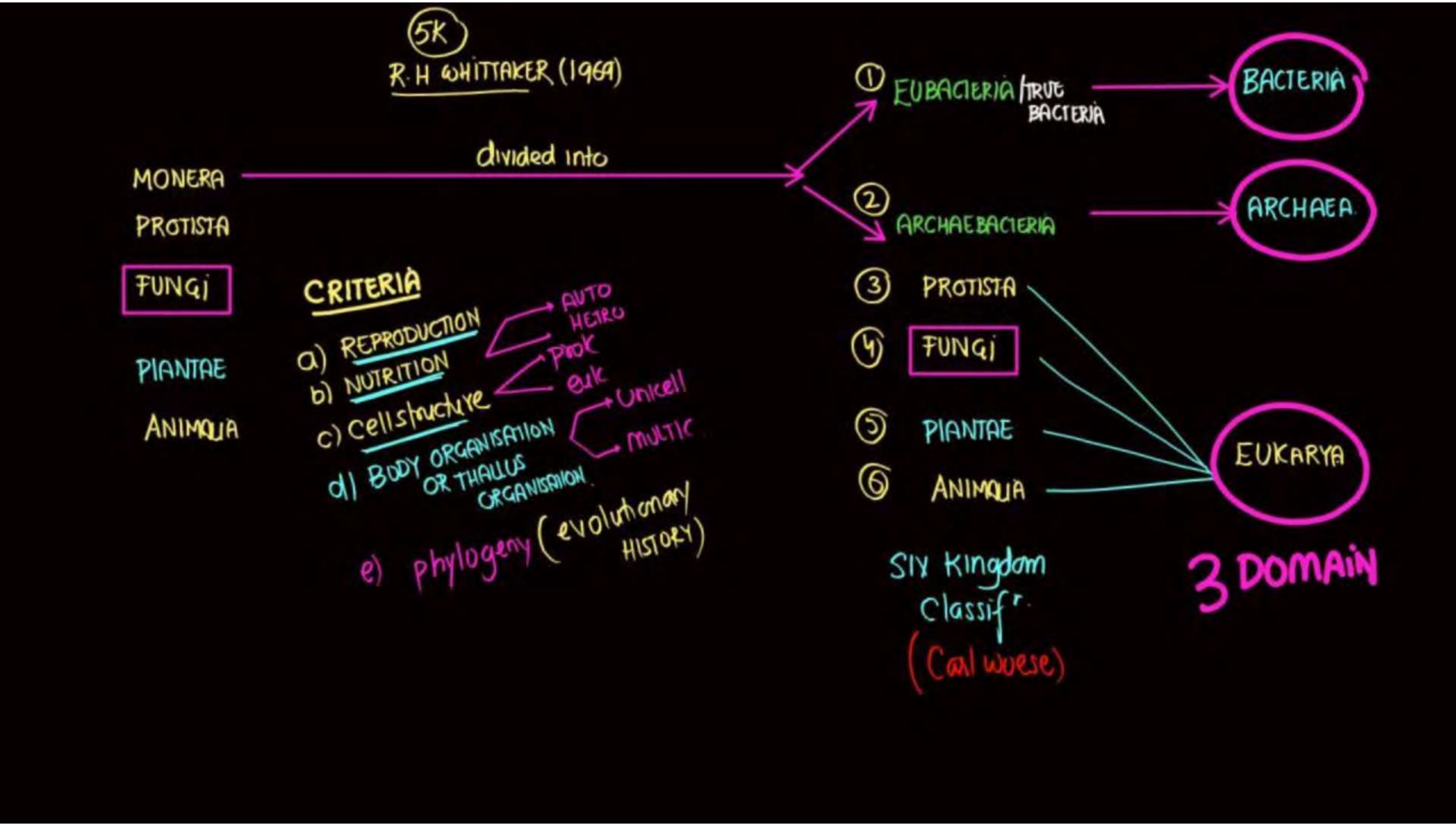
4K
Copeland

PLANTAE

ANIMALIA

PROTISTA:

MONERA: Bacteria, BGA, Archaebacteria etc.


5K
R.H WHITTAKER (1969)
MONERA
PROTISTA
FUNGI
PLANTAE
ANIMALIA
divided into
CRITERIA
a) REPRODUCTION
b) NUTRITION
c) Cell structure
d) BODY ORGANISATION OR THALLUS ORGANISATION
AUTO
HETRO
Prok
euk
Unicell
multic
e) phylogeny (evolutionary HISTORY)
① EUBACTERIA / TRUE BACTERIA
② ARCHAEBACTERIA
③ PROTISTA
④ FUNGI
⑤ PLANTAE
⑥ ANIMALIA
BACTERIA
ARCHAEA
EUKARYA
Six Kingdom Classifn
(Carl woese)
3 DOMAIN

TERMS

★ **GENETICS**: STUDY OF HEREDITY AND VARIATION

★ **HEREDITY**: TRANSMISSION OF CHARACTER FROM PARENT (ONE GENERATION) TO OFFSPRING (ANOTHER GENERATION)

★ **VARIATION**: DIFFERENCES SHOWN BY OFFSPRING (CHARACTER) WHICH ARE ABSENT IN PARENT.

★ **INHERITENCE**: PROCESS BY WHICH CHARACTER TRANSFER FROM PARENT TO OFFSPRING

GAMETES/SEXCELL → SPERM (DNA)
GAMETES/SEXCELL → EGG (DNA)

★ **FATHER OF GENETICS**: GREGOR JOHANN MENDEL.

★ **FATHER OF MODERN GENETICS/ TERM GENETICS**: BATESON.

GENE

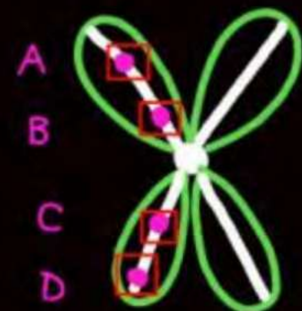
CHROMOSOME → DNA → SEGMENT OF DNA / SMALLEST PART OF DNA

↓

WHICH FORM PARTICULAR PROTEIN

↓

AND THAT PROTEIN CONTROL PARTICULAR CHARACTER.



NOTE: WHOLE DNA NOT FORM PROTEIN

TRAITS

1 GENE → 1 CHARACTER: PEA (PLANT HEIGHT) → TALL / DWARF

1 GENE : 1 CHARACTER : 2 TRAIT

1 GENE → 1 CHARACTER: SEED SHAPE → ROUND / WRINKLED

TERM GENE: JOHANSENN
→ CALLED AS FACTOR BY MENDEL.

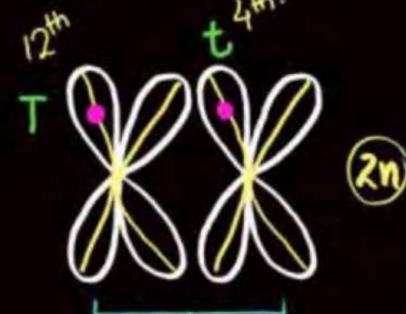
ALLELE

CLASS

1 gene —2 FORM→ 12^{th} ⇒ T allele ; 4^{th} ⇒ t allele

⇒ ALTERNATE FORM OF ONE/SAME GENE

⇒ ONE GENE : ONE CHARACTER : TWO TRAIT : TWO ALLELE



HOMOLOGOUS CHROMOSOME → SAME POSITION/ LOCUS

$2n = Tt$

TALL (Class 12^{th} : T : ताकतवर / DOMINANT

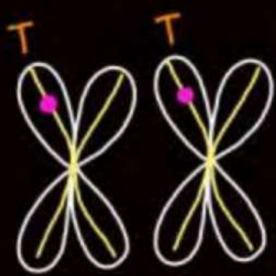
HETROZYGOUS TALL

(NON-IDENTICAL)
if DISIMILAR ALLELE PRESENT ON SAME LOCUS ON HOMOLOGOUS CHROMOSOME CALLED HETROZYGOUS CONDITION.

T : TALL TRAIT : DOMINANT ALLELE

t : DWARF TRAIT : RECESSIVE ALLELE

1 gene → 12^{th} → T
1 gene → 12^{th} → T

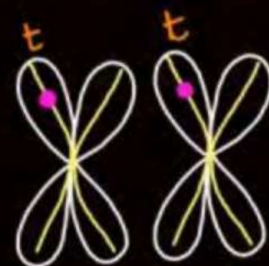


$\boxed{2n = TT}$

HOMOZYGOUS TALL

BOTH FORMS OF ONE GENE IS SIMILAR/IDENTICAL HOMOZYGOUS CONDITION.

1 gene → 4^{th} : t
1 gene → 4^{th} : t



$\boxed{\text{HOMOZYGOUS}}$

DWARF.

CONCLUSION

	TRAIT	2n = tt	EXPRESS
2n = TT	TALL	HOMOZYGOUS	DOMINANT ALLELE
2n = tt	DWARF	HOMOZYGOUS	RECESSIVE ALLELE
2n = Tt	TALL	HETROZYGOUS	DOMINANT ALLELE

Q. DOMINANT ALLELE CONTROL : DOMINANT TRAIT (TALL) T

Q RECESSIVE ALLELE CONTROL : RECESSIVE TRAIT (DWARF) T

Q. DOMINANT ALLELE EXPRESS IN HOMOZYGOUS CONDITION : T

Q DOMINANT ALLELE EXPRESS ONLY IN HOMOZYGOUS CONDITION. F

Q DOMINANT ALLELE EXPRESS ONLY IN HETROZYGOUS CONDITION : F

Q DOM. ALLELE EXPRESS IN BOTH HOMOZYGOUS & HETROZYG. COND^N T

Q DOMINANT ALLELE EXPRESS IN PRESENSE OF IDENTICAL ALLELE : 2n = TT T

Q DOMINANT ALLELE EXPRESS ONLY IN PRESENSE OF IDENTICAL ALLELE : 2n = TT F

Q DOMINANT ALLELE EXPRESS IN PRESENSE OF SIMILAR/ DISIMILAR ALLELE : T

Q RECESSIVE ALLELE EXPRESS ONLY IN PRESENSE OF IDENTICAL/ SIMILAR ALLELE T

Q RECESSIVE ALLELE ONLY EXPRESS IN HOMOZYGOUS CONDITION T

NOTE : TERM: ALLELE, HOMOZYGOUS, HETROZYGOUS, GENETICS: BATESON.

MENDELISM

* BORN, 22 JULY, 1822, AUSTRIA
* WORK: GARDEN PEA (PISUM SATIVUM)
* YERRS: 1856-1863, 7YEARS
  AUGUSTINIAN MONASTERY
* CHARACTER: 7
* CONTRASTING TRAIT: 14 / 7 PAIRS

Why PEA

* EASY TO CULTIVATE
* ANNUAL PLANT, SHORT LIFESPAN (COMPLETE THEIR CYCLE IN ONE YEAR)
* MORE SEED PRODUCED IN SHORT SPAN OF TIME
* BISEXUAL PLANT: NATURALLY SELF POLLINATION PRESENT
* CROSS POLLINATION CAN ALSO PERFORM.

TRAITS

CHARACTER	DOMINANT	RECESSIVE
① PLANT HEIGHT	TALL	DWARF
② SEED SHAPE	ROUND	WRINKLED
③ SEED COLOUR	YELLOW	GREEN.
④ FLOWER COLOUR.	VIOLET	WHITE
⑤ POD COLOUR	GREEN	YELLOW.
⑥ POD SHAPE	FULL/INFLATED	CONSTRICTED.
⑦ FLOWER POSITION	AXILLARY	TERMINAL

TECHNIQUE: EMASCULATION & BAGGING

VARIETY: 14.

Q. NO. Of TRAIT EXPRESS IN HOMOZYGOUS CONDITION.

a) DWARF (R)
b) TALL (D)
c) WRINKLED SEED (R)
d) ROUND SEED (D)
e) Violet FLOWER (D)

a): 1
b): 2
c): 3
d): 4
e) ALL — all will express whether Dominant/ RECESSIVE

Q. NO. Of TRAIT EXPRESS ONLY IN HOMOZYGOUS CONDITION.

a) 1
b) 2
c) 3
d) 4
e) ALL

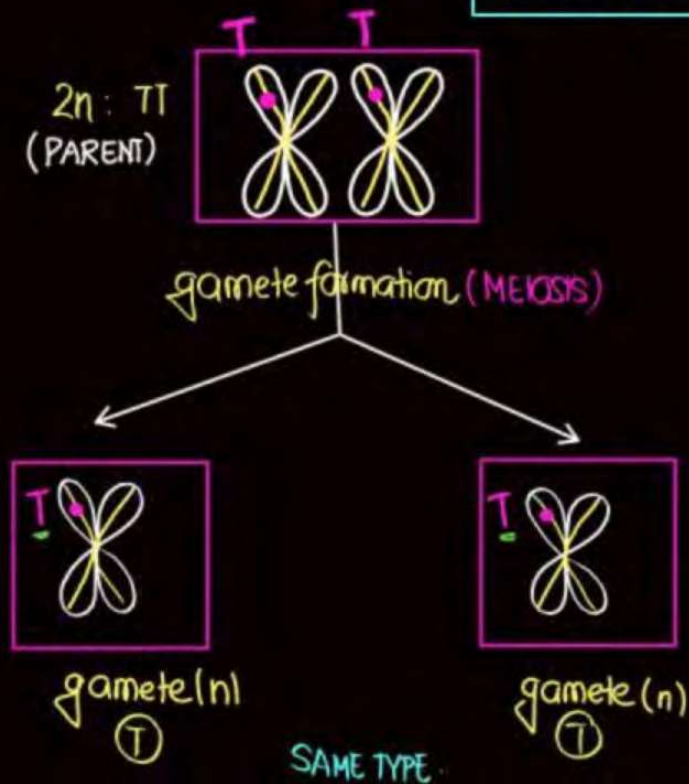
Recessive TRAIT

Q. NO. Of TRAIT EXPRESS IN HETROZYGOUS CONDITION

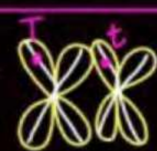
a) 1
b) 2
c) 3
d) 4
e) ALL

Dominant TRAIT

GAMETE FORMATION



- Q Chromosome seperate/segregate during gamete formation (T)
- Q Each gamete carry one of TWO CHROMOSOME (T)
- Q Chromosome / ALLELE SEGREGATE during gamete formtn, so that each gamete carry ONE ALLELE
- Q NO. of gamete : 2
- Q TYPES OF gamete : T , T



2n = Tt

no. of gamete : 2

Types of gamete : 2 T , t

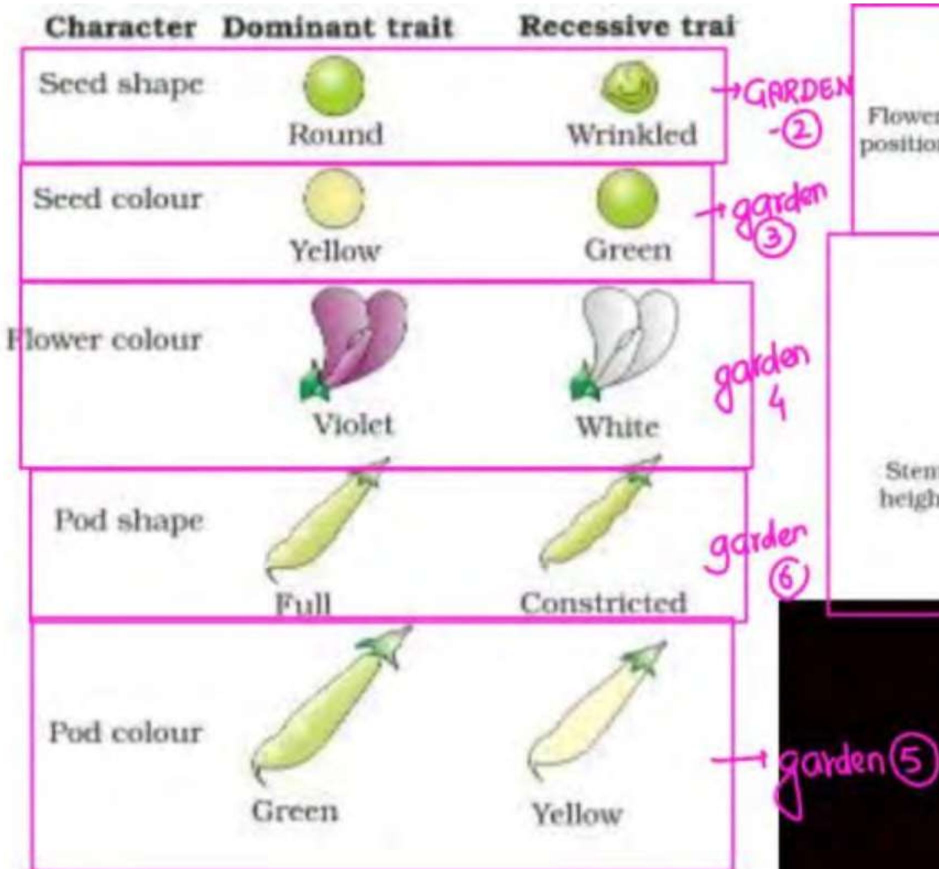
DIFFERENT TYPE

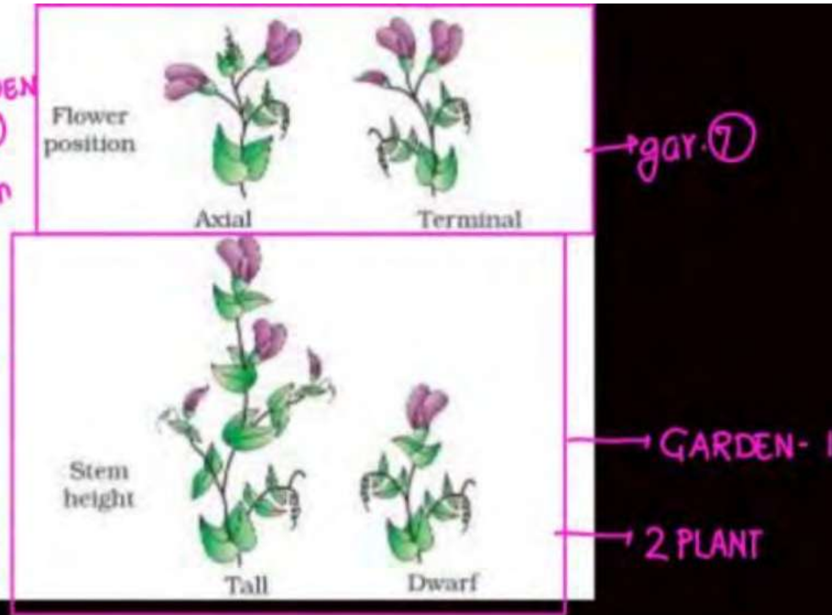
2n = tt

no : 2

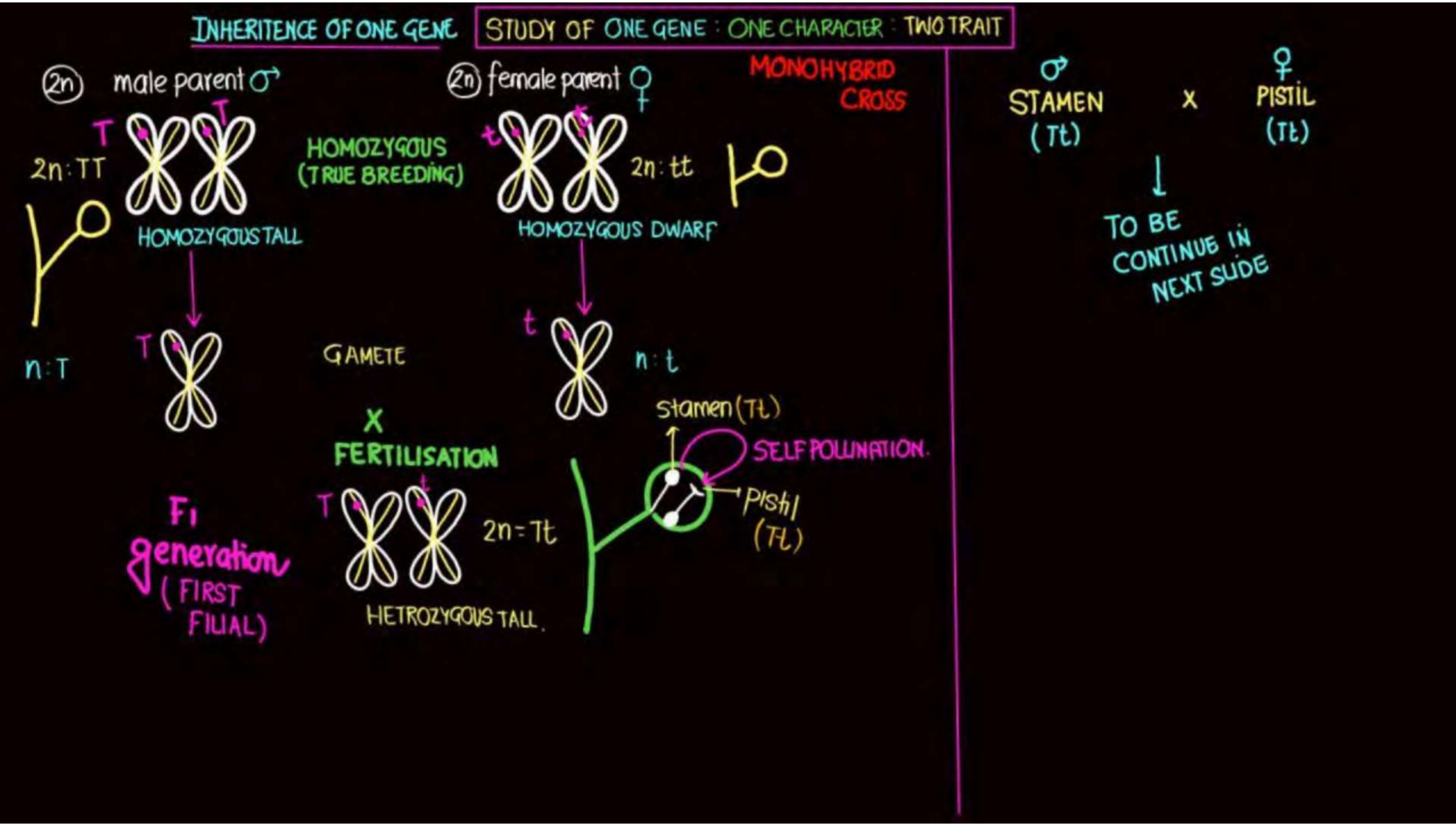
Types : 1

SAME TYPE

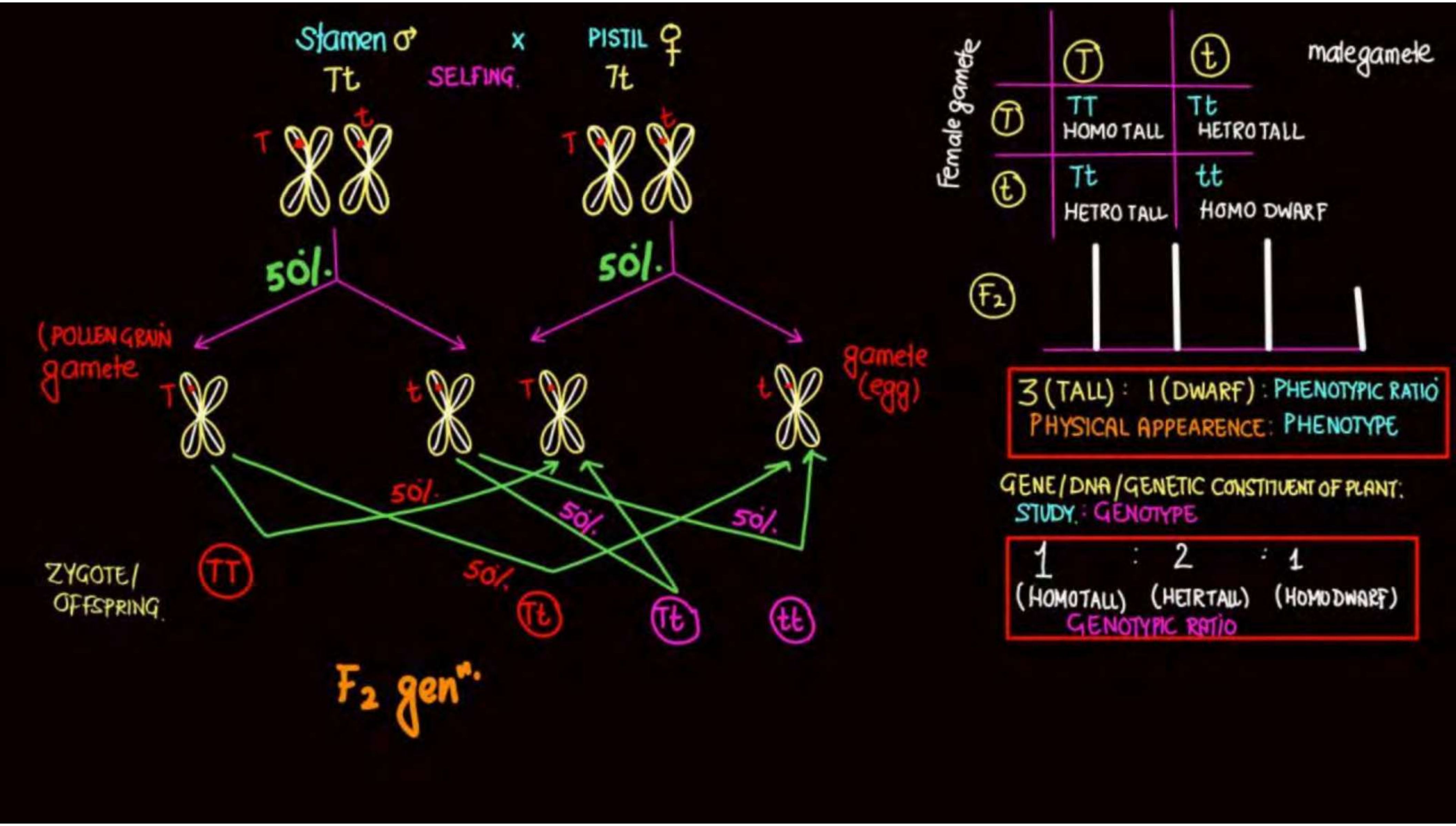

Character
Dominant trait
Recessive trai
Seed shape
Round
Wrinkled
GARDEN -②
Seed colour
Yellow
Green
garden ③
Flower colour
Violet
White
garden 4
Pod shape
Full
Constricted
garden ⑥
Pod colour
Green
Yellow
garden ⑤


Flower position
Axial
Terminal
gar. ⑦
Stem height
Tall
Dwarf
GARDEN- 1
2 PLANT


FULL



INHERITENCE OF ONE GENE
STUDY OF ONE GENE : ONE CHARACTER : TWO TRAIT
MONOHYBRID CROSS
(2n) male parent ♂
T T
2n : TT
HOMOZYGOUS TALL
HOMOZYGOUS (TRUE BREEDING)
(2n) female parent ♀
t t
2n : tt
HOMOZYGOUS DWARF
T
n : T
GAMETE
t
n : t
X
FERTILISATION
F1 generation (FIRST FILIAL)
T t
2n = Tt
HETROZYGOUS TALL.
stamen (Tt)
SELF POLLINATION.
pistil (Tt)
♂ STAMEN (Tt)
x
♀ PISTIL (Tt)
TO BE CONTINUE IN NEXT SLIDE



Stamen ♂
x
PISTIL ♀
Tt
SELFING.
Tt
T
t
T
t
50%.
50%.
(POLLEN GRAIN
gamete
gamete
(egg)
T
t
T
t
50%.
50%.
50%.
50%.
ZYGOTE/
OFFSPRING.
TT
Tt
Tt
tt
F2 genn.
Female gamete
male gamete
T
t
T
TT
HOMO TALL
Tt
HETRO TALL
t
Tt
HETRO TALL
tt
HOMO DWARF
F2
3 (TALL) : 1 (DWARF) : PHENOTYPIC RATIO
PHYSICAL APPEARENCE : PHENOTYPE
GENE/DNA/GENETIC CONSTITUENT OF PLANT:
STUDY : GENOTYPE
1 : 2 : 1
(HOMOTALL) (HETRTALL) (HOMODWARF)
GENOTYPIC RATIO

Q: NUMBER OF PHENOTYPE: 2 → TALL, DWARF

Q: NO. OF GENOTYPE: TT, Tt, tt 3

Q: TALL (INFORMATION IS NOT SPECIFIC WHETHER IT IS HOMOZYGOUS TALL / HETROZYGOUS TALL)

PHENOTYPE

Q HETROZYGOUS TALL & HOMOZYGOUS TALL

$\underbrace{\text{Tt} \qquad \text{TT}}_{\text{GENOTYPE}}$

Q GENOTYPIC RATIO OF TALL PHENOTYPE IN F-2 GEN^n

3

1 TT

2 Tt

NOTE:
1/4 : TT
2/4 : Tt
1/4 : tt

Q: 3/4 (TALL): PHENOTYPE

Q: 1/4 (TALL) TT : GENOTYPE

Female gamete / male gamete

	T	t
T	TT HOMO TALL	Tt HETRO TALL
t	Tt HETRO TALL	tt HOMO DWARF

F2

3 (TALL) : 1 (DWARF) : PHENOTYPIC RATIO
PHYSICAL APPEARENCE: PHENOTYPE

GENE/DNA/GENETIC CONSTITUENT OF PLANT:
STUDY: GENOTYPE

1 : 2 : 1
(HOMO TALL) (HETR TALL) (HOMO DWARF)
GENOTYPIC RATIO

Monohybrid cross

- ★ F_1 (Tt) Resemble with one of parent (T)
- ★ Tall (10cm) x dwarf (3cm)

  F_1 → a) 10cm ✓
  b) 3cm
  c) 6.5cm (Blending Inheritence)

- ★ NO INTERMEDIATE / NO BLENDING IN F-1 generation
- ★ ONLY ONE TRAIT (character) APPEAR IN F-1 gen^n BUT BOTH TRAIT APPEAR IN F-2 GEN^n (TALL, DWARF)

♂ $\boxed{Tt}$ x ♀ Tt / MONOHYBRID CROSS

No. of gamete: 2^n, n = no. of Hetrozygous, n=1 ⇒ $2^n = \boxed{2}$ → T, t

No. of Phenotype: 2^n ⇒ $\boxed{2}$ → Tall, dwarf

No. of genotype: 3^n ⇒ $\boxed{3}$ → Tt, TT, tt

No. of zygote: $(gamete)^2$ ⇒ $(2)^2$ = 4 → TT, Tt, Tt, tt

Q AABbCcDdEE
2^n ⇒ n = 3
2^3 ⇒ $\boxed{8}$ no. of gamete

Q Tt(♂) x Tt(♀) no. of zygote
2^n 2^n
2^1 = 2 2^1 = 2 ⇒ 2x2 = 4

REASON (MENDEL SUCCESS)

- ★ HE USED STASTICS & MATHMATICAL TOOL FOR HIS WORK (1st TIME)
- ★ HE KEPT RECORDED OF HIS EXPERIMENT
- ★ OBSERVATION / RESULT PROVED BY PROPER EXPERIMENT
- ★ LARGE SAMPLING SIZE WHICH GIVE CREDIBILITY TO DATA
  ↓
  HE REPEATED SAME EXPERIMENT ON 100 of PLANT
- ★ SO MANY CONTRASTING TRAIT IN PEA (DOMINANT / RECESSIVE TRAIT) SO EASY TO EXPLAIN DOMINANT & RECESSIVE ALLELE

PUNNET SQUARE

R.C PUNNETT, BRITISCH GENETICIST

TT tt

	T	T
t	Tt	Tt
t	Tt	Tt

→ F_1 (All Tall)

Tt × Tt

	T	t
T	TT	Tt
t	Tt	tt

⇒ graphical Representation to determine probability of genotype of offspring / zygote F_1 & F_2

⇒ Types of gamete

4.1 Mendel's Laws of Inheritance

It was during the mid-nineteenth century that headway was made in the understanding of inheritance. Gregor Mendel, conducted hybridisation experiments on garden peas for seven years (1856-1863) and proposed the laws of inheritance in living organisms. During Mendel's investigations into inheritance patterns it was **for the first time** that statistical analysis and mathematical logic were applied to problems in biology. His experiments had a large sampling size, which gave greater credibility to the data that he collected.

MENDEL: 19^{th} century.

PISUM SATIVUM.

Tall x dwarf (CROSS)/HYBRISATION.

Law of dom,
Law of segreg etc

*

TRUST

HE REPEATED SAME EXPERIMENT ON 100 of PLANT

Also, the confirmation of his inferences from experiments on successive generations of his test plants, proved that his results pointed to general rules of inheritance rather than being unsubstantiated ideas. Mendel investigated characters in the garden pea plant that were manifested as two opposing traits, e.g. tall or dwarf plants, yellow or green seeds. This allowed him to set up a basic framework of rules governing inheritance, which was expanded on by later scientists to account for all the diverse natural observations and the complexity inherent in them.

WORDS NOT SUPPORTED BY EXPERIMENT

PEA → many contrasting TRAIT

Domin TRAIT

Recessive Trait

DOMINANT

Recessive

Domin

Recessive

PHENOTYPE

EXPLAIN (DOMINANT & RECESSIVE ALLELE)

BATESON
JOHANNSEN
MORGAN

Pathway

genetics

Mendel conducted such artificial pollination/cross pollination experiments using several true-breeding pea lines. A true-breeding line is one that, having undergone continuous self-pollination, shows the stable trait inheritance and expression for several generations. Mendel selected 14 true-breeding pea plant varieties, $\boxed{\text{as pairs which were similar except for one character with contrasting traits.}}$ Some of the contrasting traits selected were smooth or wrinkled seeds, yellow or green seeds, inflated (full) or constricted green or yellow pods and tall or dwarf plants (Figure 4.1, Table 4.1).

Desired pollen grain (Tall plant) → dwarf plant

① Emasculation

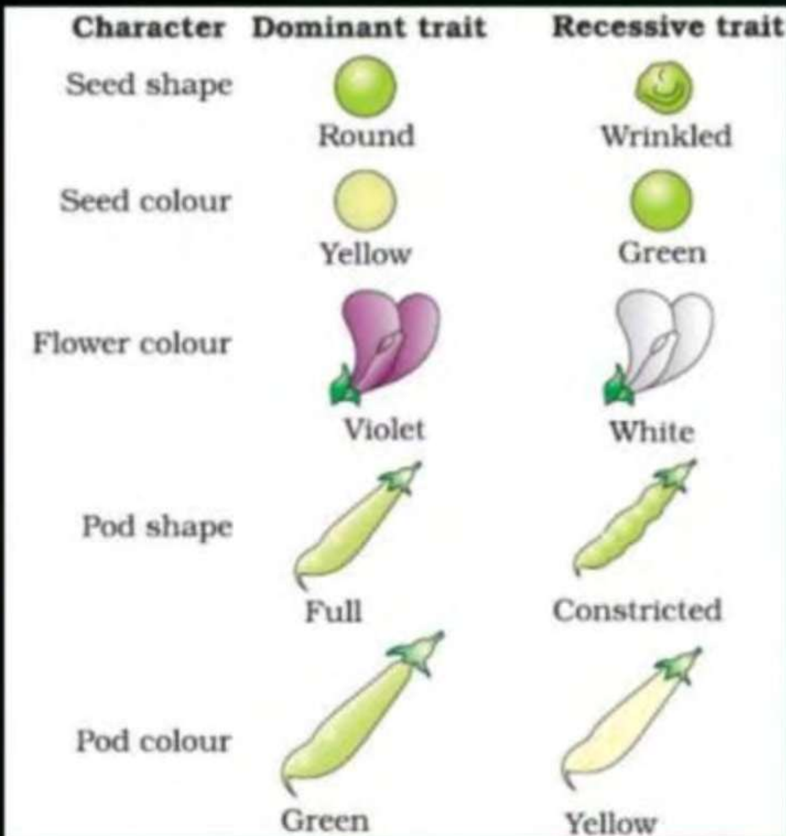
② Bagging

ROUND

TT (♂)

Parent = ?

tt (♀)



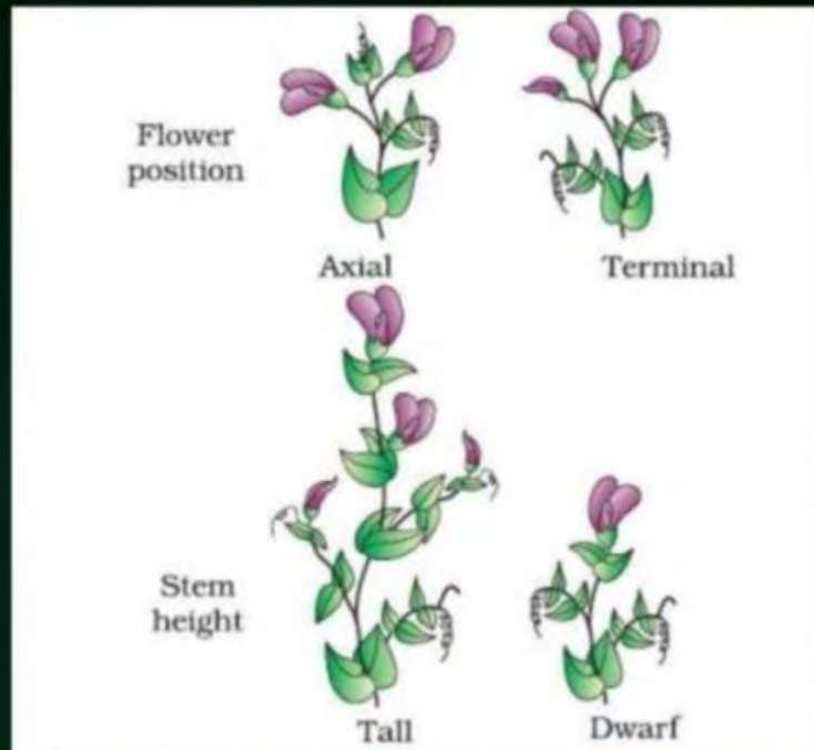


Figure 4.1 Seven pairs of contrasting traits in pea plant studied by Mendel

Table 4.1: Contrasting Traits Studied by Mendel in Pea

S.No.	Characters	Contrasting Traits
1.	*Stem height*	*Tall/dwarf*
2.	*Flower colour*	*Violet/white*
3.	*Flower position*	*Axial/terminal*
4.	*Pod shape*	*Inflated/constricted*
5.	*Pod colour*	*Green/yellow*
6.	*Seed shape*	*Round/wrinkled*
7.	*Seed colour*	*Yellow/green*

4.2 Inheritance of One Gene / MONOHYBRID CROSS.

Let us take the example of one such hybridisation experiment carried out by Mendel where he crossed tall and dwarf pea plants to study the inheritance of one gene (STUDY) (Figure 4.2). He collected the seeds produced as a result of this cross and grew them to generate plants of the first hybrid generation. This generation is also called the **Filial$_1$ progeny** or the **F$_1$**. Mendel observed that all the F_1 progeny plants were tall, like one of its parents; none were dwarf (Figure 4.3). He made similar observations for the other pairs of traits – he found that the F_1 always resembled either one of the parents, and that the trait of the other parent was not seen in them.

2 TRAIT (ONE CHARACTER)

Tall ♂ × dwarf ♀

POLLEN grain

FLOWER

seed → grow

Tt → F_1 genⁿ.

all

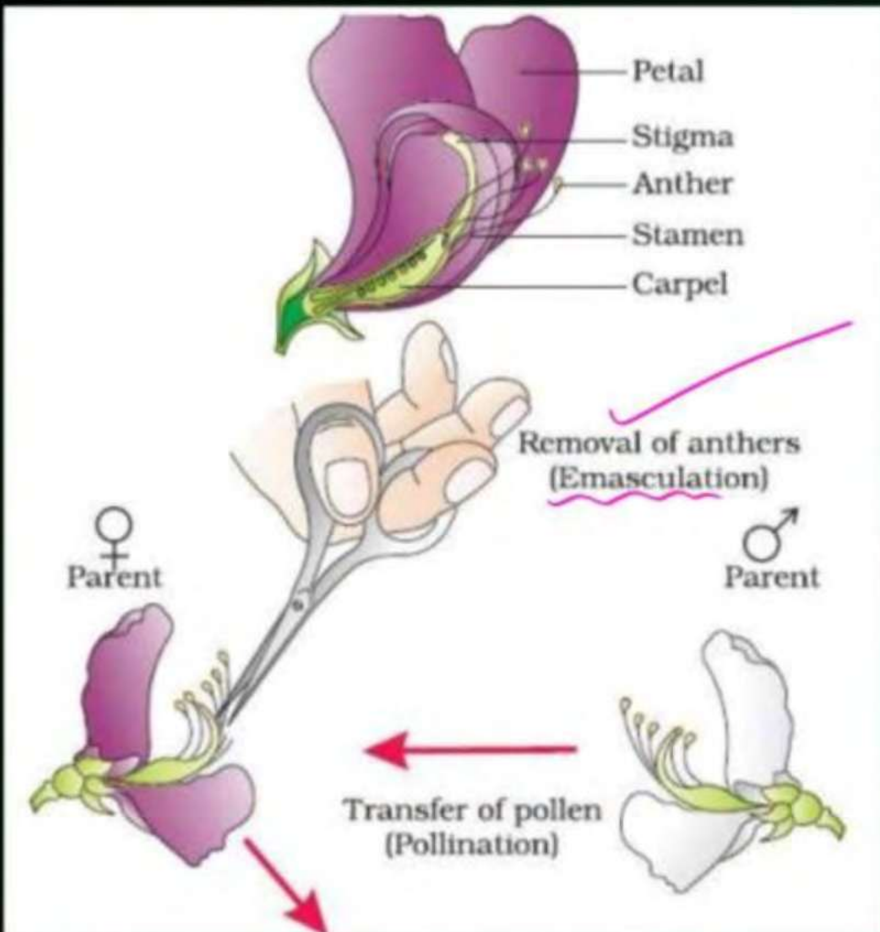
Resemblance with one parent.

ROUND SEED (RR) × wrinkled SEED (rr)

R r

Resemblance. Rr → F_1

ROUND



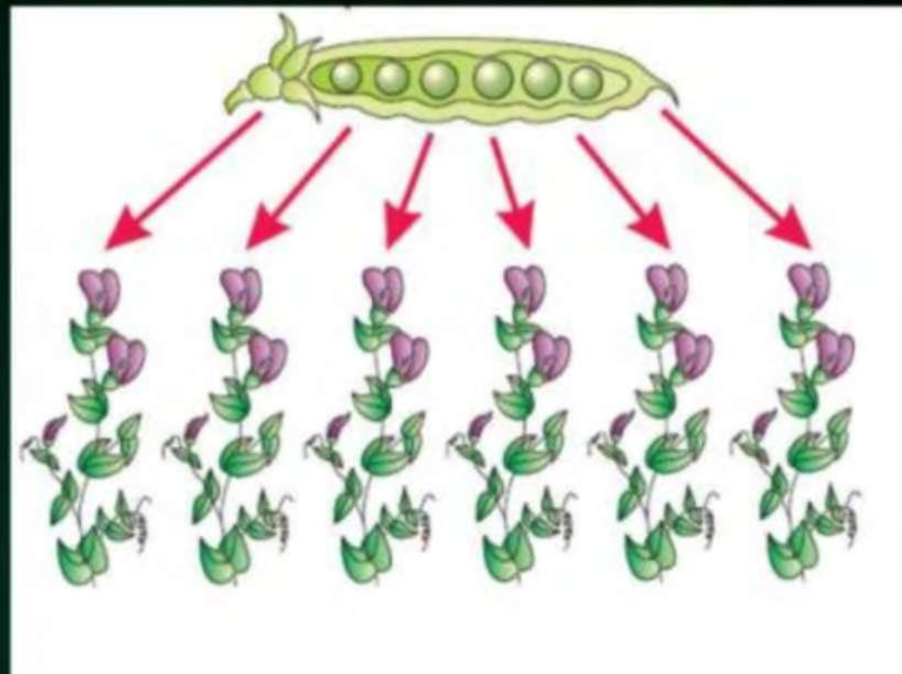


Figure 4.2 Steps in making a cross in pea

Mendel then self-pollinated the tall F_1 plants and to his surprise found that in the Filial$_2$ generation some of the offspring were 'dwarf'; the character that was not seen in the F_1 generation was now expressed. The proportion of plants that were dwarf were $1/4^{th}$ of the F_2 plants while $3/4^{th}$ of the F_2 plants were tall. The tall and dwarf traits were identical to their parental type and $\boxed{\text{did not show any}}$ $\boxed{\text{blending}}$, that is all the offspring were either tall or dwarf, none were of in-between height (Figure 4.3).

Tt × Tt

Tt, Tt

TT Tt

Tt $\boxed{\text{tt}}$

F_2 genn

dwarf

$\frac{1}{4}$

$\frac{3}{4}$ Tall

TT ♂ tt ♀

10cm TT

3cm tt

F_1 10cm

F_2: 10cm TT, Tt

3cm (tt)

6cm ×

7cm ×

8cm ×

NO BLENDING

NO INTERMEDIATE

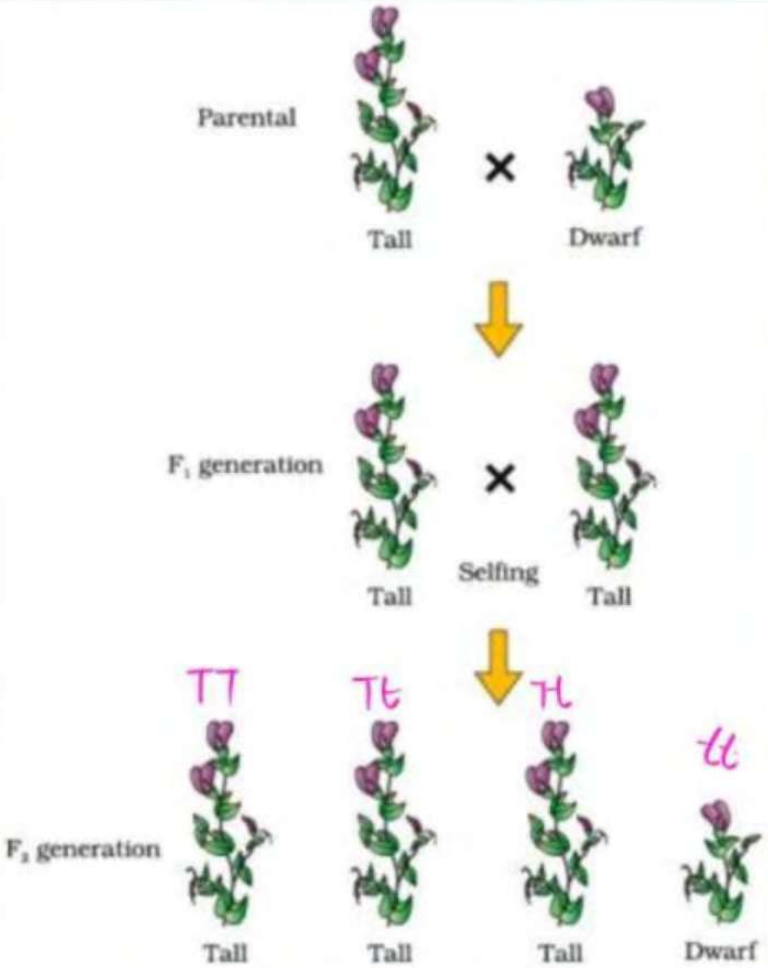


Figure 4.3 Diagrammatic representation of monohybrid cross

Similar results were obtained with the other traits that he studied: only one of the parental traits was expressed in the F_1 generation while at the F_2 stage both the traits were expressed in the proportion 3:1. The contrasting traits did not show any blending at either F_1 or F_2 stage.

Tall

Tall
dwarf

Based on these observations, Mendel proposed that something was being stably passed down, unchanged, from parent to offspring through the gametes, over successive generations. He called these things as 'factors'. Now we call them as **genes**. Genes, therefore, are the units of inheritance. They contain the information that is required to express a particular trait in an organism. Genes which code for a pair of contrasting traits are known as **alleles,** i.e., they are slightly different forms of the same gene.

sperm
egg → chromosome → DNA → gene → character.

Tall ⇒ TT/Tt
dwarf ⇒ tt

If we use alphabetical symbols for each gene, then the capital letter is used for the trait expressed at the F_1 stage and the small alphabet for the other trait. For example, in case of the character of height, **T** is used for the Tall trait and **t** for the 'dwarf', and **T** and **t** are alleles of each other. Hence, in plants the pair of alleles for height would be **TT**, **Tt** or **tt**. Mendel also proposed that in a true breeding, tall or dwarf pea variety the allelic pair of genes for height are identical or **homozygous**, **TT** and **tt**, respectively. **TT** and **tt** are called the **genotype** of the plant while the descriptive terms **tall** and **dwarf** are the **phenotype**. What then would be the phenotype of a plant that had a genotype **Tt**?

T
Tall
dwarf
t

gene
12th: T
4th: t
allele of same gene.

TT : Homo Tall
tt : Homo dwarf
genotype.

Tall

As Mendel found the phenotype of the F_1 heterozygote **Tt** to be exactly like the **TT** parent in appearance, he proposed that in a pair of dissimilar factors, one dominates the other (as in the F_1) and hence is called the **dominant** factor while the other factor is **recessive** . In this case **T** (for tallness) is dominant over **t** (for dwarfness), that is recessive. He observed identical behaviour for all the other characters/trait-pairs that he studied.

Tall

Tt

allele

factor/gene → T, t

allele

Tall

Round (Dom)

wrinkled (Recessive)

Tt

12th (dom allele

4th (Recessive allele)

factor/gene/allele/chromosomes = TRUE

TRUE

It is convenient (and logical) to use the capital and lower case of an alphabetical symbol to remember this concept of dominance and recessiveness. (Do not use **T** for tall and **d** for dwarf because you will find it difficult to remember whether **T** and **d** are alleles of the same gene/character or not). Alleles can be similar as in the case of homozygotes **TT** and **tt** or can be dissimilar as in the case of the heterozygote **Tt**. Since the **Tt** plant is heterozygous for genes controlling one character (height), it is a **monohybrid** and the cross between **TT** and **tt** is a **monohybrid cross**.

small

T
t

1 gene, 1 character
Two trait

1 gene · 1 charact (Plant Height) → Tt
Tall Trait

T
d

1 gene → A, a
1 gene → B, b
1 gene → C, c
1 gene → D, d

✓ E, e
✓ F, f

Q: E & F are

a) Two dom. allele of one gene

b) " " " " 2 gene.

From the observation that the recessive parental trait is expressed without any blending in the F_2 generation, we can infer that, when the tall and dwarf plant produce gametes, by the process of meiosis, the alleles of the parental pair separate or **segregate** from each other and only one allele is transmitted to a gamete. This segregation of alleles is a random process and so there is a 50 per cent chance of a gamete containing either allele, as has been verified by the results of the crossings.

dwarf

semidwarf X

dwarf का बाप X

dwarf से छोटा X

NO BLENDING.

2n: TT

seperation

50% 50%

T T

2n: Tt

50% 50%

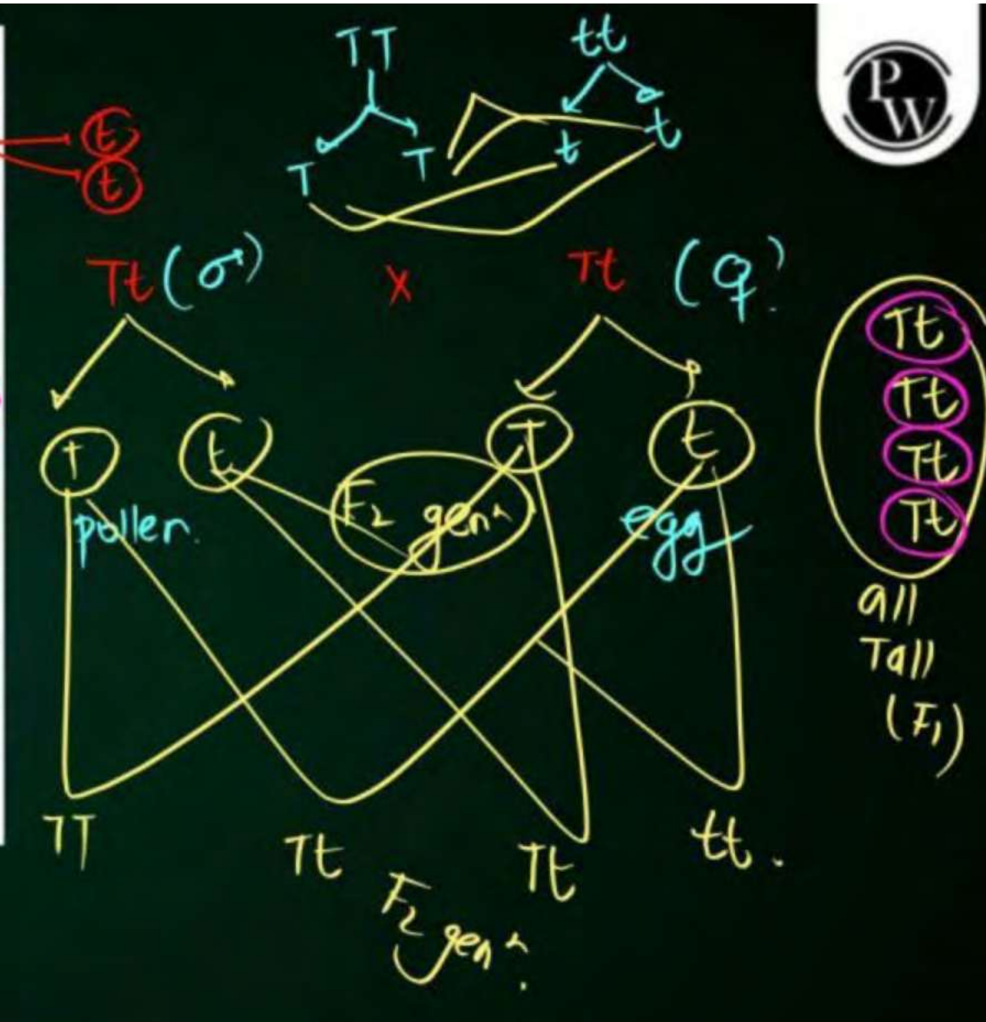
T t

2n: tt

50% 50%

t t

In this way the gametes of the tall **TT** plants have the allele **T** and the gametes of the dwarf **tt** plants have the allele **t**. During fertilisation the two alleles, **T** from one parent say, through the pollen, and **t** from the other parent, then through the egg, are united to produce zygotes that have one **T** allele and one **t** allele. In other words the hybrids have **Tt**. Since these hybrids contain alleles which express contrasting traits, the plants are **heterozygous**. The production of gametes by the parents, the formation of the zygotes, the F_1 and F_2 plants can be understood from a diagram called **Punnett Square** as shown in Figure 4.4.



It was developed by a British geneticist, Reginald C. Punnett. It is a graphical representation to calculate the probability of all possible genotypes of offspring /zygote in a genetic cross. The possible gametes are written on two sides, usually the top row and left columns. All possible combinations are represented in boxes below in the squares, which generates a square output form.

♂ gamete

♀ gamete

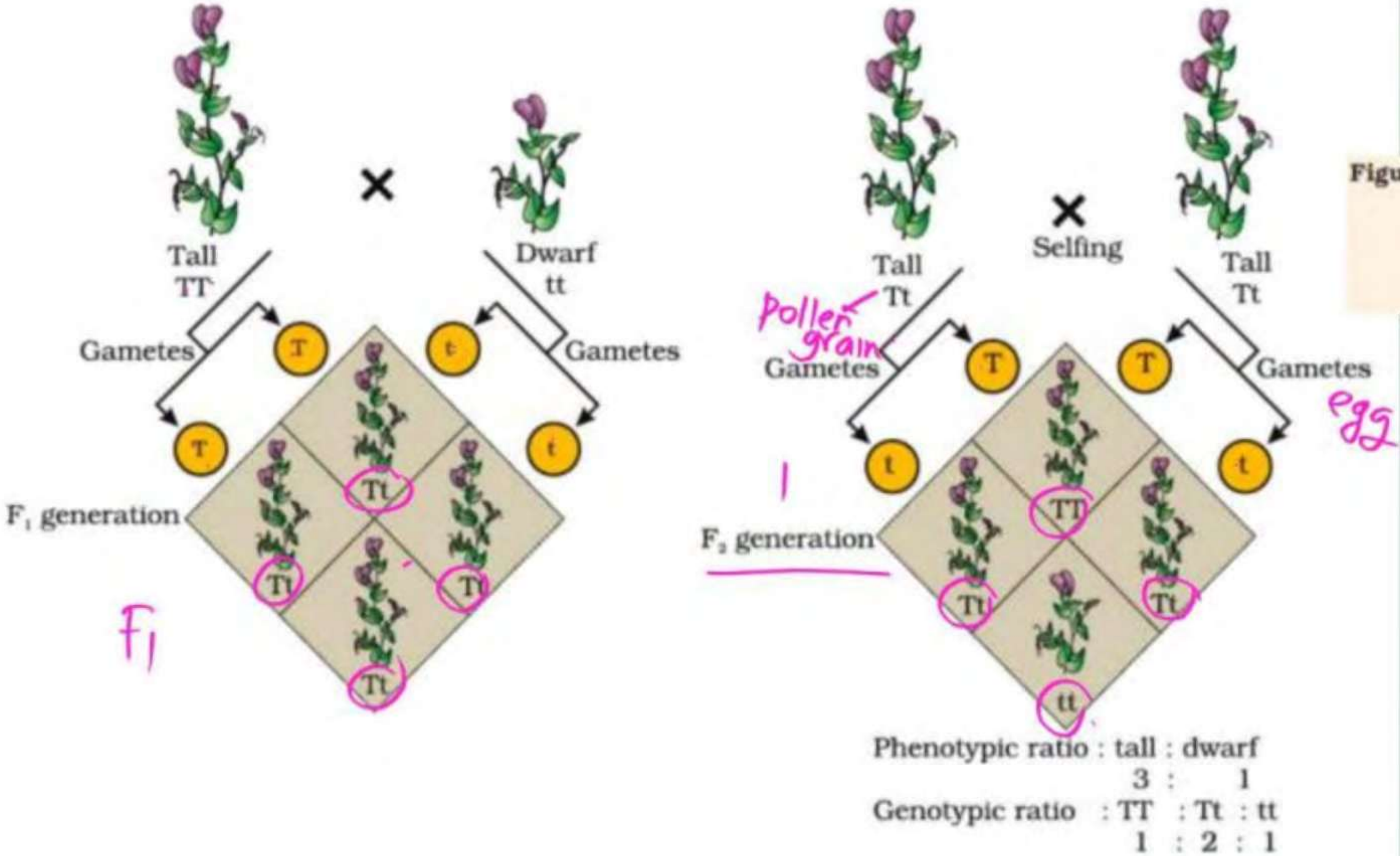


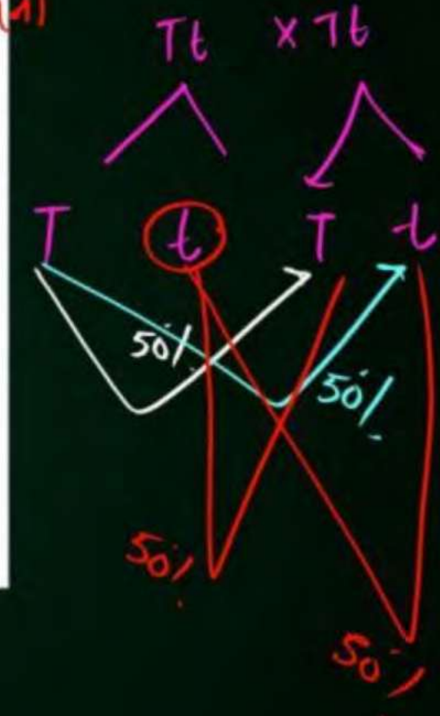
Figure 4.4 A Punnett square used to understand a typical monohybrid cross conducted by Mendel between true-breeding tall plants and true-breeding dwarf plants

The Punnett Square shows the parental tall **TT** (male) and dwarf **tt** (female) plants, the gametes produced by them and, the F_1 **Tt** progeny. The F_1 plants of genotype **Tt** are self-pollinated. The symbols ♀ and ♂ are used to denote the female (eggs) and male (pollen) of the F_1 generation, respectively. The F_1 plant of the genotype **Tt** when self-pollinated, produces gametes of the genotype **T** and **t** in equal proportion. When fertilisation takes place, the pollen grains of genotype **T** have a 50 per cent chance to pollinate eggs of the genotype **T**, as well as of genotype **t**. Also pollen grains of genotype **t** have a 50 per cent chance of pollinating eggs of genotype **T**, as well as of genotype **t**. As a result of random fertilisation, the resultant zygotes can be of the genotypes **TT**, **Tt** or **tt**.

Tt

Like beget like.

पैदा करना



From the Punnett square it is easily seen that $1/4^{th}$ of the random fertilisations lead to **TT**, 1/2 lead to **Tt** and $1/4^{th}$ to **tt**. Though the F_1 have a genotype of **Tt**, but the phenotypic character seen is 'tall'. At F_2, $3/4^{th}$ of the plants are tall, where some of them are **TT** while others are **Tt**. Externally it is not possible to distinguish between the plants with the genotypes **TT** and **Tt**. Hence, within the genopytic pair **Tt** only one character '**T**' tall is expressed. Hence the character **T** or 'tall' is said to dominate over the other allele **t** or 'dwarf' character. It is thus due to this dominance of one character over the other that all the F_1 are tall (though the genotype is **Tt**) and in the F_2 $3/4^{th}$ of the plants are tall (though genotypically 1/2 are **Tt** and only $1/4^{th}$ are **TT**). This leads to a phenotypic ratio of $3/4^{th}$ tall : (1/4 **TT** + 1/2 **Tt**) and $1/4^{th}$ **tt**, i.e., a 3:1 ratio, but a genotypic ratio of 1:2:1.

TT : Tall
Tt : Tall
genotype diff
Phenotype same

Tall

TT (1)

Tt (2)

The 1/4 : 1/2 : 1/4 ratio of **TT**: **Tt**: **tt** is mathematically condensable to the form of the binomial expression $(ax + by)^2$, that has the gametes bearing genes **T** or **t** in equal frequency of ½. The expression is expanded as given below :

$(1/2\mathbf{T} + 1/2\,\mathbf{t})^2 = (1/2\mathbf{T} + 1/2\mathbf{t}) \times (1/2\mathbf{T} + 1/2\mathbf{t}) = 1/4\,\mathbf{TT} + 1/2\mathbf{Tt} + 1/4\,\mathbf{tt}$

$\left(\frac{1}{2}T + \frac{1}{2}t\right)^2 \Rightarrow a^2 + b^2 + 2ab$

BINOMIAL EXPRESSION

$\Rightarrow \frac{1}{2}T \times \frac{1}{2}T + \frac{1}{2}t \times \frac{1}{2}t + 2 \times \frac{1}{2}T \times \frac{1}{2}t$

$\Rightarrow \frac{1}{4}TT + \frac{1}{4}tt + \frac{2}{4}Tt$

MONOHYBRID CROSS M·C

ON BASIS OF M·C MENDEL
GIVES TWO RULES CALLED
LAW OF INHERITENCE

⇒ 1st Law: LAW OF DOMINANCE

⇒ 2nd Law: LAW OF SEGREGATION.
(PURITY OF GAMETES)

LAW OF DOMINANCE

★ CHARACTER CONTROLLED BY SEPERATE ONIT (DISCRETE) CALLED FACTOR.

★ FACTORS OCCUR IN PAIR
TT / Tt / tt

★ IN DISIMILAR PAIR OF FACTOR

Tt

dominant allele | Recessive allele

★ EXPLAIN ONLY ONE TRAIT (CHARACTER), TALL IN F-1 genⁿ AND BOTH TRAIT IN F_2 genⁿ (TALL, DWARF)

★ ONLY DOMINANT ALLELE HENCE DOMINANT TRAIT EXPRESS IN F-1 GENⁿ.

★ ALSO EXPLAIN 3:1 IN F-2 GENⁿ.

★ THIS LAW IS NOT UNIVERSAL LAW. IT HAS EXCEPTION.

INCOMPLETE DOMINANCE
CODOMINANCE
?

LAW OF SEGREGATION.

* This law Based on fact that allele do not show Blending (NO MIXING OF ALLELE / NO INTERMEDIATE HEIGHT / NO 7/8 Cm) AND BOTH CHARACTER (TRAIT) RECOVERED IN F_2 (TALL & DWARF) ALTHOUGH ONLY ONE TRAIT EXPRESS IN F_1 (TALL)
* PARENTS CONTAIN TWO ALLELE / TWO FACTOR DURING GAMETE FORMATION
* ONLY ONE CHROMOSOME / FACTOR / ALLELE ENTER INTO EACH GAMETES.

* TT → T, T (50%) — HOMOZYGOUS PARENT → ONE TYPE OF GAMETE
  Tt → T, t (50%) — HETROZYGOUS PARENT → TWO TYPE OF GAMETE.
  tt → t, t (50%) — HOMOZYGOUS PARENT → ONE TYPE OF GAMETE

* UNIVERSAL LAW.

BACK CROSS → TEST CROSS
BACK CROSS → OUTCROSS

TEST CROSS

Violet FLOWER × Recessive parent

$\boxed{WW}$ × ww

↓

Ww

(All violet FLOWER)

VIOLET FLOWER
(PHENOTYPE)

↓

IT CAN BE HOMOZYGOUS VIOLET / HETROZYGOUS VIOLET.

WW / Ww

↓

USED TO DETERMINE GENOTYPE OF UNKOWN PARENT.

Violet flower × Recessive parent

$\boxed{Ww}$ × ww

	W	w
w	Ww 50%	ww 50%
	VIOLET	WHITE

$\boxed{1 : 1}$

NOTE: $\boxed{\text{TALL}}$ (F_1 genⁿ)

TALL x tt

TALL: 50%
DWARF: 50%

Genotype: Tt

NOTE: TALL (F_2 genⁿ)

TALL x tt

All TALL PLANT ONLY

Genotype: TT.

* TO FIND THE GENOTYPE OF UNKNOWN PARENT (F_1/F_2).

याद रखो

$\boxed{F_1 \text{ X Recessive parent}}$

$\boxed{\text{Tt X tt}}$

Tt : 50% (TALL)
tt : 50% (DWARF)

MONOHYBRID TEST CROSS: $\boxed{1:1}$

Phenotype: 2 Tall, dwarf
genotype: 2 Tt, tt
Phenotypic Ratio: 1 : 1 (TALL & DWARF)
Genotypic Ratio: 1:1 (Tt & tt)

SAME

OUT CROSS.

$\boxed{F_1 \text{ X HOMOZYGOUS DOMINANT}}$

Tt X TT

	T
T	TT
t	Tt

Phenotype: 1 (TALL)
Genotype: 2 TT, Tt

$\boxed{\text{genotypic Ratio: 1 : 1}}$

Exception of MENDELISM

INCOMPLETE DOMINANCE

* CORRENS
* EXAMPLE: (1) MIRABILIS JALAPA / 4 O'CLOCK PLANT

  (2) ANTIRRHINUM MAJUS / DOG FLOWER / SNAPDRAGON.

HOMOZYGOUS STATE

RED — RR

WHITE — rr

Red flower × White flower

RR × rr

(R) × (r)

$\boxed{Rr} \longrightarrow F_1$

PINK

* MIXING OF ALLELE / INTERMEDIATE / BLENDING
* F_1 do not Resemble either of Two parent

Rr (♂) × Rr (♀)

	R	r
R	RR (Red)	Rr (PINK)
r	Rr (PINK)	rr (White)

F_2

No. of phenotype: 3 → Red, PINK, WHITE

No. of genotype: 3 → RR, Rr, rr

Phenotypic Ratio:	1 :	2 :	1
	(Red)	(PINK)	(White)
genotypic Ratio:	1 :	2 :	1
	RR	Rr	rr

Same.

4.2.1 Law of Dominance

(i) Characters are controlled by discrete units called **factors**.

(ii) Factors occur in pairs.

(iii) In a dissimilar pair of factors one member of the pair dominates (dominant) the other (recessive).

The law of dominance is used to explain the expression of only one of the parental characters in a monohybrid cross in the F_1 and the expression of both in the F_2. It also explains the proportion of 3:1 obtained at the F_2.

Tall

4.2.2 Law of Segregation

DWARF Tall, dwarf

This law is based on the fact that the alleles do not show any blending and that both the characters are recovered as such in the F_2 generation though one of these is not seen at the F_1 stage. Though the parents contain two alleles during gamete formation, the factors or alleles of a pair segregate from each other such that a gamete receives only one of the two factors. Of course, a homozygous parent produces all gametes that are similar while a heterozygous one produces two kinds of gametes each having one allele with equal proportion.

TT 10cm

tt 3cm

Tt : 10cm

ONLY ONE ALLELE EXPRESS

MIX (NO)

7cm/8cm (NO)

Tt

50% T

50% t

TT / tt

50% T

50% T

50% t

50% t

MULTIPLE ALLELE

★ ONE GENE : USUALLY TWO ALLELE : ONE CHARACTER
BUT

★ ONE GENE : MORE THAN TWO ALLELE : ONE CHARACTER

★ I gene : 3 ALLELE : ABO BLOOD group.

★ I^A : 12th : Dominant

★ I^B : 12th : Dominant

★ I^O : 4th : Recessive

★ OUT OF THREE ALLELE ONLY TWO ALLELE PRESENT ON HOMOLOGOUS SITE / SAME LOCUS ON HOMOLOGOUS CHROMOSOME

★ BOTH DOMINANT ALLELE EXPRESS EQUALLY, 50% CONTRIBUTION BY BOTH ALLELE / BOTH ALLELE DO NOT INHIBIT EACH OTHER & INDEPENDENTLY EXPRESS : **CODOMINANCE.**

A BLOOD

HOMOZYGOUS

Genotype

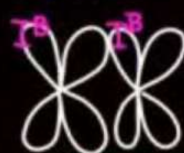
I^AI^A & I^AI^O

HETROZYGOUS.

EXPRESS : DOMINANT ALLELE

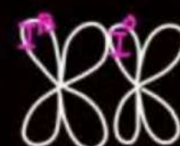
Q : My Blood group is A : Phenotype
I am Hetrozygous for Blood group 'A' : I^AI^O Genotype.

B BLOOD



HOMOZYGOUS

I^BI^B & I^BI^O



HETROZYGOUS

AB BLOOD

I^AI^B

O BLOOD

I^OI^O / ii

STUDY IN POPULATION

CODOMINANCE

CONCEPT

AB BLOOD group

$I^A I^A \rightarrow I^A$

$I^B I^B \rightarrow I^B$

50% ← $\boxed{I^A I^B}$ → 50%

⇒ PROGENY RESEMBLE TO BOTH PARENT 50% EACH.

⇒ BOTH ALLELE EXPRESS EQUALLY

NOTE:

* F_1 Resemble : ONLY ONE PARENT
  COMPLETE DOMINANCE
* " " : NONE OF TWO PARENT / INTERMEDIATE
  INCOMPLETE DOMINANCE
* " " : BOTH PARENT EQUALLY
  CODOMINANCE.

SICKLE CELL ANEMIA

$Hb^A\ Hb^A$: NORMAL.

$Hb^S\ Hb^S$: DEATH.

$Hb^A\ Hb^S$

$\boxed{\begin{array}{l}50\%\ Hb : \text{GOOD} \\ 50\%\ Hb : \text{DEFECTIVE}\end{array}}$

CARRIER CODOMINANCE

Hb^A : NORMAL

Hb^S : DEFECTIVE ALLELE

$Hb^A Hb^S \times Hb^A Hb^S$

	Hb^A	Hb^S
Hb^A	$Hb^A Hb^A$	$Hb^A Hb^S$
Hb^S	$Hb^A Hb^S$	$Hb^S Hb^S$

DEATH

Lethal gene : Which cause death in Homozygous Condition.

NOTE

A

→ A SUGAR.
→ membrane

RBC

B

→ B sugar.

O

→ NO SUGAR.

AB

→ A
→ B

] → SLIGHTLY DIFFERENT FORM OF SUGAR.

③ Coat colour in cattle.

RED	white
RR	WW
↓	↓
R	W

$\boxed{RW} \longrightarrow F_1$

ROAN (RED & WHITE) CODOMINANCE

RW X RW

	R	W
R	RR RED	RW ROAN
W	RW ROAN	WW WHITE

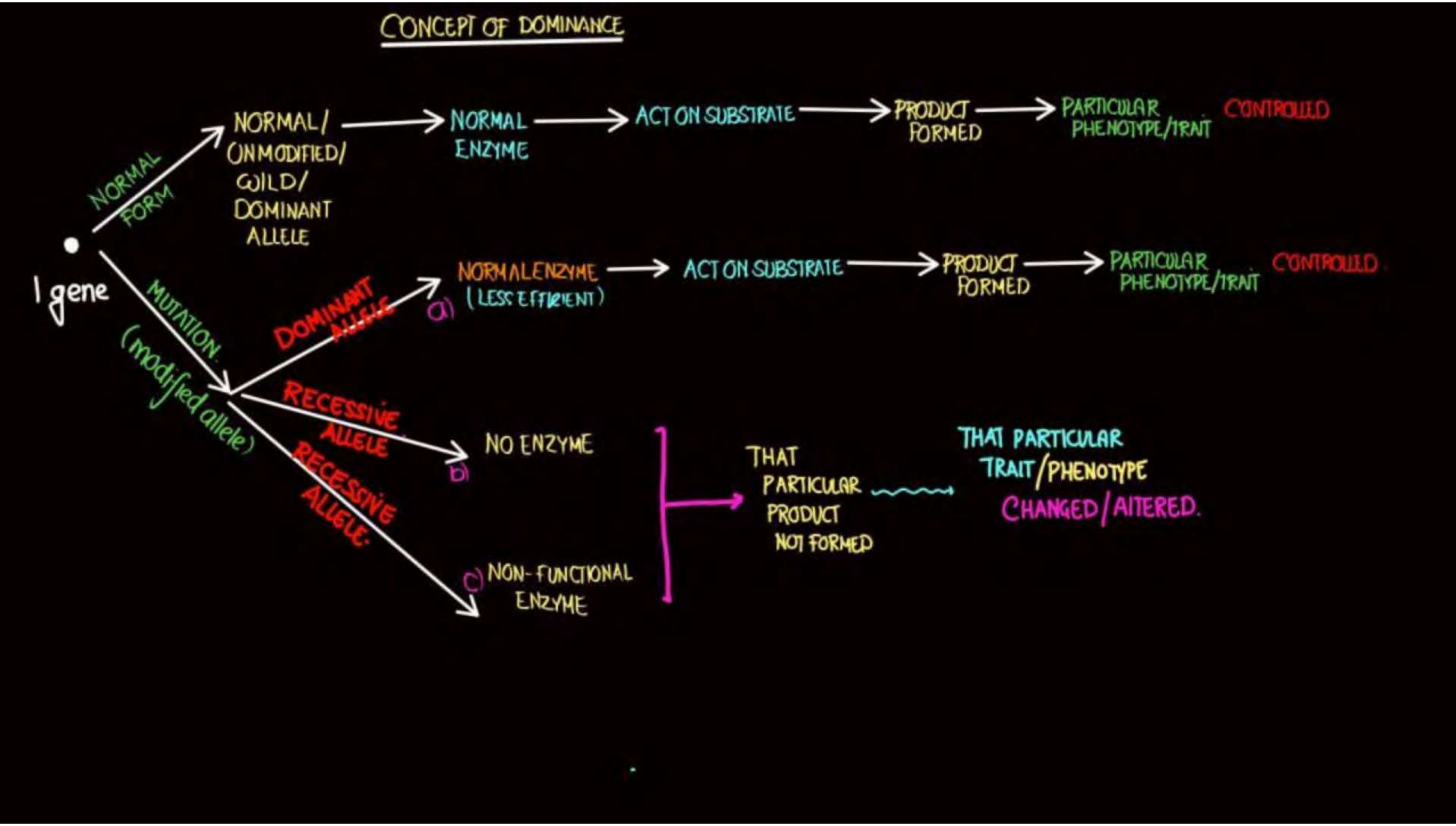
PHENOTYPIC RATIO : 1(RED) : 2(ROAN) : 1(WHITE)
GENOTYPIC RATIO : 1(RR) : 2(RW) : 1(WW)

OUT OF NCERT

⇒ Eye colour in drosophila
⇒ self incompatibility
⇒ Coat colour in Rabbit

[MULTIPLE ALLELE

⇒ MN BLOOD GROUP : CODOMINANCE.


CONCEPT OF DOMINANCE
1 gene
NORMAL FORM
NORMAL/ UNMODIFIED/ WILD/ DOMINANT ALLELE
NORMAL ENZYME
ACT ON SUBSTRATE
PRODUCT FORMED
PARTICULAR PHENOTYPE/TRAIT
CONTROLLED
MUTATION
(modified allele)
DOMINANT ALLELE
a) NORMAL ENZYME (LESS EFFICIENT)
ACT ON SUBSTRATE
PRODUCT FORMED
PARTICULAR PHENOTYPE/TRAIT
CONTROLLED.
RECESSIVE ALLELE
b) NO ENZYME
RECESSIVE ALLELE.
c) NON-FUNCTIONAL ENZYME
THAT PARTICULAR PRODUCT NOT FORMED
THAT PARTICULAR TRAIT/PHENOTYPE CHANGED/ALTERED.

PLEIOTROPY

★ NORMALY ONE GENE CONTROL ONE CHARACTER

★ ONE GENE CONTROL MORE THAN ONE CHARACTER / TRAIT / PHENOTYPE

★ STARCH SYNTHESIS CONTROLLED BY ONE GENE & HAS TWO ALLELE
- B → STARCH SYNTHESIS (MORE)
- b → STARCH (LESS/NO SYNTHESIS

	SEED STARCH	SIZE	SHAPE
BB	Maximum	LARGE	ROUND
Bb	INTERMEDIATE	INTERMEDIATE	ROUND
bb	MINIMUM	small	WRINKLED

SIZE OF SEED (1 TRAIT / PHENOTYPE

Large seed → BB → B

small seed → bb → b

INCOMPLETE DOMINANCE

Bb ⟶ F_1

(INTERMEDIATE SIZE

Bb X Bb

	B	b
B	BB (L)	Bb (I)
b	Bb (I)	bb (S)

⇒ P.R : 1 (L) : 2 (I) : 1 (S)

⇒ GR : 1 (BB) : 2 (Bb) : 1 (bb)

SHAPE OF SEED / TRAIT / PHENOTYPE

ROUND SEED

BB

WRINKLED SEED

bb

Law of dominance

Bb → F_1

ROUND.

Bb x Bb

	B	b
B	BB ROUND	Bb ROUND
b	Bb ROUND	bb WRINKLED

$\boxed{\text{PR: } 3 : 1 \quad \text{GR: } 1 : 2 : 1}$

RUPESH SIR
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Physics Wallah
@PWRUPESHSIR

INHERITENCE OF TWO GENE

STUDY OF : TWO GENE : TWO CHARACTER : FOUR TRAIT : DIHYBRID CROSS

GENE	Character	TRAIT DOMINANT	TRAIT RECESSIVE	CROSS
•	seed shape	ROUND	WRINKLED	M·C
•	seed colour	yellow	green	M·C
2 GENE	2 CHARACTER	4 TRAIT		MC + MC = DC

PARENT

PURE (TRUE BREEDING)

♂ ROUND, YELLOW
SHAPE COLOUR

RRYY

RY

♀ WRINKLED, GREEN
SHAPE COLOUR.

rryy

ry

gametes.

GENOTYPE ← $\boxed{RrYy}$ ⟶ F_1

ROUND, YELLOW
SHAPE COLOUR → PHENOTYPE

RrYy $\times$ RrYy

50% 50% 50% 50%

R r Y y

50% 50% 50% 50%

RY Ry rY ry

25% 25% 25% 25%

pollen grain
(male gametes)

rY

Ry ry

RY

egg
(female gamete)

Q. probability of formation of each gamete: ry

$\Rightarrow \frac{1}{4} \times 100$

$\Rightarrow 25\%$

	RY	Ry	rY	ry
RY	RRYY RY	RRYy RY	RrYY RY	RrYy RY
Ry	RRYy RY	RRyy RG	RrYy RY	Rryy RG
rY	RrYY RY	RrYy RY	rrYY WY	rrYy WY
ry	RrYy RY	Rryy RG	rrYy WY	rryy WG

Phenotype — GENOTYPE

- ROUND YELLOW ⇒ 9
  - RRYY : 1
  - RRYy : 2
  - RrYY : 2
  - RrYy : 4 *
- ROUND GREEN ⇒ 3
  - RRyy : 1
  - Rryy : 2
- WRINKLED YELLOW ⇒ 3
  - rrYY : 1
  - rrYy : 2
- WRINKLED GREEN ⇒ 1
  - rryy : 1

Phenotypic Ratio : 9 : 3 : 3 : 1

1 DC : MC + MC

: (3:1) (3:1)

: **9 : 3 : 3 : 1**

Genotypic Ratio

1 DC : MC + MC

: (1:2:1) (1:2:1)

: **1 : 2 : 1 : 2 : 4 : 2 : 1 : 2 : 1**

Q1 Two dominant trait controlled by same gene in DC (TRUE/ FALSE)

FALSE : $\boxed{\text{DIFFERENT GENE : CORRECT}}$

WRINKLED & GREEN

Q2 Two Recessive trait controlled by same gene in DC (TRUE/FALSE)

FALSE $\boxed{\text{DIFFERENT GENE : CORRECT}}$

Q.3 Ratio of two dominant trait controlled by two different gene

ROUND : 9+3 ⇒ 12

YELLOW : 9+3 ⇒ 12

$\boxed{1:1}$

Q.4 Ratio of two recessive trait controlled by two difference gene

WRINKLED : 3+1 ⇒ 4

GREEN : 3+1 ⇒ 4

$\boxed{1:1}$

Q.5 Ratio of two trait controlled by same gene

ROUND (D) : WRINKLED (R) ⇒ 12 : 4 ⇒ $\boxed{3:1}$

YELLOW (D) : GREEN (R) ⇒ 12 : 4 ⇒ $\boxed{3:1}$

Q.6 No. of plant which are hetrozygous for both trait. RrYy ⇒ 4

Q.7 No. of plant which are homozygous for both trait.

RRYY 1

RRyy 1

rrYY 1

rryy 1

⇒ 4

Q.8 No. of plant hetrozygous for 1st trait & homozygous for 2nd trait

RrYY ⇒ 2

Rryy ⇒ 2

⇒ 4

Q.9 No. of plant homozygous for 1st trait & heterozygous for 2nd trait.

RRYy 2

rrYy 2

⇒ 4

Q. No. of plant : Double Recessive in F_2 generation.

rryy ⇒ 1

Q. Ratio of parental to recombinant in F_2 generation.

~~10~~ ~~6~~ Crossing over (NEW)

5 3

$\boxed{5 : 3}$

Q. Number of plant in which all allele are in identical condition 2

1 : RRYY : DOMINANT

1 : rryy : Recessive

~~RRyy~~

DIHYBRID TEST CROSS

F_1 × Recessive parent

⇒ RrYy × rryy.

	ry	
RY	RrYy	RY
Ry	Rryy	RG
rY	rrYy	WY
ry	rryy	WG.

no. of phenotype : 4

no. of genotype : 4

Phenotypic Ratio : 1 : 1 : 1 : 1
RY RG WY WG.

Geno Ratio : 1 : 1 : 1 : 1

INDEPENDENT ASSORTMENT → EXPRESS.

On Basis of Dihybrid cross. Second sets of generalisation given

3rd Law

* When we study Two gene / Two character Together, even then Both gene / character / TRAIT EXPRESS INDEPENDENTLY OF EACH OTHER

RrYy ⟶ F_1

ROUND TRAIT — YELLOW TRAIT

BOTH TRAIT HAVE DIFFERENT GENE

* BOTH GENE DO NOT INHIBIT EXPRESSION OF EACH OTHER.
* NOT A UNIVERSAL LAW
* EXCEPTION: **LINKAGE** ?
* THIS LAW CAN'T BE EXPLAIN ON BASIS OF MONOHYBRID CROSS (TRUE)
* MENDEL EXPLAINED LAW OF DOMINANCE & LAW OF SEGREGATION ON BASIS OF MONOHYBRID CROSS (TRUE)
* All THREE LAW CAN BE EXPLAINED ON BASIS OF DIHYBRID CROSS (TRUE)

POLYGENIC INHERITENCE | QUANTITATIVE INHERITENCE

★ According to MENDEL: EACH CHARACTER HAS TWO DISTINCT TRAIT

eg: Tall & dwarf, ROUND & WRINKLED.
violet/purple & white

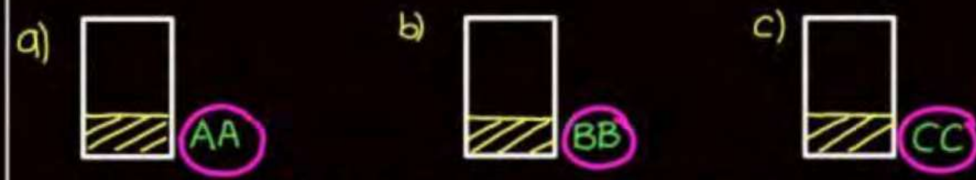
⇒ QUALITATIVE INHERITENCE

BUT

⇒ SOME CHARACTER (HUMAN SKIN COLOUR) have many TRAITS (BUT NOT TWO DISTINCT TRAIT)

eg: HUMAN HEIGHT.

⇒ THESE CHARACTER CONTROLLED BY MULTIPLE GENE / MANY GENE. CALLED POLYGENIC INHERITENCE



★ SAME QUANTITY: MELANIN PIGMENT (DARK COLOUR)

★ EACH DOMINANT ALLELE FORM SAME AMOUNT OF MELANIN

VERY DARK: COMPLETE FILL

NEED DOMINANT ALLELE: 6

★ 3 PAIR OF GENE: TOTAL 6 GENE

NOTE: DEPENDS UPON QUANTITY OF DOMINANT ALLELE NOT RECESSIVE ALLELE

Eg: HUMAN SKIN COLOUR.

VERY DARK (NEGRO) × VERY LIGHT (ALBINO)

AABBCC × aabbcc

AABBCC → $\boxed{ABC}$

aabbcc → $\boxed{abc}$

AaBbCc

$\boxed{AaBbCc} \longrightarrow F_1$

INTERMEDIATE/MULATO.

AaBbCc (♂) × AaBbCc (♀)

	ABC 3	ABc 2	AbC 2	Abc 1	aBC 2	aBc 1	abC 1	0 abc
ABC 3	6	5	5	4	5	4	4	3
ABc 2	5	4	4	3	4	3	3	2
AbC 2	5	4	4	3	4	3	3	2
Abc 1	4	3	3	2	3	2	2	1
aBC 2	5	4	4	3	4	3	3	2
aBc 1	4	3	3	2	3	2	2	1
abC 1	4	3	3	2	3	2	2	1
abc 0	3	2	2	1	2	1	1	0

PHENOTYPIC

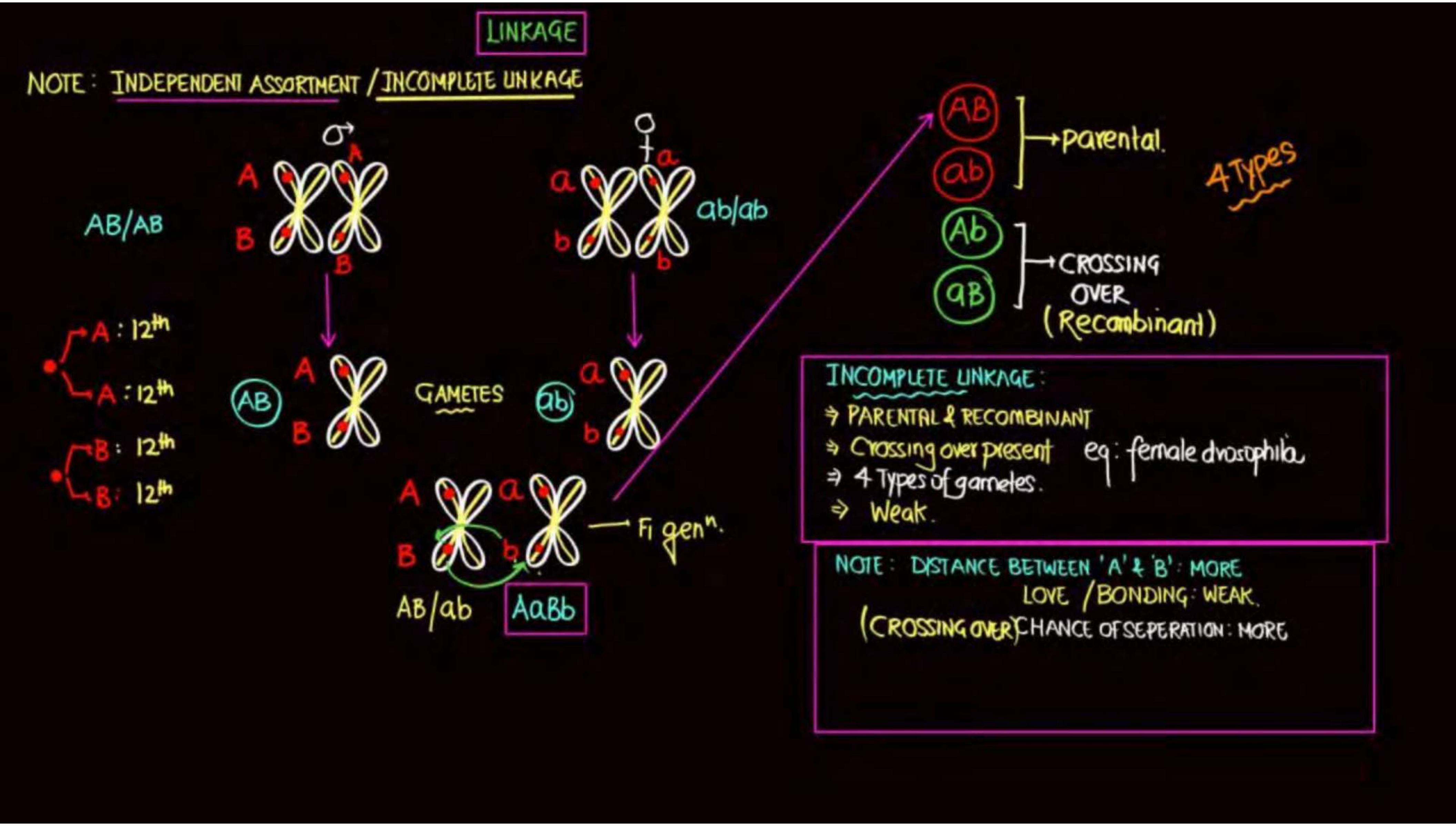
VERY D : 1
DARK : 6
FAIR·DARK : 15
INTERMEDIATE : 20
FAIRLY LIGHT : 15
LIGHT : 6
VERY LIGHT : 1

no. of phenotype:
$\Rightarrow 2n+1$
n: pair of polygene
n: 3
$\Rightarrow 2 \times 3 + 1 \Rightarrow 7$
no. of genotypes $\Rightarrow$: 3^n
$\Rightarrow 3^3$: 27

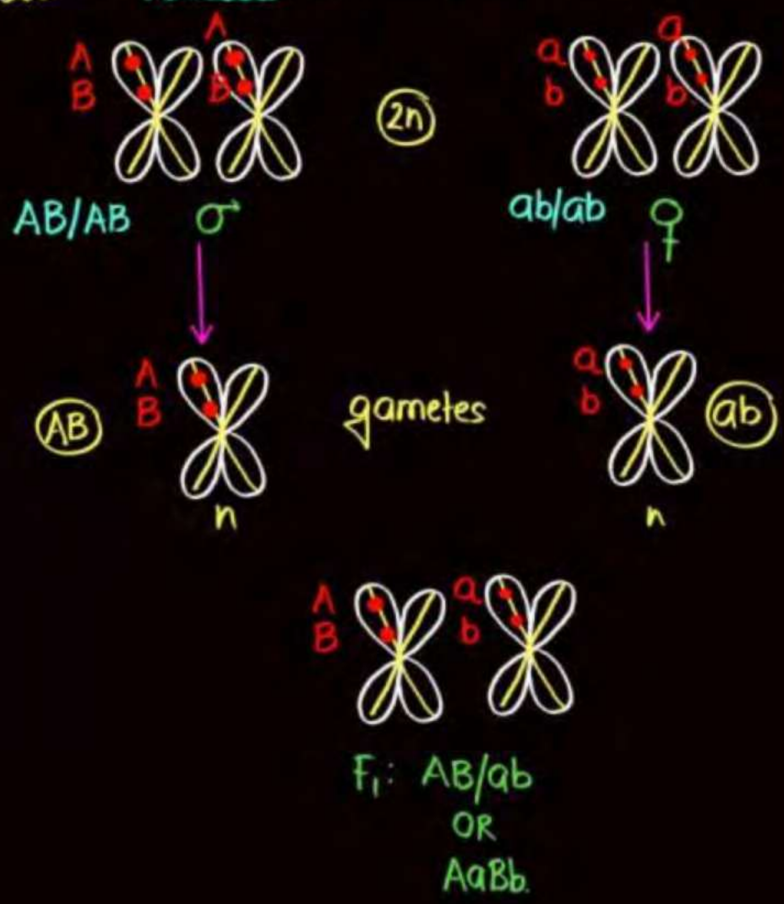
⇒ ALSO ROLE OF ENVIRONMENT.

⇒ CUMULATIVE / ADDITIVE EFFECT.

Each dominant allele contribute
its ROLE & FULY TRAIT (VERY DARK)
APPEAR, WHEN ALL DOMINANT
ALLELE CONTRIBUTE / PRESENT


LINKAGE
NOTE: INDEPENDENT ASSORTMENT / INCOMPLETE LINKAGE
AB/AB
ab/ab
A : 12th
A : 12th
B : 12th
B : 12th
AB
GAMETES
ab
A
B
a
b
AB/ab
AaBb
F1 genn.
AB
ab
parental.
Ab
aB
CROSSING OVER (Recombinant)
4 Types
INCOMPLETE LINKAGE:
⇒ PARENTAL & RECOMBINANT
⇒ Crossing over present
eg: female drosophila
⇒ 4 Types of gametes.
⇒ Weak.
NOTE: DISTANCE BETWEEN 'A' & 'B': MORE
LOVE / BONDING: WEAK.
(CROSSING OVER) CHANCE OF SEPERATION: MORE

NOTE: COMPLETE LINKAGE : RARE



⇒ DISTANCE B/W A&B : LESS.
LOVE / BONDING : MORE
CHANCE OF SEPERATION : 0%
CROSSING OVER : ABSENT
(RECOMBINATION).

NO. OF GAMETE : AB , ab ⇒ 2 ⇒ All are parental 100%

★ Tendency of Two gene Remain Together & inherit Together. Called LINKAGE (TERM: MORGAN)

eg: MALE DROSOPHILA

★ RARE / IT IS NOT COMMON.

★ STRONG.

★ NO INDEPENDENT ASSORTMENT.

★ NO RECOMBINANT

$$\boxed{C.O \propto \frac{1}{\text{LINKAGE}}}$$

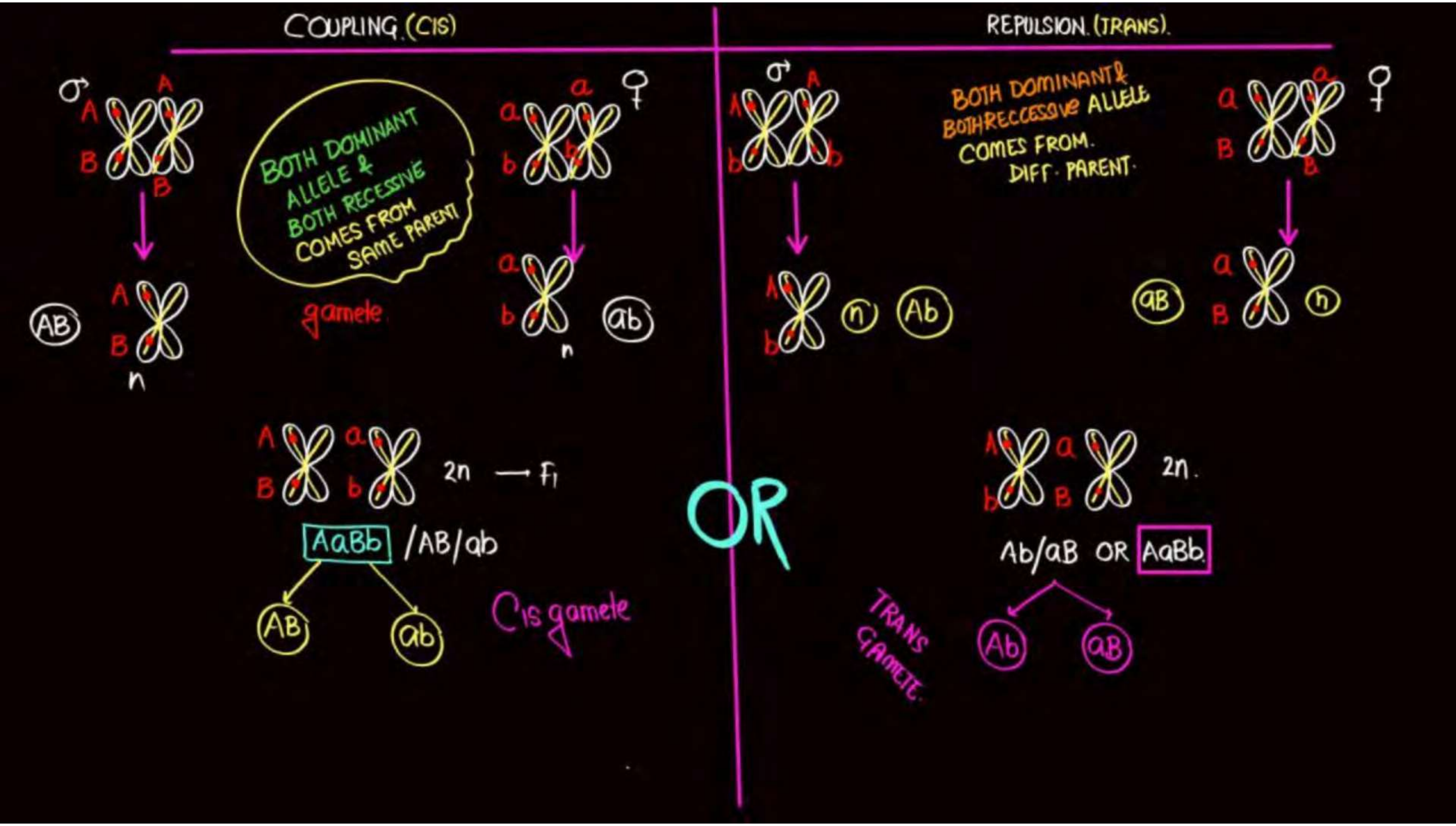
⇒ DISTANCE ↑, C.O ↑, LINKAGE ↓ (WEAK)

⇒ DISTANCE ↓, C.O ↓, LINKAGE ↑ (STRONG)

⇒ INCOMPLETE LINKAGE :

⇒ RECOMBINANT (NEW $\leq 50\%$

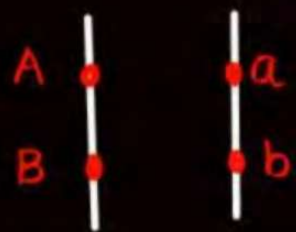
⇒ RECOMBINANT CAN'T EXCEEDE MORE THAN 50%



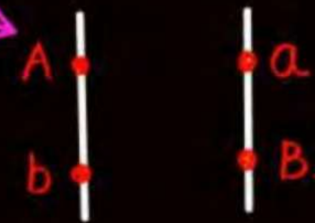
COUPLING. (CIS)
REPULSION. (TRANS).
BOTH DOMINANT ALLELE & BOTH RECESSIVE COMES FROM SAME PARENT
gamete
AB
ab
n
AaBb /AB/ab
2n → F1
AB
ab
Cis gamete
OR
BOTH DOMINANT & BOTH RECCESSIVE ALLELE COMES FROM. DIFF. PARENT.
Ab
aB
2n.
Ab/aB OR AaBb
TRANS GAMETE.
Ab
aB

Question :

AaBb. number of gamete : (These are linked gene).



OR.



2

AB , ab

Cis Type

Ab , aB

2

TRANS TYPE.

Q.1 Gamete formed by $\boxed{\text{AaBb}}$, if complete linkage present.

AB

ab

A | | a

B | | b.

2

Q.2 Gametes formed by $\boxed{\text{AaBb}}$, if independ assortment / incomplete linkage present.

AB

Ab

aB

ab

4

CR. OVER ✓

Q.3 AaBbCc types of gametes if last two genes are linked.

Aa → Follow indep. assort.

BbCc → LINKAGE

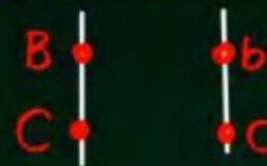
$\Rightarrow 2^n$

$n = 1$

$\Rightarrow 2^1 = 2$

2 gam.

$2 \times 2 = 4$



Aa

A a

BC bc

ABC

AbC

aBC

abc

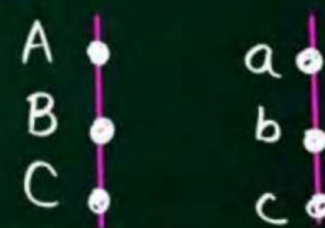
$\Rightarrow 4$

Q.4 AaBbCc types of gametes if all genes are linked.

2

ABC

abc



Q. No. of gametes formed by AaBb$\boxed{\text{CcDd}}$

(a) If last two genes are linked ⇒.

(b) If independe assort present

AaBbCcDd

$\Rightarrow 2^n$

$\Rightarrow n = 4$

$\Rightarrow 2^4 \Rightarrow 16$

AaBb$\boxed{\text{CcDd}}$.

Indep assort

$\Rightarrow 2^n$

$\Rightarrow n : 2$

$\Rightarrow 2^2 = 4$

Linkage

CD

cd

2

$4 \times 2 \Rightarrow 8$

AB.
Ab
aB
ab

ABCD
ABcd
AbCD
Abcd
aBCD
aBcd
abCD
abcd

LINKAGE

Q $RrYy \times RrYy$

a) F_2 Ratio: 9:3:3:1 (If independent assortment OCCUR)

b) If LINKAGE PRESENT

	RY	ry
RY	RRYY	RrYy
ry	RrYy	rryy

$\boxed{\text{PR: 3:1} \quad \text{GR: 1:2:1}}$

NOTE: RATIO OF DIHYBRID CROSS DURING LINKAGE EQUAL TO NORMAL MONOHYBRID CROSS

Q Ratio of Dihybrid Test cross, if Linkage present

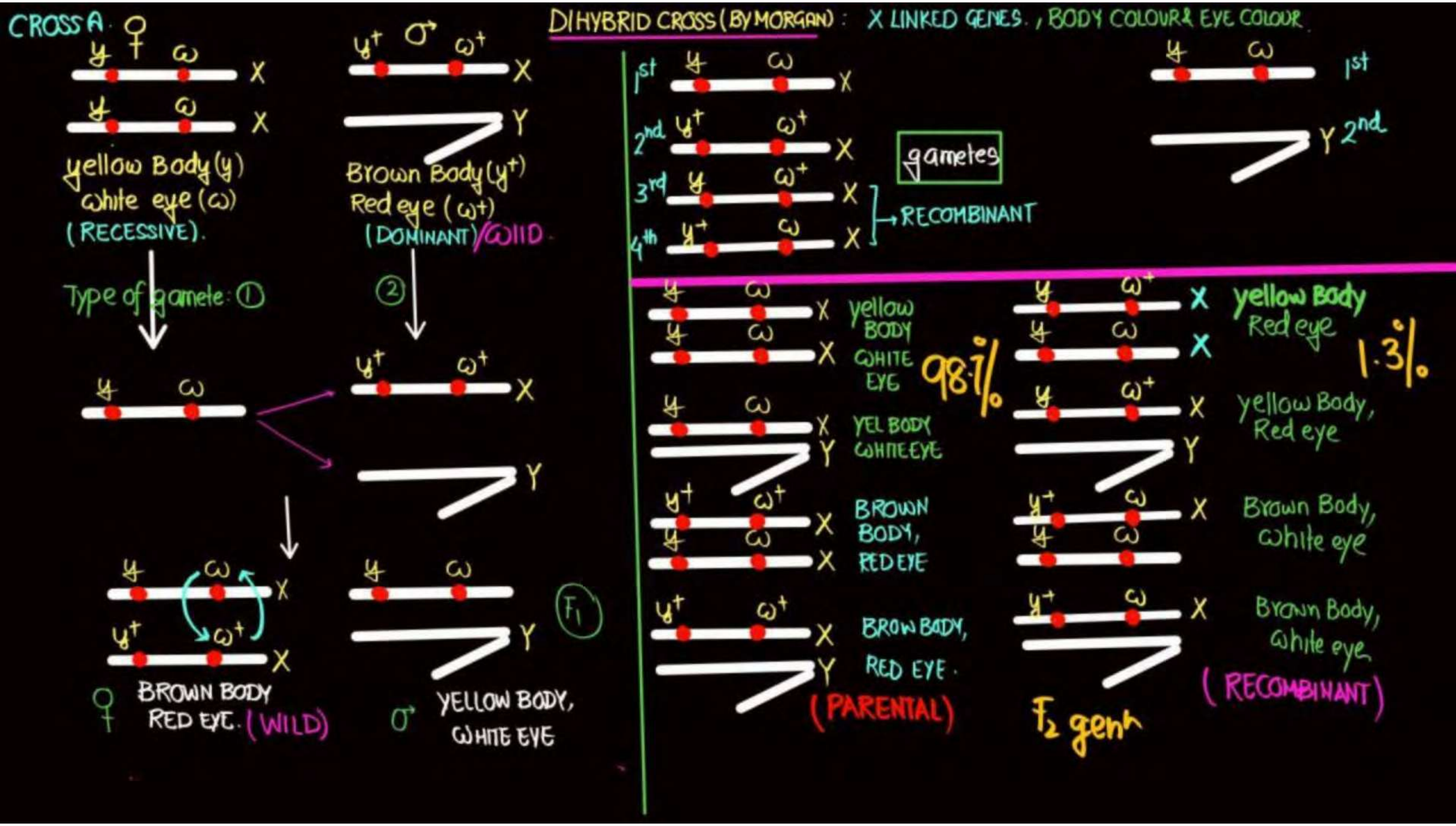
$F_1 \times$ Reces

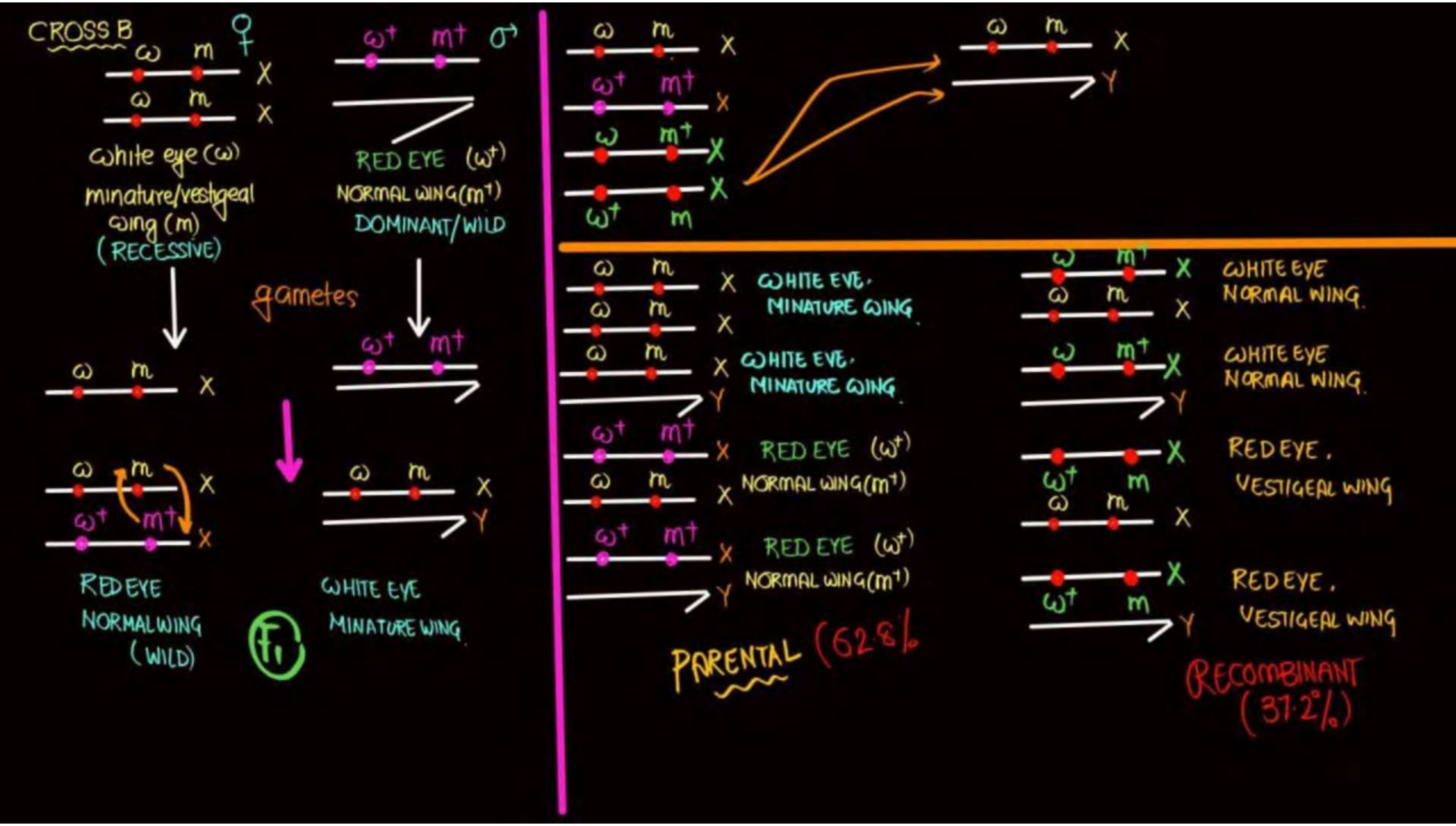
$\Rightarrow RrYy \times rryy$

	ry
RY	RrYy
ry	rryy

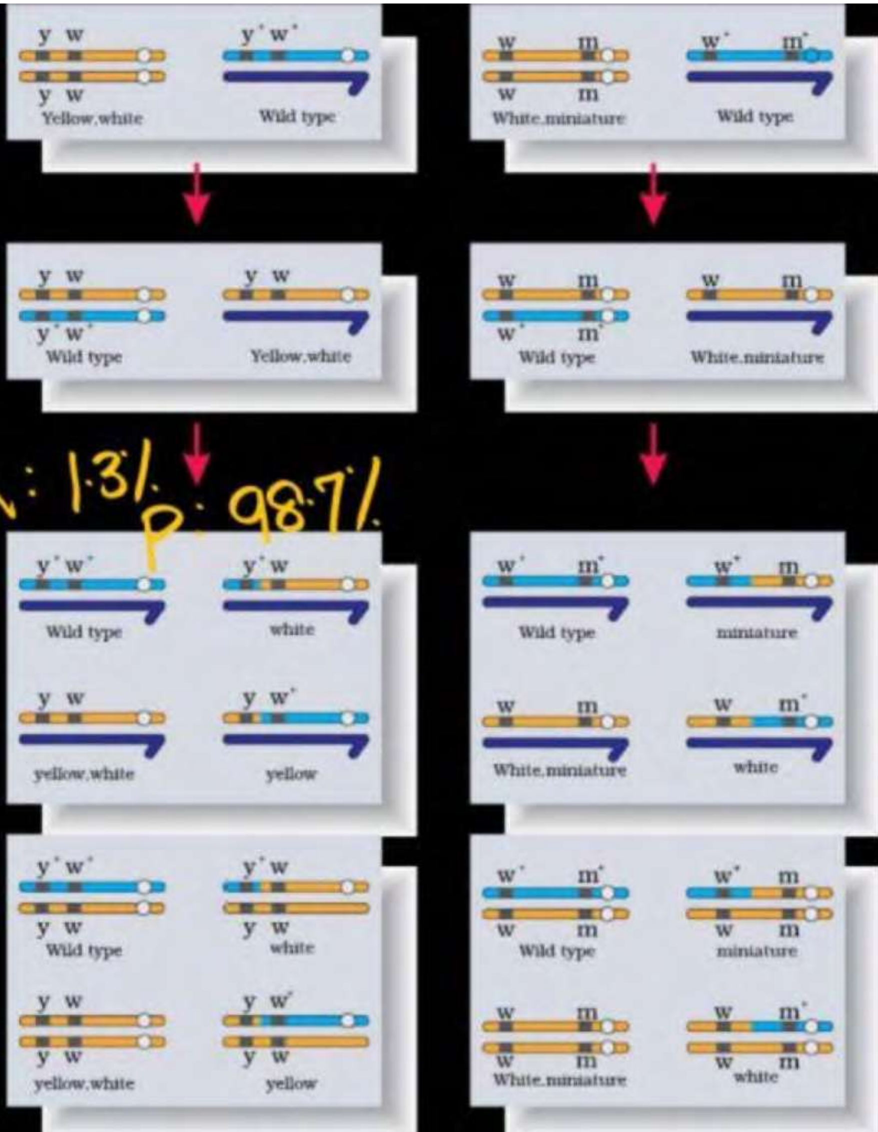
$\boxed{\text{PR \& GR: 1:1}}$

NOTE: RATIO OF DIHYBRID TEST CROSS DURING LINKAGE EQUAL TO NORMAL MONOHYBRID TEST CROSS


CROSS A
DIHYBRID CROSS (BY MORGAN): X LINKED GENES., BODY COLOUR & EYE COLOUR
♀ y ω X
y ω X
yellow Body (y)
white eye (ω)
(RECESSIVE).
♂ y+ ω+ X
Y
Brown Body (y+)
Red eye (ω+)
(DOMINANT)/WILD
Type of gamete: ①
②
y ω
y+ ω+ X
Y
y ω X
y+ ω+ X
♀ BROWN BODY RED EYE. (WILD)
y ω
Y
♂ YELLOW BODY, WHITE EYE
F1
1st y ω X
2nd y+ ω+ X
3rd y ω+ X
4th y+ ω X
RECOMBINANT
gametes
y ω 1st
Y 2nd
yellow BODY WHITE EYE
YEL BODY WHITE EYE
BROWN BODY, RED EYE
BROW BODY, RED EYE.
98.7%
(PARENTAL)
yellow Body Red eye
1.3%
yellow Body, Red eye
Brown Body, white eye
Brown Body, white eye
(RECOMBINANT)
F2 genn


CROSS B
ω m ♀
X
ω m
X
White eye (ω)
minature/vestigeal
wing (m)
(RECESSIVE)
ω⁺ m⁺ ♂
RED EYE (ω⁺)
NORMAL WING (m⁺)
DOMINANT/WILD
gametes
ω m
X
ω⁺ m⁺
ω m
X
ω⁺ m⁺
X
ω m
X
Y
RED EYE
NORMAL WING
(WILD)
F1
WHITE EYE
MINATURE WING
ω m
X
ω⁺ m⁺
X
ω m⁺
X
X
ω⁺ m
ω m
X
Y
WHITE EYE,
MINATURE WING
WHITE EYE,
MINATURE WING
RED EYE (ω⁺)
NORMAL WING (m⁺)
RED EYE (ω⁺)
NORMAL WING (m⁺)
PARENTAL (62.8%
WHITE EYE
NORMAL WING.
WHITE EYE
NORMAL WING.
RED EYE,
VESTIGEAL WING
RED EYE,
VESTIGEAL WING
RECOMBINANT
(37.2%)

R : 1.3%
P : 98.7%



62.8% = P
37.2% : R.

Topic : NCERT BOOSTER

(Tt)

4.3.2 Chromosomal Theory of Inheritance

seperate

death: 1884.
after 16 years.

(1) Mendel published his work on inheritance of characters in $\boxed{1865}$ but for several reasons, it remained $\boxed{\text{unrecognised till 1900.}}$ Firstly, communication was not easy (as it is now) in those days and his work could not be widely publicised. (2) Secondly, his concept of **genes** (or **factors**, in Mendel's words) as stable and discrete units that controlled the expression of traits and, of the pair of alleles which did not 'blend' with each other, $\boxed{\text{was not accepted by his contemporaries}}$ as an explanation for the apparently continuous variation seen in nature.

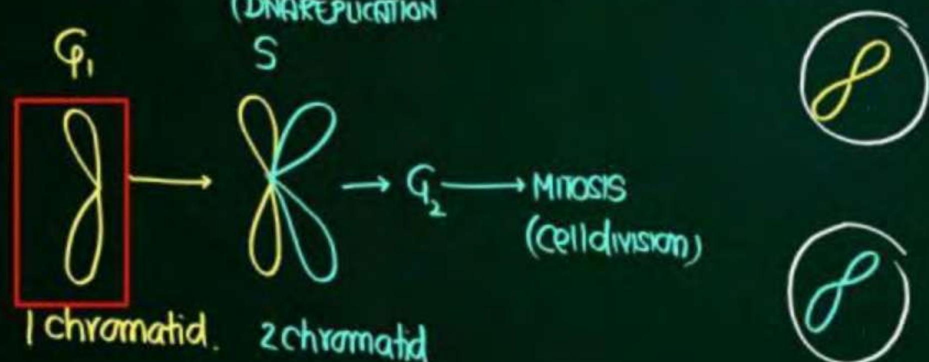
NO BLENDING

Thirdly, Mendel's approach of using mathematics to explain biological phenomena was totally new and unacceptable to many of the biologists of his time. Finally, though Mendel's work suggested that factors (genes) were discrete units, he could not provide any physical proof for the existence of factors or say what they were made of.

In 1900, three Scientists (de Vries, Correns and von Tschermak) independently rediscovered Mendel's results on the inheritance of characters. Also, by this time due to advancements in microscopy that were taking place, scientists were able to carefully observe cell division. This led to the discovery of structures in the nucleus that appeared to double and divide just before each cell division. These were called **chromosomes** (*colored bodies*, as they were visualised by staining). By 1902, the chromosome movement during meiosis had been worked out.

Basic dye.

DNA Replication.

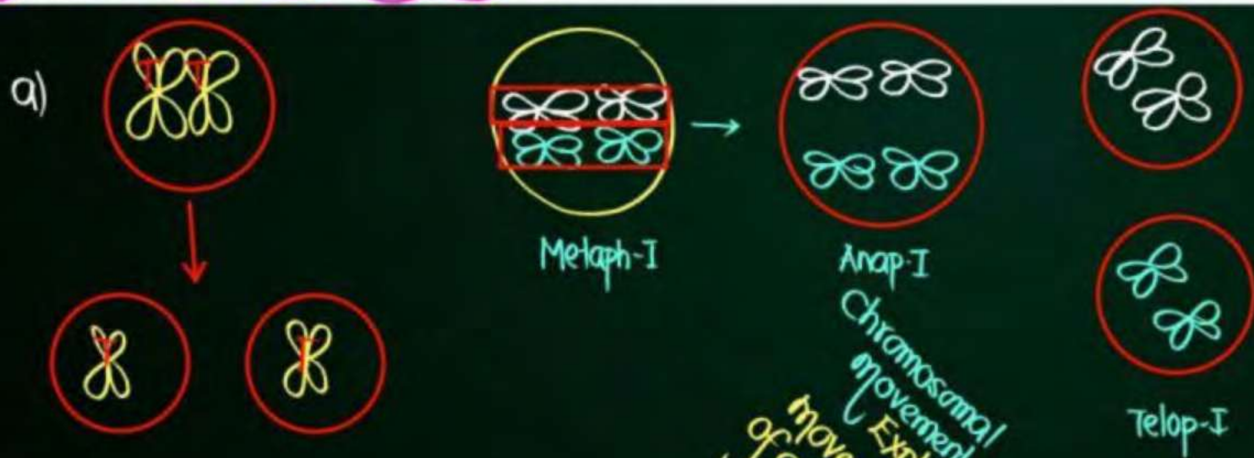


Anaphase-I

↓

Chromosome move opposite pole.

Walter Sutton and Theodore Boveri noted that the behaviour of chromosomes was parallel to the behaviour of genes and used chromosome movement (Figure 4.8) to explain Mendel's laws (Table 4.3). Recall that you have studied the behaviour of chromosomes during mitosis (equational division) and during meiosis (reduction division). The important things to remember are that chromosomes as well as genes occur in pairs. The two alleles of a gene pair are located on homologous sites on homologous chromosomes.



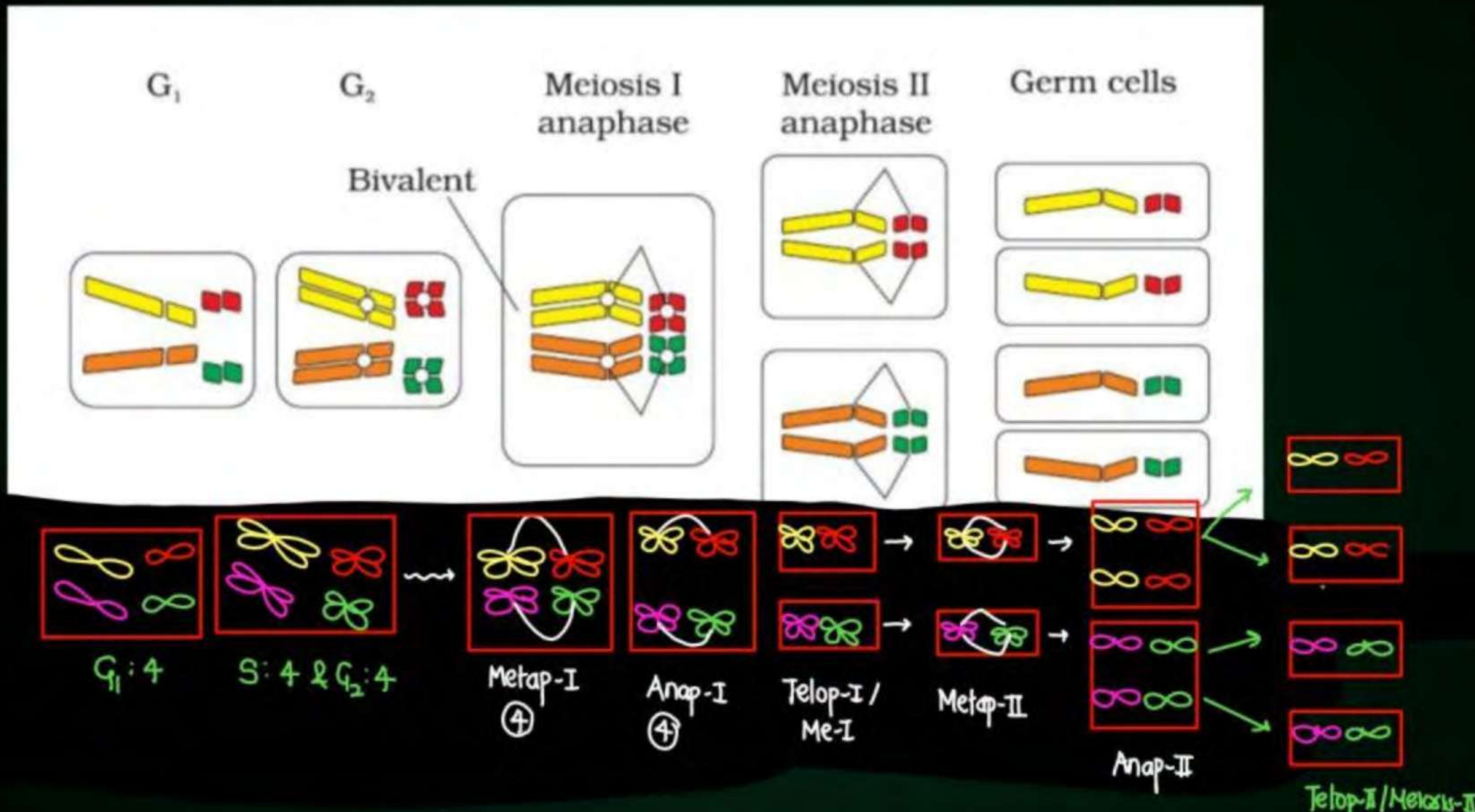
Chromosomal movement
Explain.
movement of allele/gene/factor.

Figure (a)

⇒ chromosome & gene : occur in pairs
OR ALLELE/FACTOR.

⇒ DURING GAMETE FORMATION
chromosome seperate/
segregate (Anap-I)
so allele/gene/factor
seperate

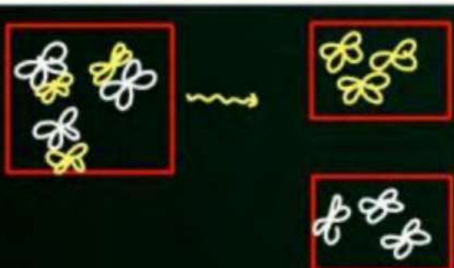
⇒ Each gamete receive
one chromosome/
one allele/one factor

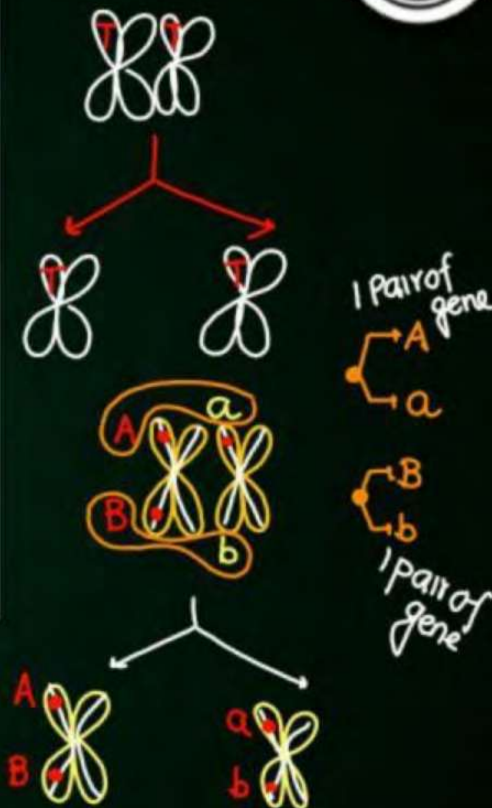


G1
G2
Meiosis I anaphase
Meiosis II anaphase
Germ cells
Bivalent
G1 : 4
S : 4 & G2 : 4
Metap-I
4
Anap-I
4
Telop-I / Me-I
Metap-II
Anap-II
Telop-II / Meiosis-II

Table 4.3: A Comparison between the Behaviour of Chromosomes and Genes

A (Chromosome)	B (gene).
Occur in pairs	*Occur in pairs* TT Tt tt
Segregate at the time of gamete formation such that only one of each pair is transmitted to a gamete	*Segregate at gamete formation and only one of each pair is transmitted to a gamete*
Independent pairs segregate independently of each other	*One pair segregates independently of another pair*
Can you tell which of these columns A or B represent the chromosome and which represents the gene? How did you decide?	





During Anaphase of meiosis I, the two chromosome pairs can align at the metaphase plate independently of each other (Figure 4.9). To understand this, compare the chromosomes of four different colour in the left and right columns. In the left column (Possibility I) orange and green is segregating together. But in the right hand column (Possibility II) the orange chromosome is segregating with the red chromosomes.

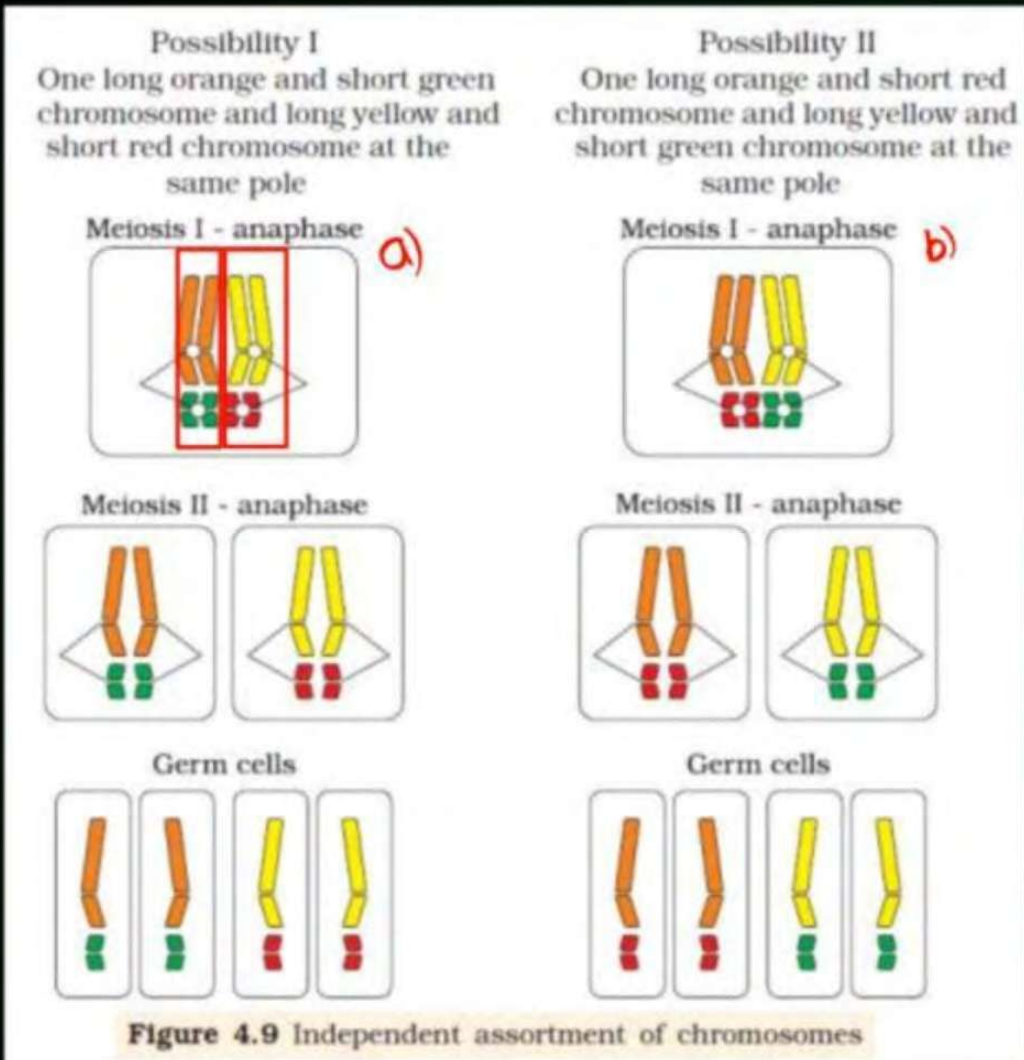
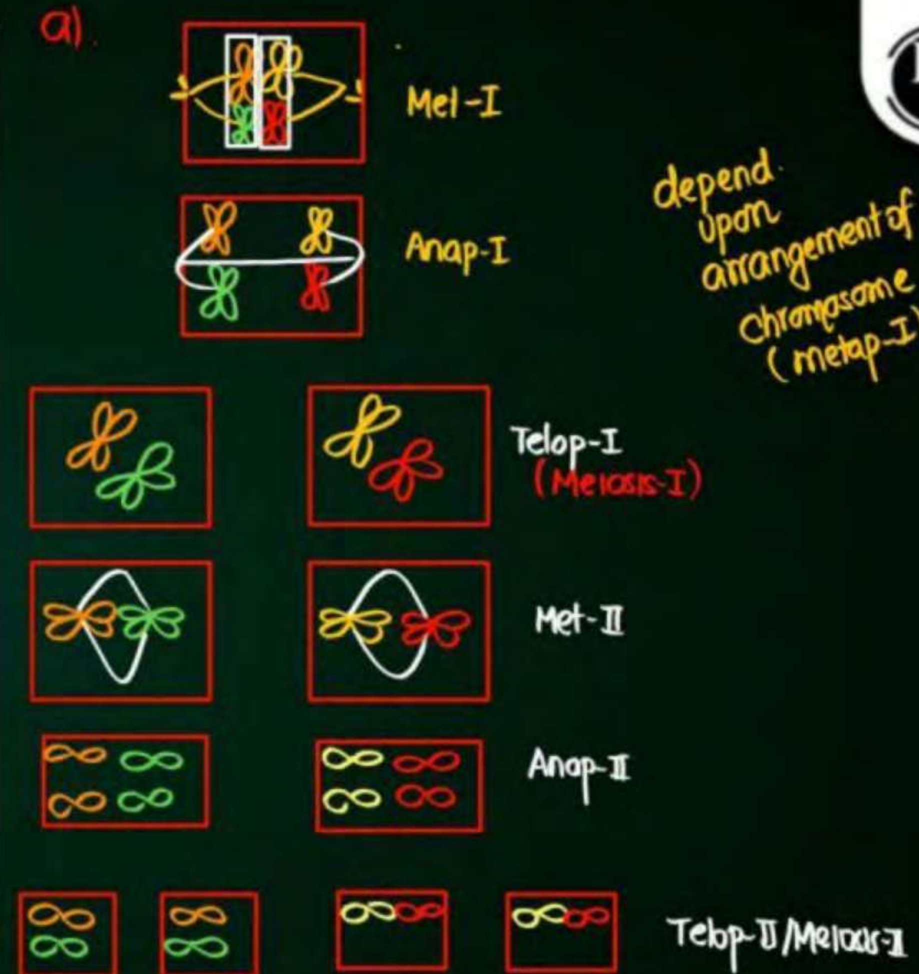


Figure 4.9 Independent assortment of chromosomes



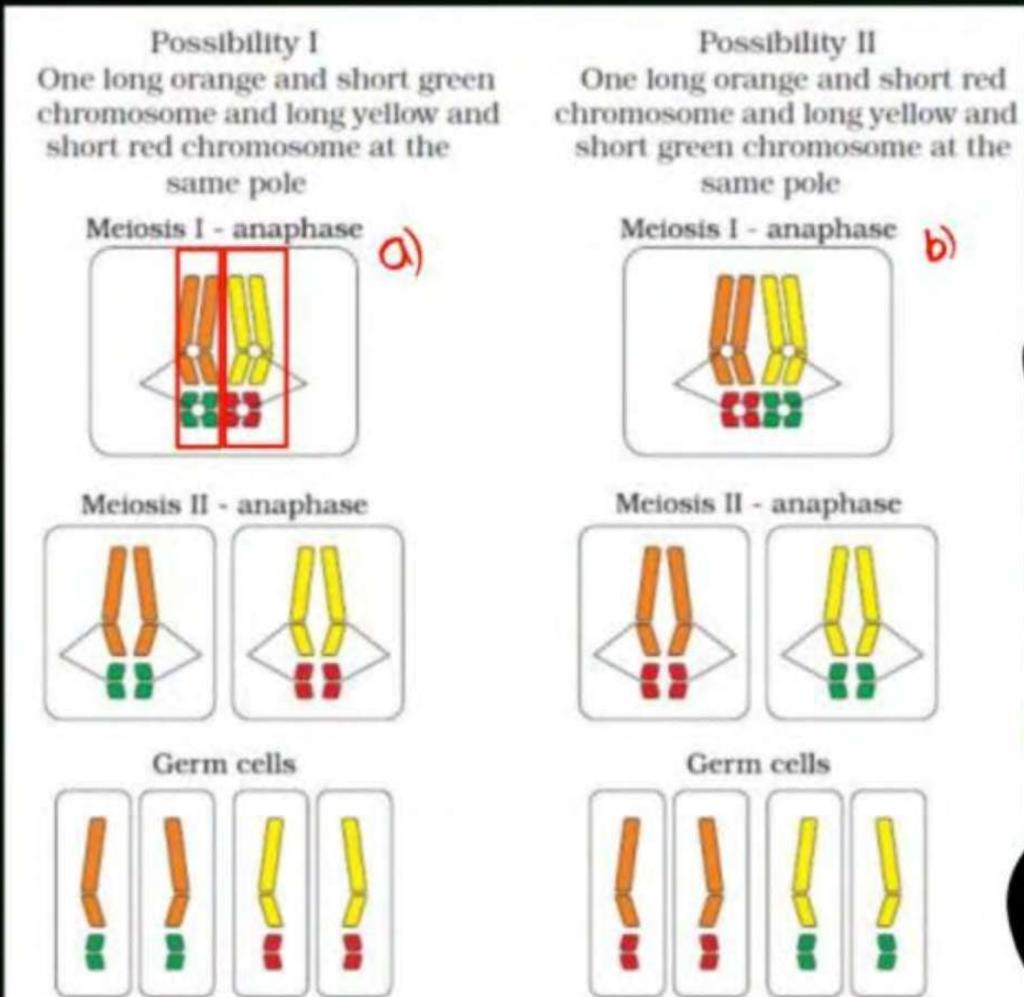
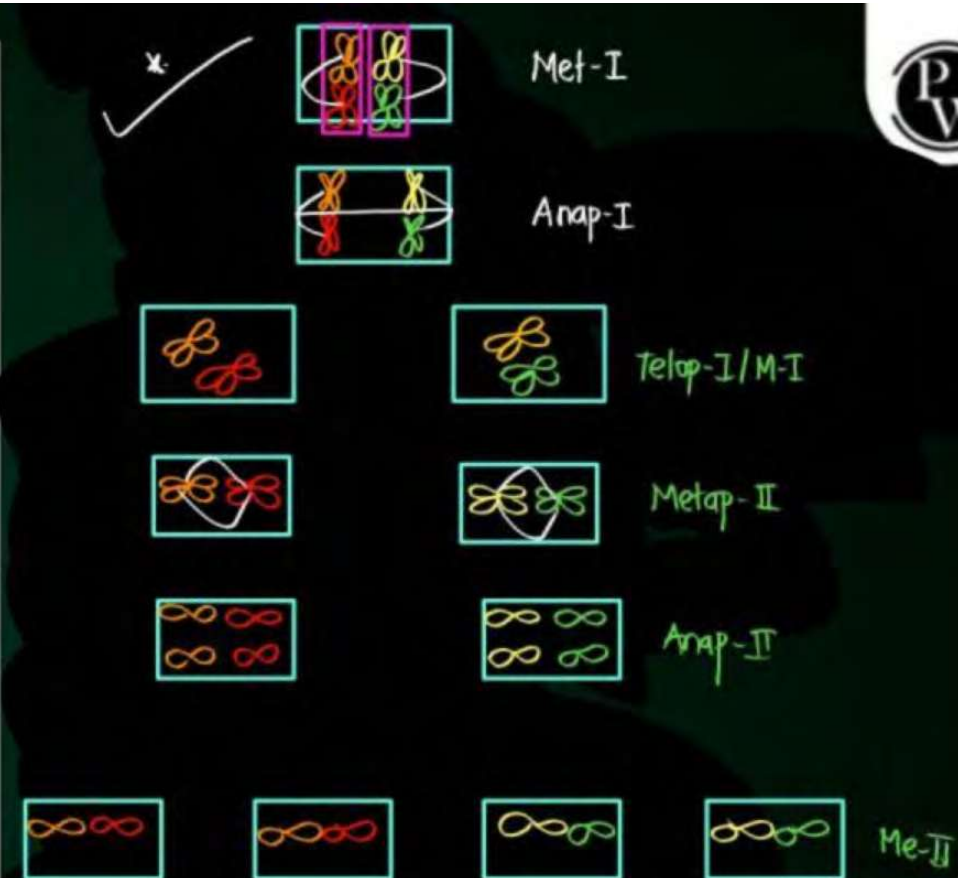


Figure 4.9 Independent assortment of chromosomes



Following this synthesis of ideas, experimental verification of the chromosomal theory of inheritance by Thomas Hunt Morgan and his colleagues, led to discovering the basis for the variation that sexual reproduction produced. Morgan worked with the tiny fruit flies, ***Drosophila melanogaster*** (Figure 4.10), which were found very suitable for such studies. (1) They could be grown on simple synthetic medium in the laboratory. Banana (2) They complete their life cycle in about two weeks, and a single mating could produce a large number of progeny flies. 100 offspring Also, (3) there was a clear differentiation of the sexes – the male and female flies are easily distinguishable. Also, it has many types of hereditary variations that can be seen with low power microscopes. (4)

Small size

Large size

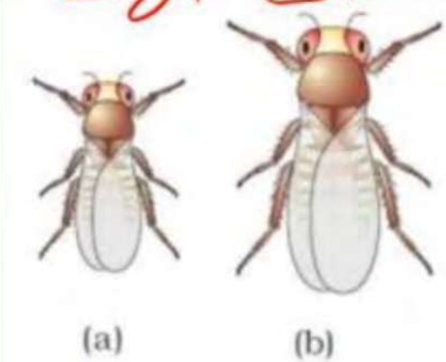
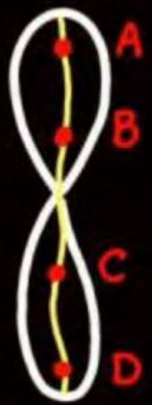


Figure 4.10 *Drosophila melanogaster* (a) Male (b) Female

Recombination frequency



DISTANCE

⇒ A-D > A-C > A-B

⇒ position of gene on chromosome (chromosomal map/genetic map) give the idea of Recombination frequency or cross over frequency.

CROSS OVER/RECOM FREQUENCY

⇒ A-D > A-C

(LINKAGE LESS) LINKAGE MORE

⇒ Chances of seperation of Two genes By crossing over.

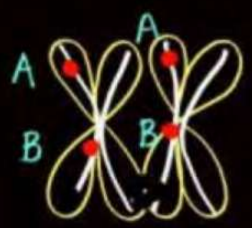
Q Distance Between Two gene on same Chromosome a) > Distance Between Two gene on diff Chromosome b)

STRONG LINKAGE

a) distance more

~~b)~~ distance less (STRONG LINKAGE)

LINKAGE GROUP.

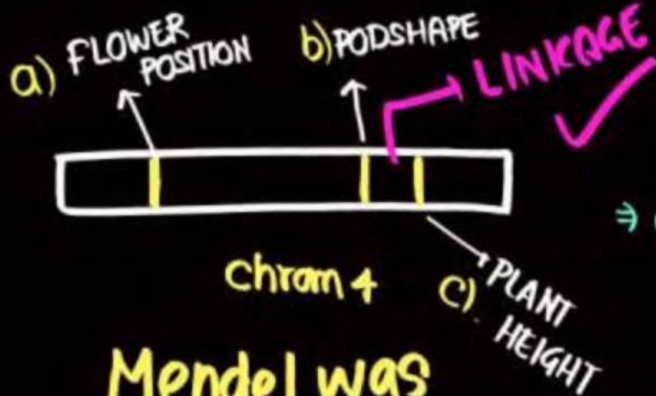


⇒ no. of gene present on homologous Chromosome consider as one linkage group

⇒ $\frac{\text{no. of chromosome}}{2}$

⇒ $\frac{2}{2}$ ⇒ 1

⇒ equal to Haploid set of chromosome



Mendel was Lucky: He didn't study PODSHAPE & PLANT HEIGHT TOGETHER

⇒ pea:

2n: 14 chromosome.

L.G: 14/2 ⇒ 7

⇒ HUMAN.

Male: 46: 44 + XY ⇒ 22+1+1 ⇒ 24.

Female: 46: 44 + XX ⇒ 22+1 ⇒ 23

Ques. of day:

HUMAN SPERM: LINKAGE group: 23.

Sex determination

★ HENKING : STUDY : FEW INSECTS

X CHROMOSOME

50% SPERM : PRESENT
50% SPERM : ABSENT

★ 'X' BODY.

CHROMOSOMAL BASIS OF SEX DETERMINATION

(1) XX-XO TYPE
(2) XX-XY TYPE
(3) ZZ-ZW TYPE
(4) ZO-ZZ TYPE

ZO-ZZ TYPE

ZO : FEMALE, (A+Z), (A+O), HETROGAMETIC, TWO TYPES, SEX DETERMINED
ZZ : MALE (A+Z) (A+Z), HOMOGAMETIC, ONE TYPES
eg : BUTTERFLY

XX - XY TYPE

HUMAN : 46
44 (AUTOSOME) 22 PAIRS ; XX/XY SEX CHROMOSOME

♂ : 22 Pairs + XY
♀ : 22 Pairs + XX

♂ (AA + XY) ⇒ (A+X) & (A+Y)
♀ (AA + XX) ⇒ (A+X) & (A+X)

♂ : (22+X) & (22+Y), HETROGAMETIC — 2 TYPE, NO: 2
♀ : (22+X) & (22+X), HOMOGAMETIC — 1 TYPE, NO: 2

⇒ few insects (drosophila), HUMAN

⇒ Y shorter than 'X'
⇒ SEX determined By MALE (HETROGAMETIC)

Q Family, 4 SONS PRESENT, THEY ARE EXPECTING 5th CHILD ⇒ SON.
a) 50% b) 100% c) 0%

XX - XO TYPE

MOST OF INSECT, GRASSHOPPER

⇒ XX : FEMALE, HOMOGAMETIC, 1 TYPE OF GAMETE
AA+XX ⇒ (A+X) (A+X) : 100% EGG : 'X'

⇒ AA+XO ⇒ (A+X) (A+O) : 50% SPERM 'X', 50% SPERM X absent
HETROGAMETIC : 2 TYPES
SEX DETERMINED : MALE
BOTH HAVE UNEQUAL NO. OF CHROMOSOME

ZZ - ZW TYPE

ZZ : MALE, HOMOGAMETIC, (A+Z), (A+Z), 1 TYPE
ZW : FEMALE, HETROGAMETIC, (A+Z) (A+W), 2 TYPE (SEX DETERMINED BY FEMALE
Eg : BIRDS.

HONEY BEE HAPLOID, DIPLOID MECHANISM.

FEMALE
QUEEN
2n = (32 chromosome)

MALE (DRONE)
n = 16

MEIOSIS

MITOSIS

16 (egg)

16 (egg)

16 male gamete

FERTILISATION

UNFERTILISED EGG
PARTHENOGENESIS

MALE/DRONE

2n = 32 ⇒ QUEEN
⇒ WORKERS [FEMALE]

NO FATHER
NO SON.

HAS GRANDFATHER
HAVE GRANDSON.

CHROMOSOMAL DISORDER

NOTE : CHROMOSOME 'C'

⇒ 45 (loss of C) ⇒ 47 (gain of 'C') → PATTERN OF 'C' CHANGE

REASON

ANEUPLOIDY

* chromosome/chromatid fail to seperate during meiosis so it leads to abnormal gamete.

⇒ n : 23 (NORMAL)

⇒ n-1 ⇒ 23-1 ⇒ $\boxed{22}$

⇒ n+1 ⇒ 23+1 ⇒ $\boxed{24}$

→ abnormal gamete.

NOTE : (n) ♂ & (n-1) ♀

TYPE-1 Hypoploidy

⇒ $\boxed{(2n-1)}$ loss of one Chromosome:

⇒ (2x23-1)

⇒ 46-1 ⇒ $\boxed{45}$ (MONOSOMY)

(n-1) ♂ (n-1) ♀

⇒ $\boxed{2n-2}$

⇒ 46-2

⇒ $\boxed{44}$

loss of TWO CHROMOSOME (NULLISOMY)

TYPE-II (HYPERPLOIDY)

⇒ (n) x (n+1) TRISOMY

⇒ $\boxed{2n+1}$ ⇒ 46+1 ⇒ $\boxed{47}$

⇒ (n+1) x (n+1)

⇒ 2n+2 ⇒ 46+2 ⇒ $\boxed{48}$

TETRASOMY

POLYPLOIDY

⇒ failure of cytokinesis in Telophase. Increase in set of chromosome.

⇒ common in plants.

$\boxed{2n : 10}$ n : 5 → VEGETATIVE REPRODUCTION.

3n : 15 → ODD NUMBER (STERILE)

4n : 20 → EVEN NUMBER (FERTILE)

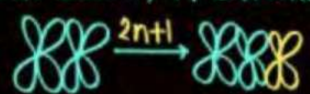
$\boxed{2n : 4}$ n : 2

3n : 6

4n : 8

DOWN SYNDROME AUTOSOMAL

* LANGDON DOWN, 47 chromosome, TRISOMY (2n+1) ⇒ 46+1 ⇒ 47

* 21 ⇒ 

Q : Female down syndrome aff., male : NORMAL, Child : affected?

⇒ (AA+X) (A+X) (A+X) (A+Y)

AAA+XX	AAA+XY	AA+XX	AA+XY
44+1 + 2	44+1+1+1	44+2	44+2
⇒ $\boxed{47}$ ✓	$\boxed{47}$ ✓	$\boxed{46}$	$\boxed{46}$

⇒ $\frac{2}{4} \times 100$ ⇒ 50%

$\boxed{\text{KLINFELTER S.}}$ MALE

⇒ ♀ gamete ♂ gamete

(A + X) A+XY

normal fertilisation

$\boxed{AA + XXY}$ ⇒ 44 + 1+1+1 ⇒ $\boxed{47}$

ALLOSOMAL TRISOMY

SEX-CHROMOSOMAL.

A + XX (A + Y)

(abnormal) x

$\boxed{AA + XXY}$ ⇒ 47

Extra 'X' chromosome in male

$\boxed{\text{TURNER SYNDROME}}$ Female.

⇒ 45, Loss of 1 chromosome, MONOSOMY.

♂ ♀

(A + X) (A + O)

$\boxed{AA + XO}$ ⇒ 44 + 1 ⇒ 45

♂ ♀

(A + O) (A + X)

$\boxed{AA + XO}$ 44 + 1 ⇒ 45.

45, $\underbrace{XO}$

(person) karyotype

Q a) 45 + XO ⇒ 46 ✗

b) 44 + XO ⇒ 45 ✓

c) 45, XO ✓

d) All

e) Both b & C ✓

DOWN SYNDROME

1. Short stature with small Round Head
2. Furrowed Tongue
3. partially open mouth
4. Broad palm with palm crease
5. physical, psychomotor, mental development is Retarded.
6. Mongolian idiocy

KLINFELTER SYNDROME

a) Sterile male
b) Undeveloped Testis
c) Mental Retardation
d) Overall masculine development But Feminine development (development of Breast)

↓

Gynaecomastia.

TURNER

Sterile Female,
Rudimentary ovary,
Lack of secondary sexual character.


Single palmar crease
Normal palm creases

GENETIC DISORDER → MENDELIAN D & CHROMOSOMAL D.

* Gene → MUTATION (CHANGE) → M.D
* parents $\xrightarrow{\text{Transfer}}$ offspring

FOLLOW PRINCIPLES OF INHERITENCE

* STUDY : HELP : PEDIGREE ANALYSIS

NOTE : AUTOSOME : 1→22 PAIRS (44)

1 gene → A, A ; → A, a ; → a, a

A : autosomal dominant

a : autosomal Recessive

* AUTO. GENE : PRESENT : AUT CHROM
* AA , Aa
* aa

Phenylketonuria, SICKLE CELL ANEMIA, THALLASEMIA, CYSTIC FIBROSIS

* AUTOSOMAL RECESSIVE D.
* person : aa (affected)

* AA (NORMAL)
* Aa (Hetrozygous/carrier)

TRAIT PRESENT (UNAFFECTED)

Case-I

♂ AA ♀ AA

↓

AA NORMAL

Case-II

♂ (AA) ♀ (Aa)

A → A, a

AA : Normal

Aa : Normal

NOTE : If BOTH PARENT CARRIER, DISORDER TRANSFER TO OFFSPRING.

♂ (Aa) ♀ Aa

	A	a
A	AA	Aa
a	Aa	aa

$\Rightarrow \frac{1}{4} \times 100 \Rightarrow 25\%$

affected child.

* affected male child

$\frac{1}{4} \times \frac{1}{2} \Rightarrow \frac{1}{8}$

PHENYLKETONURIA

★ AUTO. RECESS. DIS. , aa

★ Phenyl alanine $\xrightarrow[\text{hydroxylase}]{\text{Phenylalanine}}$ Tyrosine
(NORMAL PERSON.

★ Enzyme NOT FORMED (AFFECTED)

★ Phenyl alanine & its product Phenylpyruvic acid accumulation increase.

★ Excreted out in URINE
depigmentation of skin, Hair, mental Retardation
(more than one effect)
Pleiotropy

★ inborn error of protein metabolism

SICKLECELLANEMIA (SCA)

★ $Hb^A Hb^A$: NORMAL
★ $Hb^S Hb^S$: AFFECTED (Abnormal Hb)
★ $Hb^A Hb^S$: SCA (TRAIT PRESENT) BUT NOT AFFECTED (NORMAL) CARRIER

★ $Hb^A Hb^S$ (♂) $Hb^A Hb^S$ (♀)

	Hb^A	Hb^S
Hb^A	$Hb^A Hb^A$	$Hb^A Hb^S$
Hb^S	$Hb^A Hb^S$	$\boxed{Hb^S Hb^S}$

SCA

$Hb^A Hb^S$
50% → Hb^A
50% → Hb^S (MUTANT/ AFFECTED ALLELE

Hb: NORMAL IN RBC ⟶ BICONCAVE SHAPE
Hb: Abnormal in RBC ⟶ aggregate/polymerise so Shape of RBC ⇒ SICKLE SHAPED.

BLOOD VESSELS

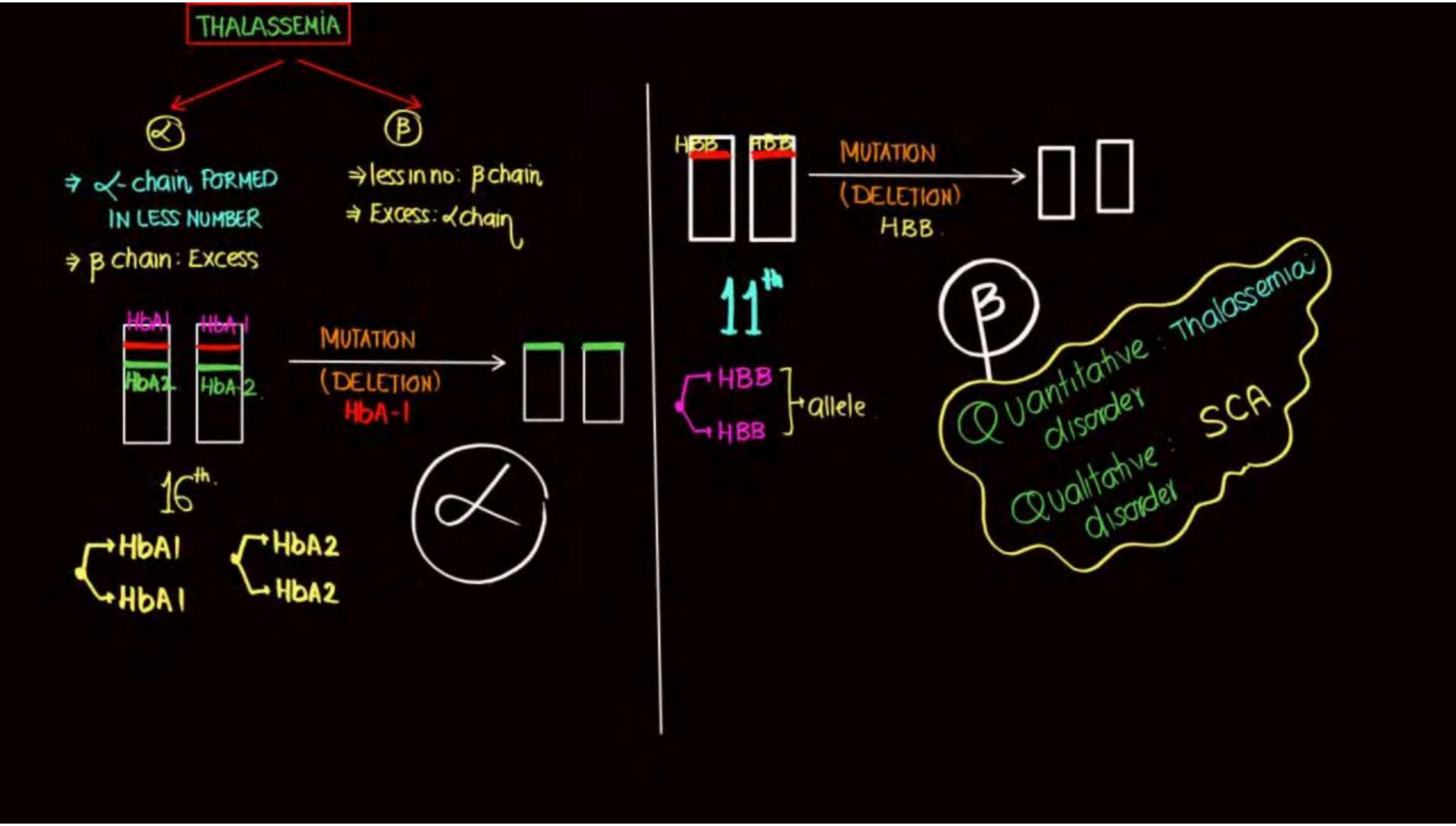
⇒ BLOOD SUPPLY : IMPROPER TO TISSUE, ORGAN
⇒ DO NOT GET PROPER O_2.

★ SCA : abnormal Hb FORMED.

★ CTC $\xrightarrow[\text{Base}]{\text{Single}}$ CAC (SUBSTITUTION/POINT M) [DNA]

★ GAG $\xrightarrow[\text{change}]{\text{Codon}}$ GUG (RNA)

★ GLUTAMIC ACID $\xrightarrow[\text{of } \beta\text{- hB chain}]{6^{th}\text{ position}}$ VALINE



THALASSEMIA
α
β
⇒ α- chain, FORMED IN LESS NUMBER
⇒ β chain: Excess
⇒ less in no: β chain
⇒ Excess: α chain
HbA1
HbA-1
HbA2
HbA-2
MUTATION
(DELETION)
HbA-1
16th
HbA1
HbA1
HbA2
HbA2
α
HBB
HBB
MUTATION
(DELETION)
HBB
11th
HBB
HBB
allele
β
Quantitative disorder : Thalassemia
Qualitative disorder : SCA

PROTEIN

Hb

amino acid chain

α globulin chain

β globulin chain

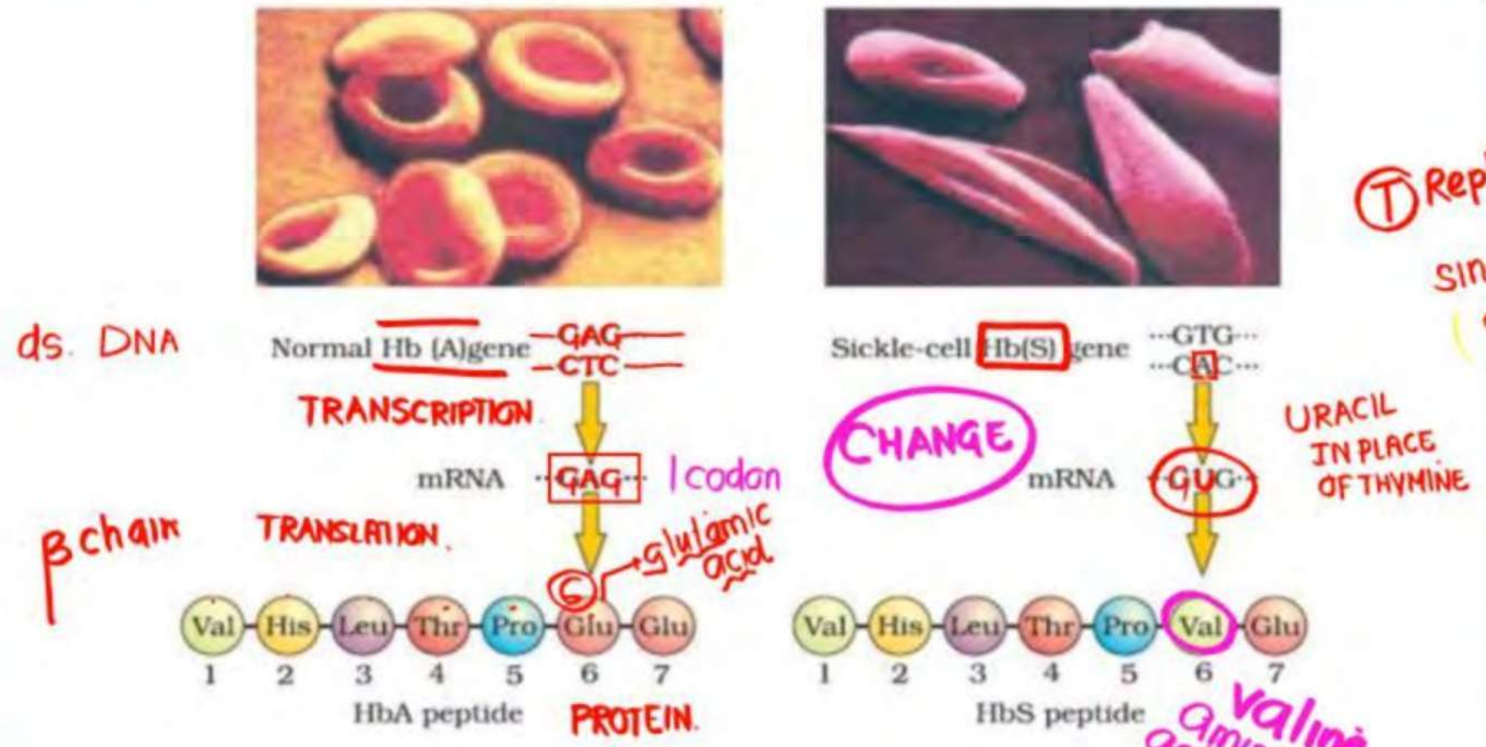


Figure 4.15 Micrograph of the red blood cells and the amino acid composition of the relevant portion of β-chain of haemoglobin: (a) From a normal individual; (b) From an individual with sickle-cell anaemia

T Replace by A in DNA

Single Base Replace

(SUBSTITUTION TYPE OF MUTATION)

POINT MUTATION.

MENDELIAN DISORDER

COLOUR BLINDNESS , HEMOPHILIA → CONTROLLED BY GENE PRESENT ON 'X' CHROMOSOME / SEX CHR. (Recessive)

sex linked inheritence : inherit from one genⁿ to another by sex 'chr'

hemizygous

X^cY : affected male

homozygous ← X^cX^c : affected female

XX : Normal female

XY : Normal male

X^cX : Carrier female (NORMAL). (Hetrozygous)

Recessive (NOT EXPRESS) SUPPRESS BY dominant gene

dominant

⇒ person not able to differentiate B/w RED & GREEN COLOUR

⇒ common in male

Case-I

Female (carrier) X^cX — male Normal XY

X^cX X^cY XX XY

25% PROGENY : AFFECTED
25% " : Carrier
50% " : NORMAL

50% SON : AFFECTED

Case-II

X^cX — X^cY

X^cX^c → affected daughter
X^cY
X^cX
XY

Case-I : MOTHER (AFFECTED) FATHER (NORMAL)

X^cX^c XY

X^cX
X^cY
X^cX
X^cY

100% SON : AFFECTED
100% DAUGHTER : CARRIER.

∴ MOTHER (AFFECTED) ♀ → SON (AFFECTED) & ♂ DAUGHTER (CARRIER) → daughter (carrier) ♀

X^cY (affected) XX (NORMAL)

X^cX
X^cX
XY
XY

100% D : CARRIER
100% S : NORMAL

CRISS CROSS INHERITENCE

Case-II FATHER (AFFECTED) MOTHER (NORMAL)

X^cY XX

X^cX
X^cX
XY
XY

FATHER (AFFECTED) → DAUGHTER (CARRIER) → SON (affected)

SON (NORMAL)

daughter (carrier)

CRISS CROSS INHERITENCE

X^cX XY

X^cX
X^cY → affected
XX
XY

Haemophilia

* Royal disease, Queen victoria (carrier).
* Types:
  - (A): VIII absent: Antihemophilic globulin
  - (B): IX absent: Plasma thromboplastin component.
* Blood continue to flow, if cuts

Myotonic dystrophy

AUTOSOMAL DOMINANT

AA/Aa: affected.

aa: Normal.

⇒ No proper muscle contraction.

pedigree analysis

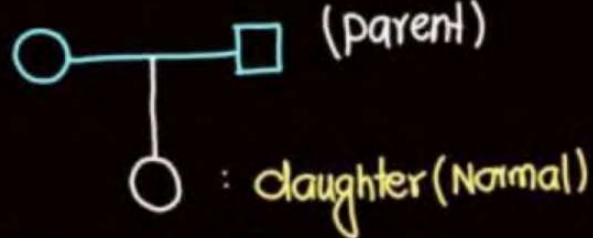
Symbol

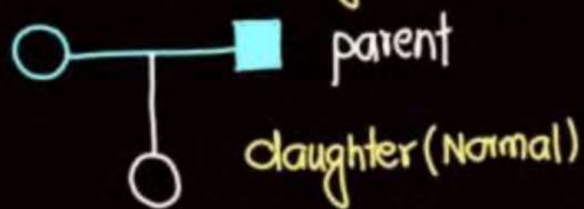
○ : Normal Female

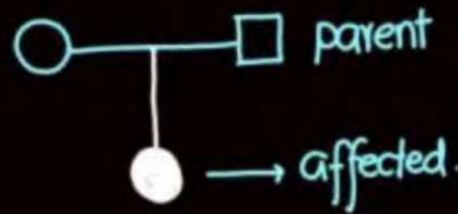
□ : Normal male

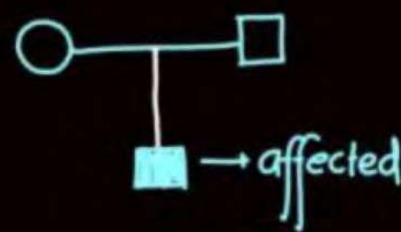
● : affected female

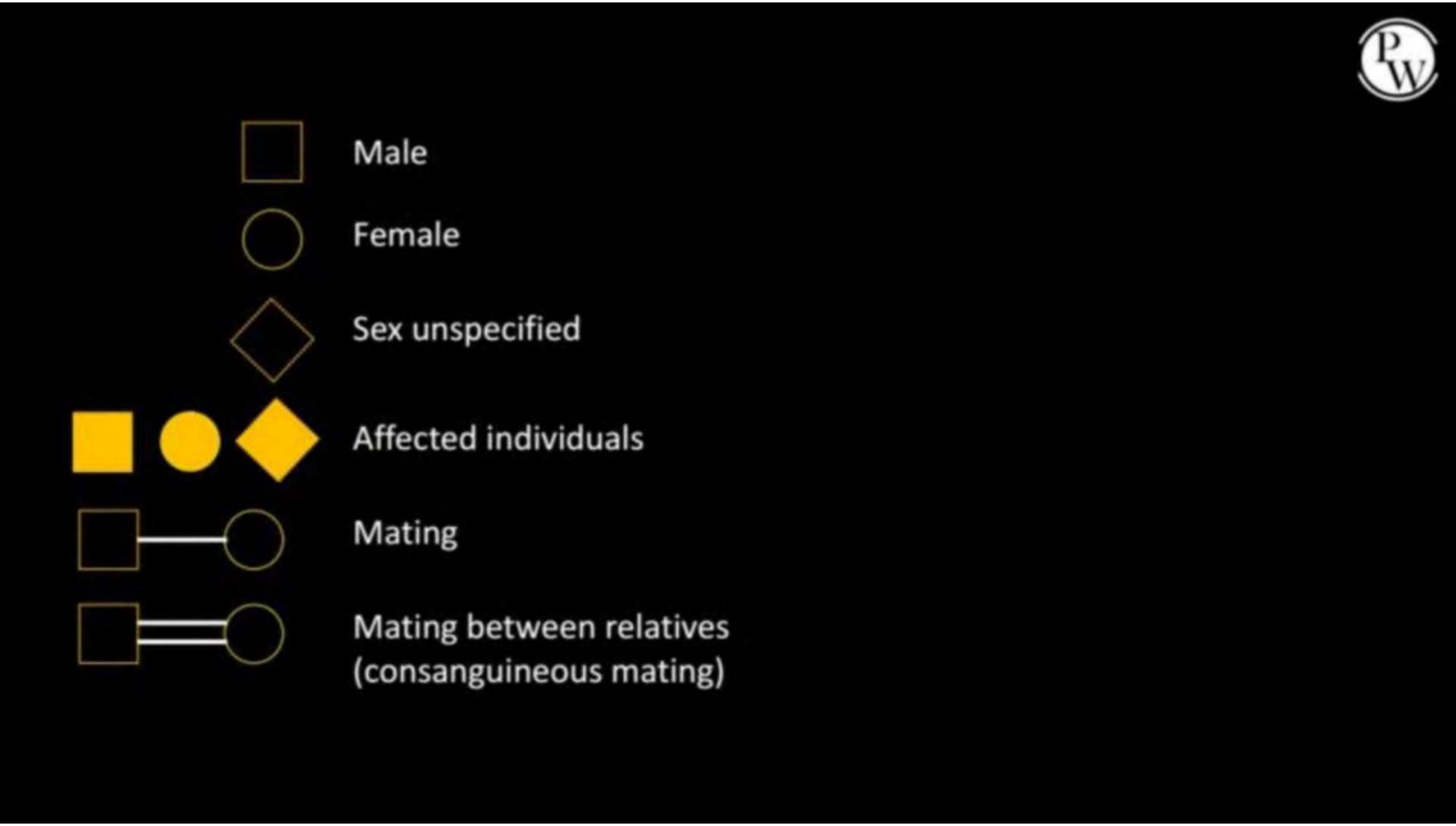
■ : affected male

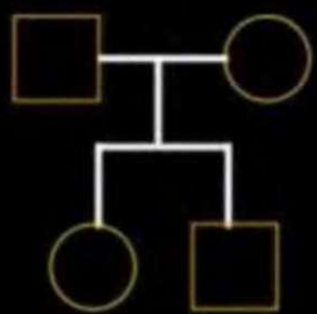




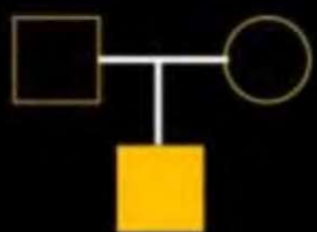





Male
Female
Sex unspecified
Affected individuals
Mating
Mating between relatives
(consanguineous mating)

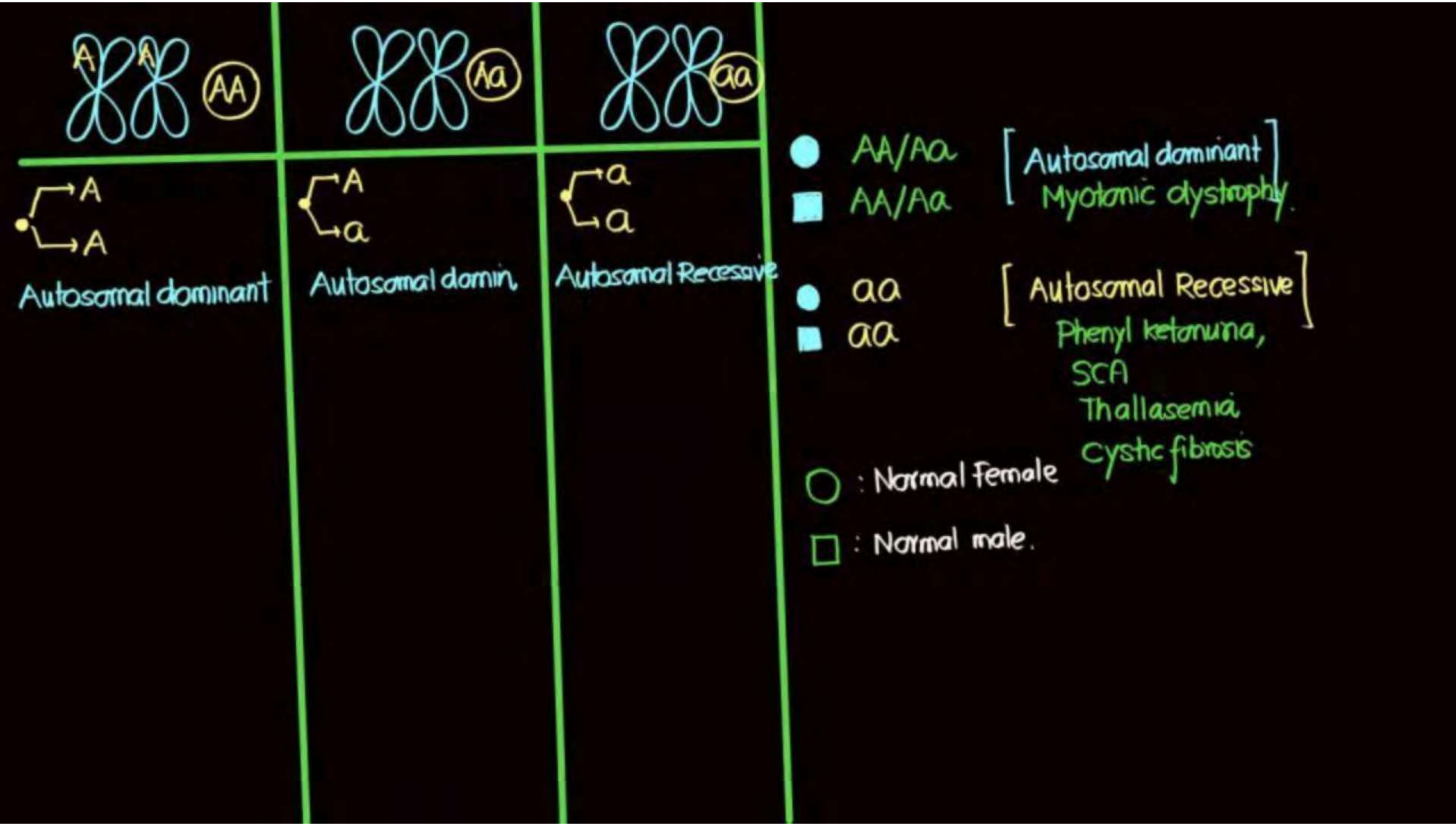


Parents above and children below
(in order of birth-left to right)



Parents with male child affected with disease

Five unaffected offspring


AA
Aa
aa
A
A
A
a
a
a
Autosomal dominant
Autosomal domin.
Autosomal Recessive
AA/Aa
AA/Aa
Autosomal dominant
Myotonic dystrophy.
aa
aa
Autosomal Recessive
Phenyl ketonuria,
SCA
Thallasemia
Cystic fibrosis
: Normal female
: Normal male.

Let us check for Autosomal Recessive disorder

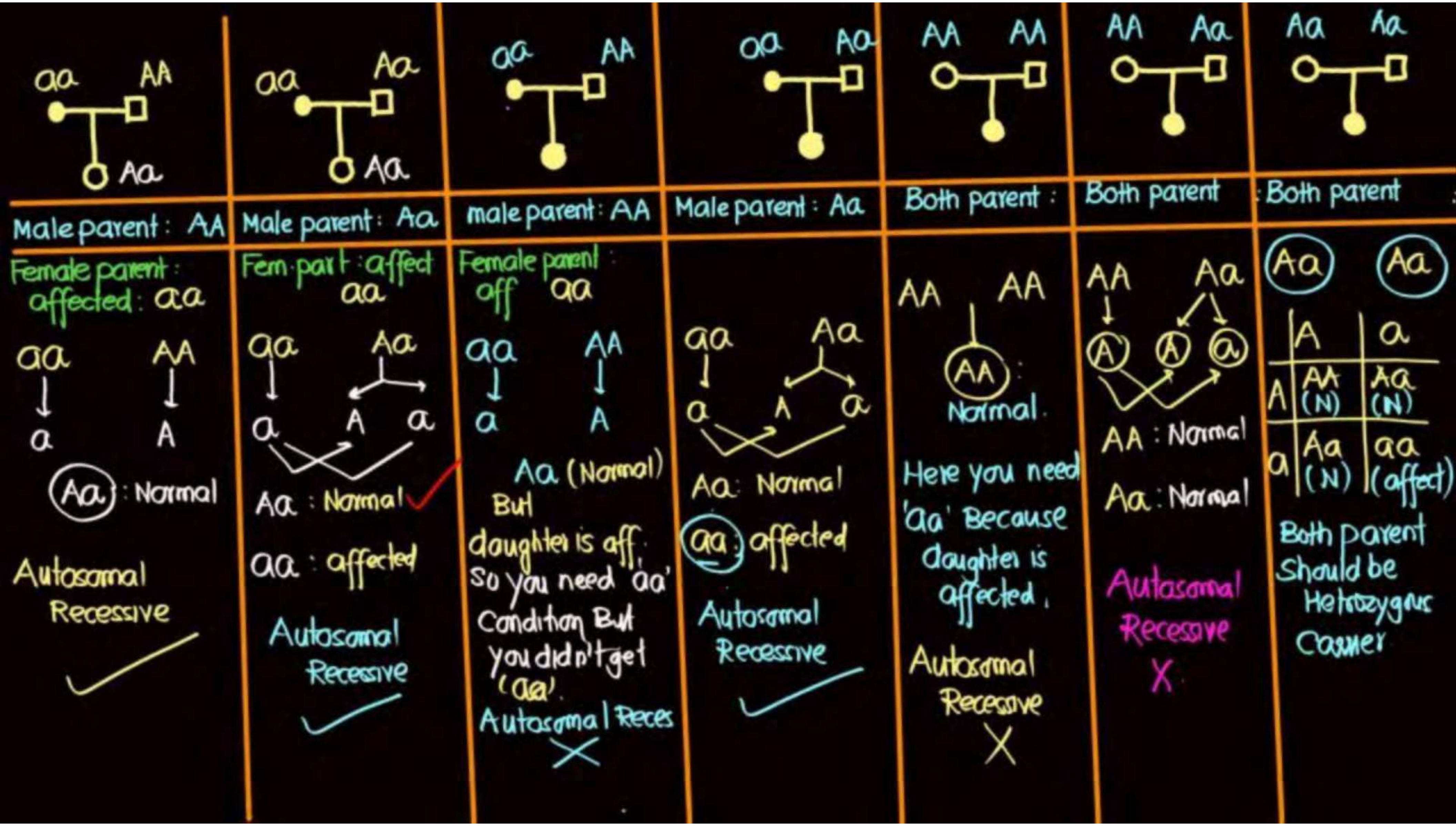
confirm

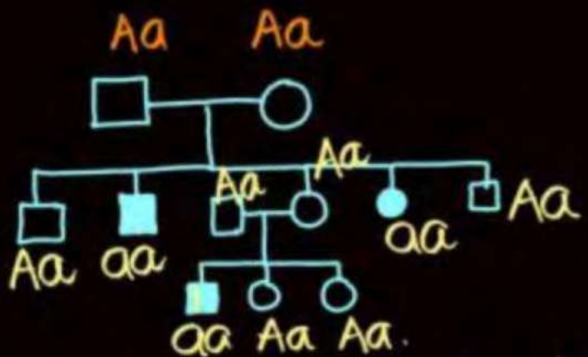
○ : Aa / AA → Term & Condition ?

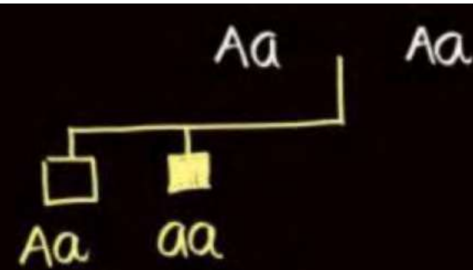
□ : Aa / AA

● : aa : affected

■ : aa : affected


aa AA
Aa
Male parent: AA
Female parent: affected: aa
aa AA
a A
Aa : Normal
Autosomal Recessive
aa Aa
Aa
Male parent: Aa
Fem. part: affect aa
aa Aa
a A a
Aa : Normal
aa : affected
Autosomal Recessive
aa AA
male parent: AA
Female parent off aa
aa AA
a A
Aa (Normal)
But daughter is aff. so you need 'aa' Condition But you didn't get 'aa'.
Autosomal Reces
aa Aa
Male parent: Aa
aa Aa
a A a
Aa: Normal
aa: affected
Autosomal Recessive
AA AA
Both parent:
AA AA
AA
Normal.
Here you need 'aa' Because daughter is affected.
Autosomal Recessive
AA Aa
Both parent
AA Aa
A A a
AA : Normal
Aa : Normal
Autosomal Recessive
Aa Aa
Both parent
Aa Aa
A a
A AA (N) Aa (N)
a Aa (N) aa (affect)
Both parent should be Hetrozygous Carrier





Aa	Aa
AA (N)	Aa (N)
Aa (N)	aa (A)

Q is it autosomal Recessive? ⇒ yes.

Hint-① If Both parent : Normal (Carrier/Hetrozygous) & sons/daughter : affected or Normal

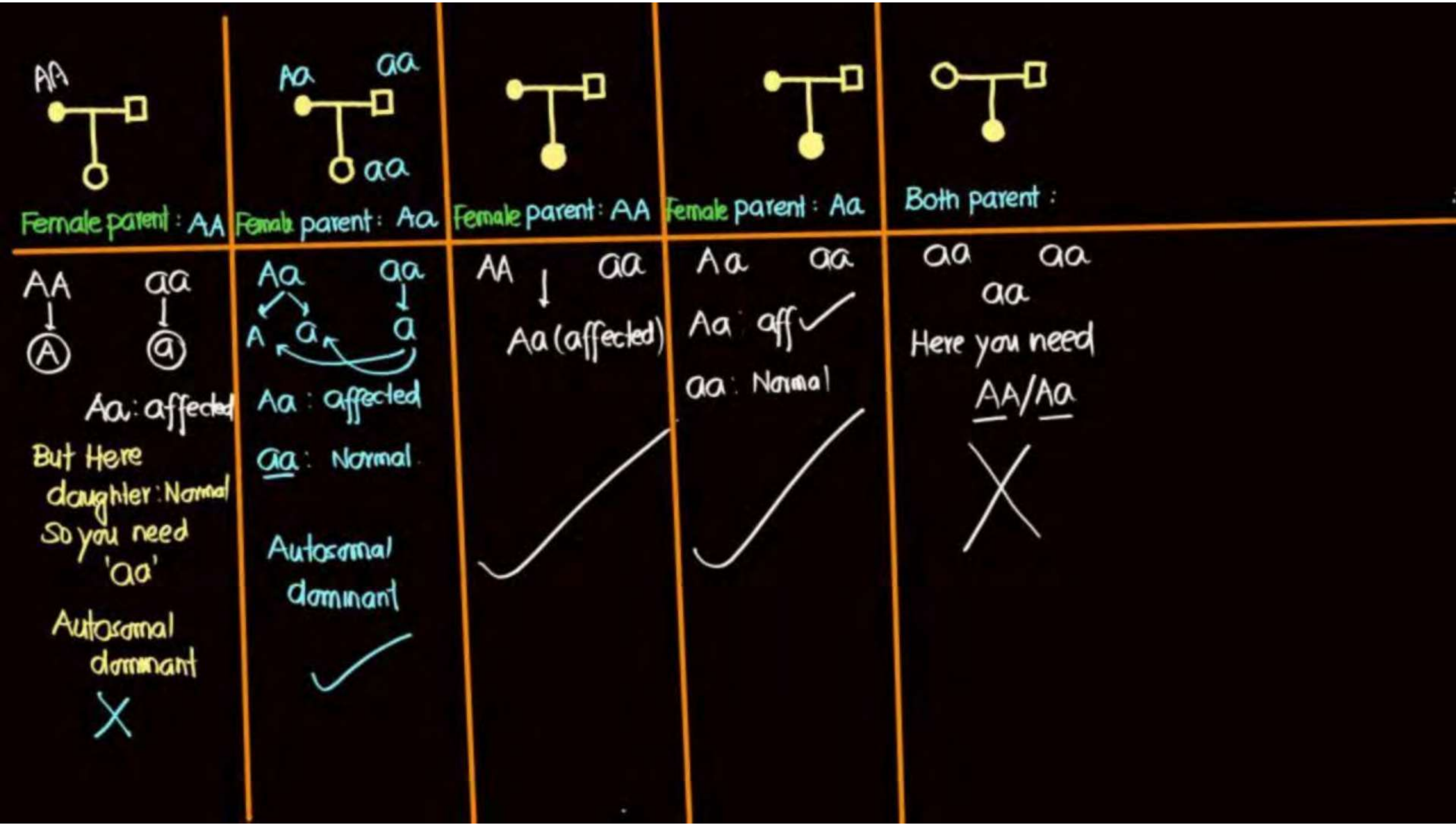
Hint-② : ○/□ : Aa
●/■ : aa

Autosomal Recessive

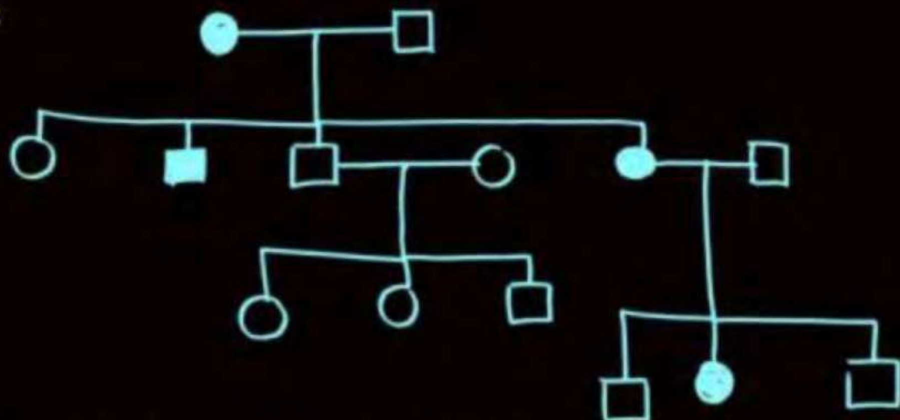
Let us check for Autosomal dominant

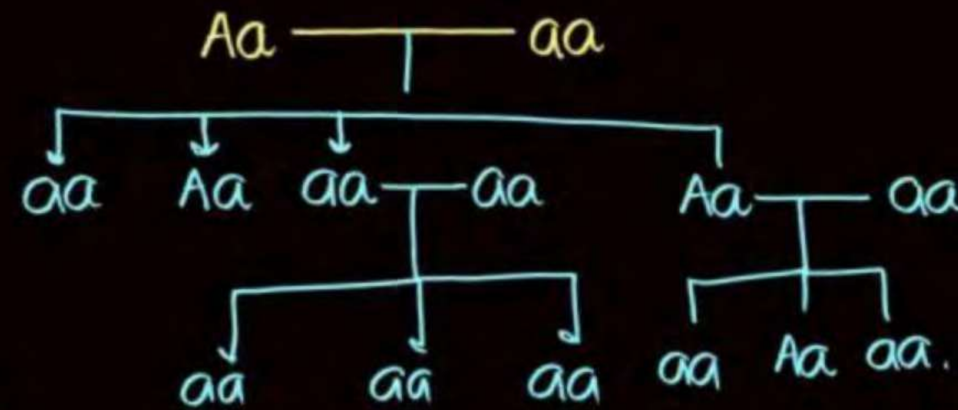
●/■ : AA/Aa (affected)

○/□ : aa (Normal).


AA
Female parent : AA
AA aa
A a
Aa : affected
But Here daughter : Normal
So you need 'aa'
Autosomal dominant
Aa aa
aa
Female parent : Aa
Aa aa
A a a
Aa : affected
aa : Normal
Autosomal dominant
Female parent : AA
AA aa
Aa (affected)
Female parent : Aa
Aa aa
Aa : aff
aa : Normal
Both parent :
aa aa
aa
Here you need
AA/Aa

Autosomal dominant	Autosomal Recessive
●/■ : Aa	●/■ : aa
○/□ : aa	○/□ : Aa
	If Both parent : Normal/ Carrier/ Hetrozygous.
	son/ daughter : affected.





is it Autosomal dominant?

●/■ : Aa

○/□ : aa

yes

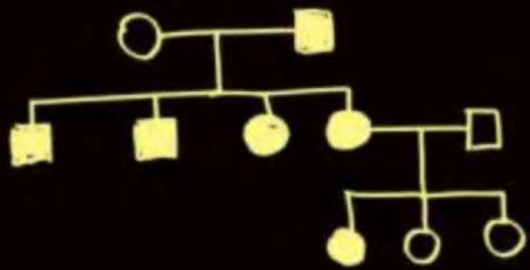
	A	a
a	Aa (A)	aa (N)
a	Aa (A)	aa (N)

aa x aa

a a

aa

Normal



is it autosomal Recessive
is it autosomal Dominant
Both.

auto. Recessive

●/■ : aa
○/□ : Aa

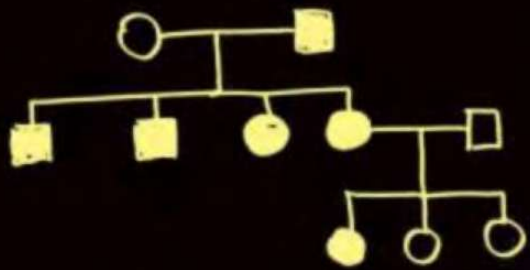
yes

Aa — aa

aa aa aa aa — Aa

aa Aa Aa

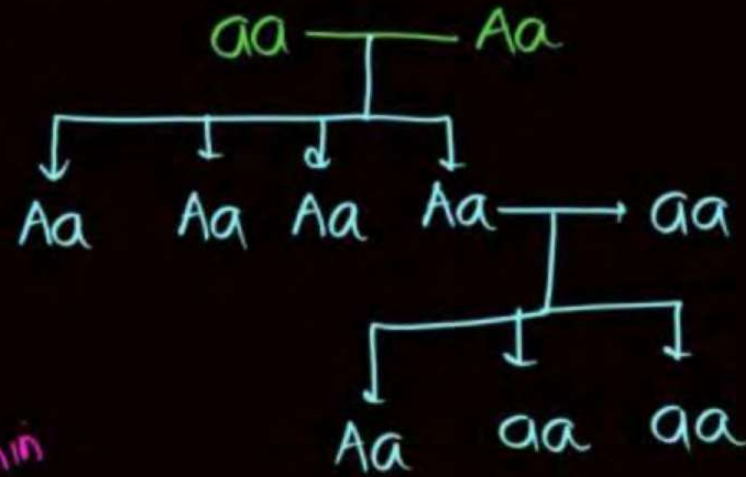
	A	a
a	Aa N	aa a
a	Aa N	aa a



is it autosomal Recessive
is it autosomal Dominant
Both.

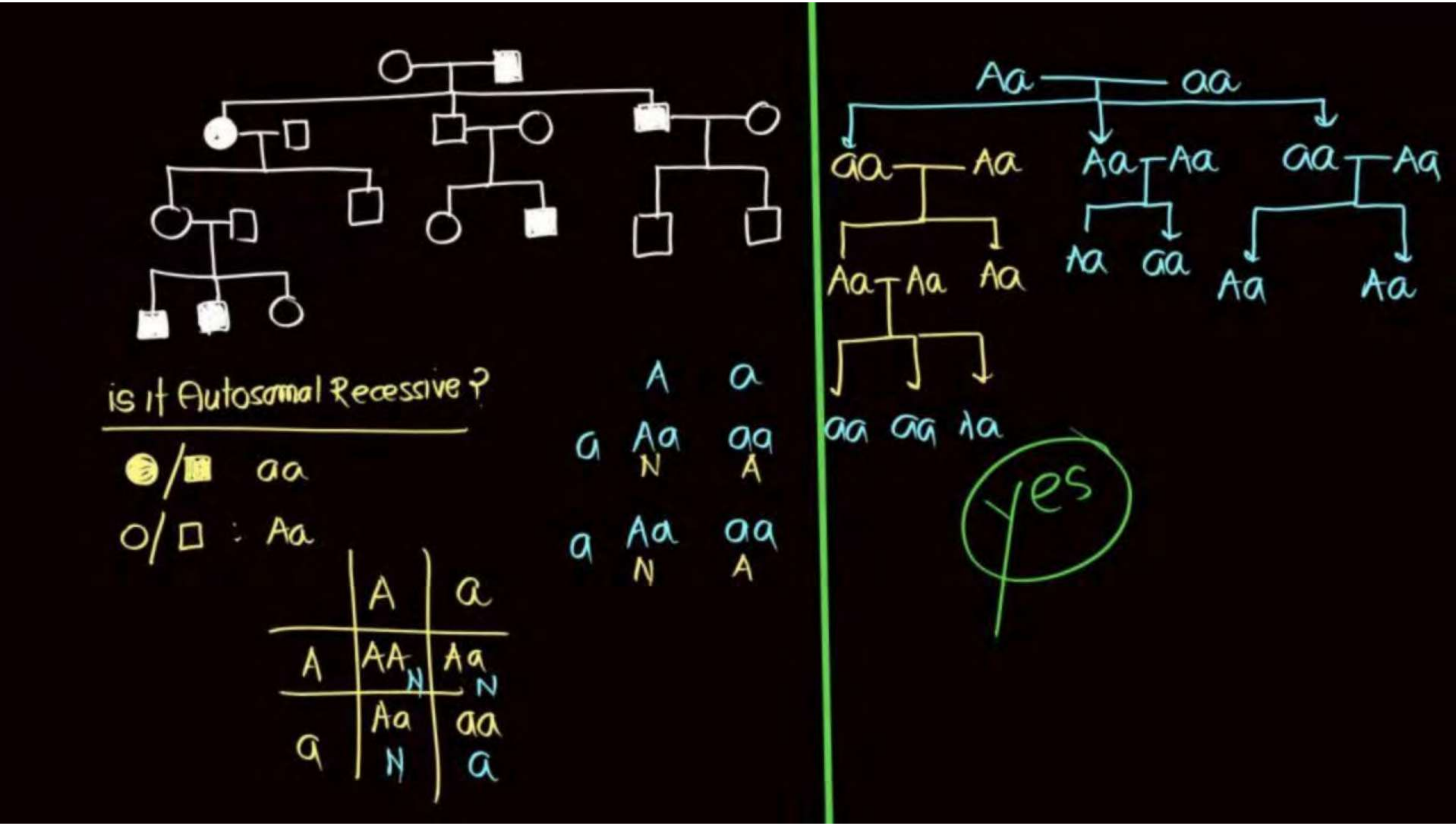
Aut. Dominant

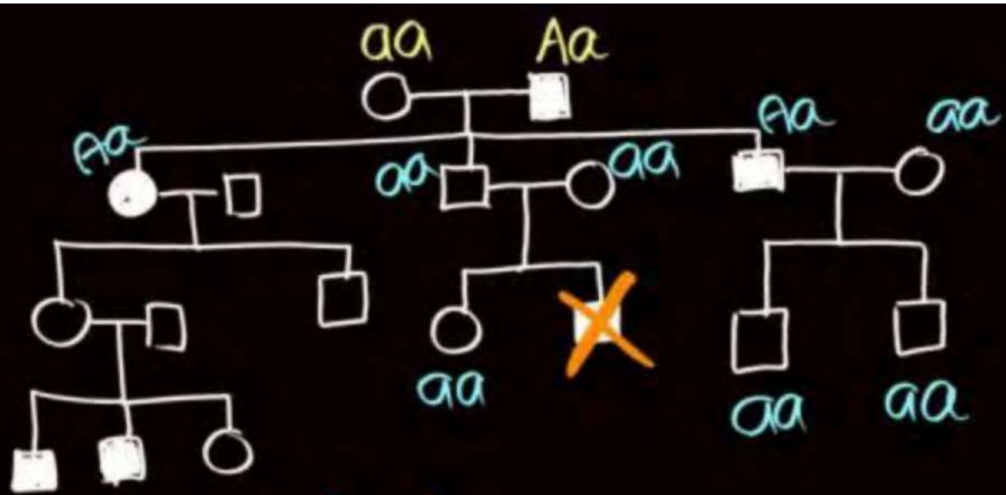
●/■ : Aa
○/□ : aa



	A	a
a	Aa a	aa N
a	Aa a	aa N.

Auto domin


is it Autosomal Recessive?
aa
: Aa
A a
A AA Aa
a Aa aa
N N N a
A a
a Aa aa
N A
a Aa aa
N A
Aa aa
aa Aa Aa Aa aa Aa
Aa Aa Aa Aa aa Aa Aa
aa aa Aa
yes



Is it autosomal dominant?

●/■ : Aa

○/□ : aa

	a	a
A	Aa	Aa
a	aa N	aa N

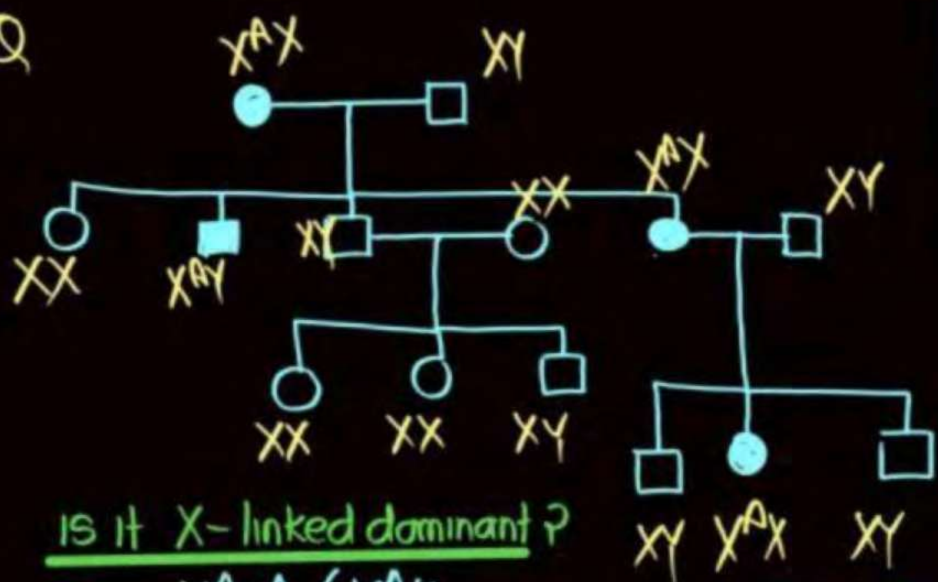
aa × aa

↓ ↓

a a

aa (Normal)

Q



Is it X-linked dominant?

● → X^AX^A / X^AX

■ → X^AY

○ → XX

□ → XY

yes

~~X^AX^A~~ XY

X^AX X^AY X^AX X^AY X

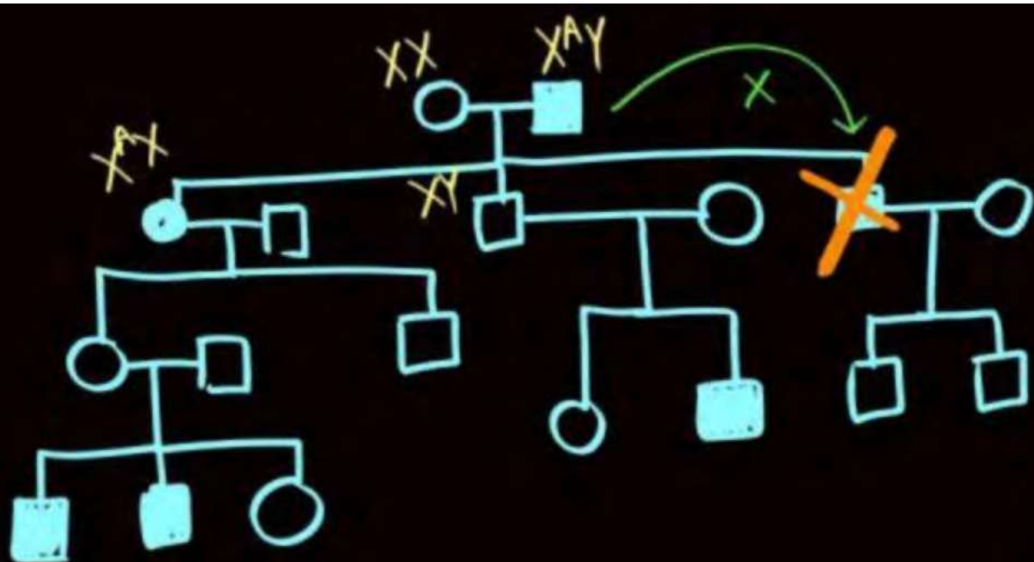
aff aff aff aff

X^AX XY

X^AX X^AY XX XY

aff aff Nor Nor

Fem male Fem male.



NO.

Is it X linked dominant?

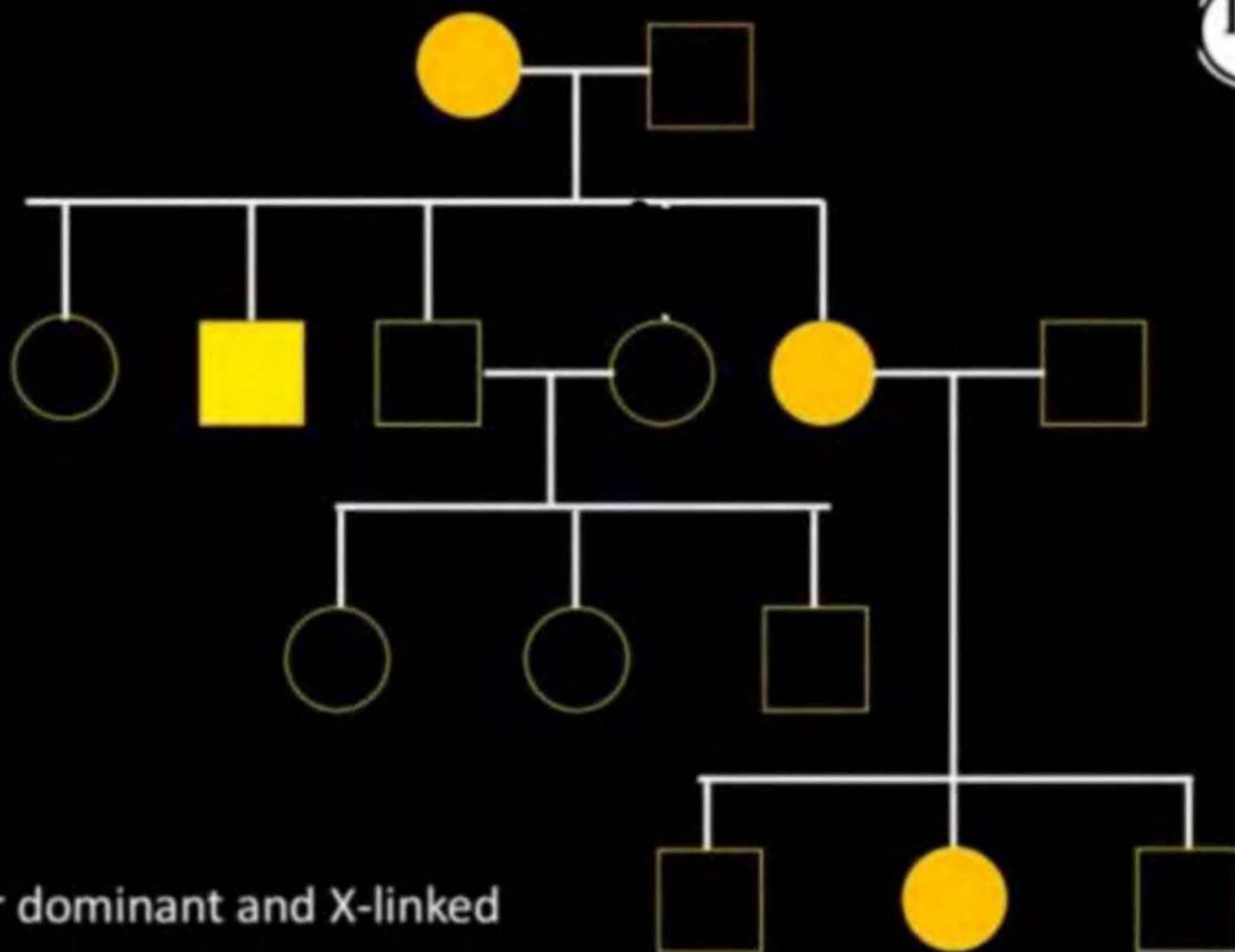
Short cut:

$XX \qquad X^AY$

a $X^AX \quad XY$ N

a $X^AX \quad XY$ N

alredy solved.



(1) Dominant and X-linked
(2) Dominant and autosomal or dominant and X-linked
(3) Recessive and X-linked
(4) Recessive and Y-linked

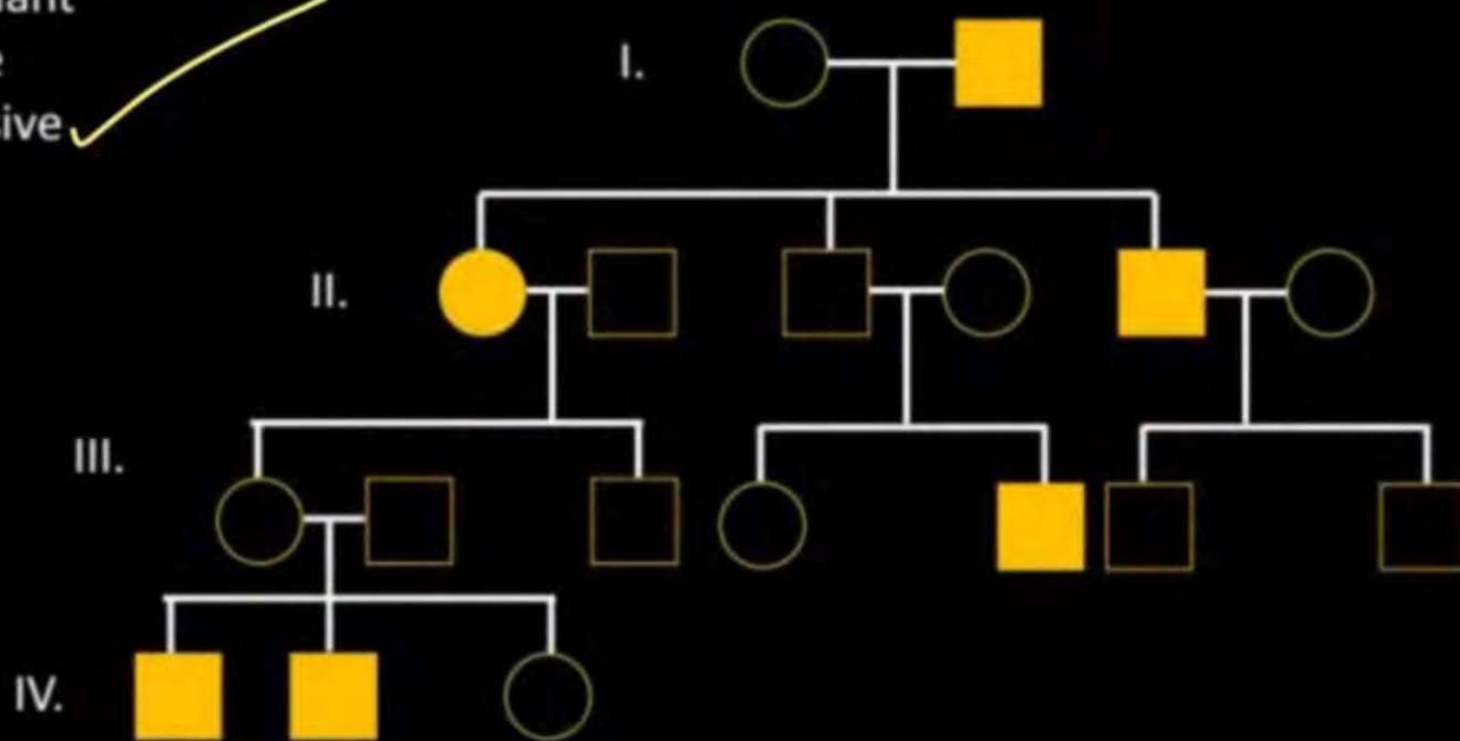
In the following human pedigree, the filled symbols represent the affected individuals. Identify the type of given pedigree. [Re-AIPMT-2015]

(1) X-linked dominant

(2) Autosomal dominant

(3) X-linked recessive

(4) Autosomal recessive



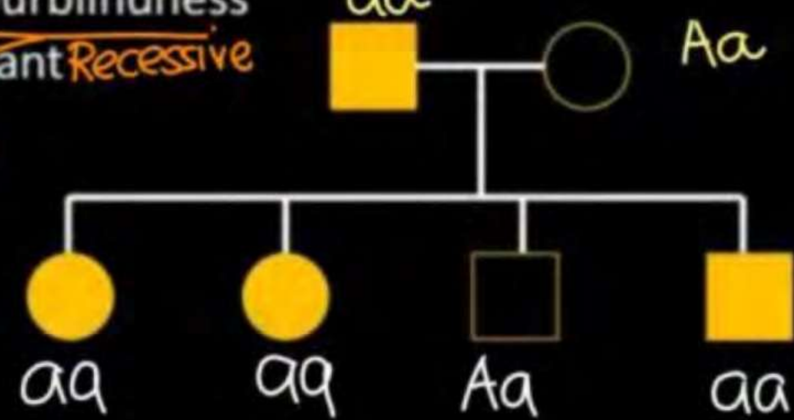
#Q. Study the pedigree chart of a certain family given below and select the correct conclusion which can be drawn for the character

(1) The female parent is heterozygous

~~(2)~~ The parents could ~~not~~ have had a normal daughter for this character

(3) The trait under study could ~~not~~ be colourblindness

~~(4)~~ The male parent is homozygous ~~dominant~~ Recessive



Female parent : Normal : Aa
(heterozygous)
(Autosomal Recessive)
affected : aa

	a	a
A	Aa N	Aa N
a	aa A	aa A

X^aY X^aX

aff X^aX^a X^aX car/N.

aff male X^aY XY Normal male

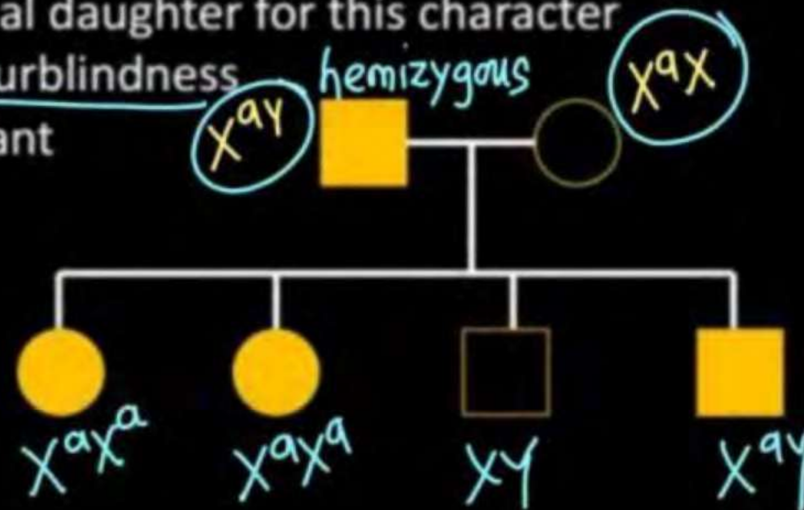
#Q. Study the pedigree chart of a certain family given below and select the correct conclusion which can be drawn for the character

(1) The female parent is heterozygous

(2) The parents could not have had a normal daughter for this character

(3) The trait under study could ~~not~~ be colourblindness

(4) The male parent is homozygous dominant



Colourblind: X linked Recessive

● : X^aX^a

⊙ : Carrier X^aX (Normal)

○ : XX/X^aX

■ : X^aY

□ : XY

Let us check for option (a)

	A	a
A	AA (N)	Aa (N)
a	Aa (N)	aa (aff.)

#Q. Study the pedigree chart. What does it show? (2009)

(1) Inheritance of a condition like phenylketonuria as an autosomal recessive trait

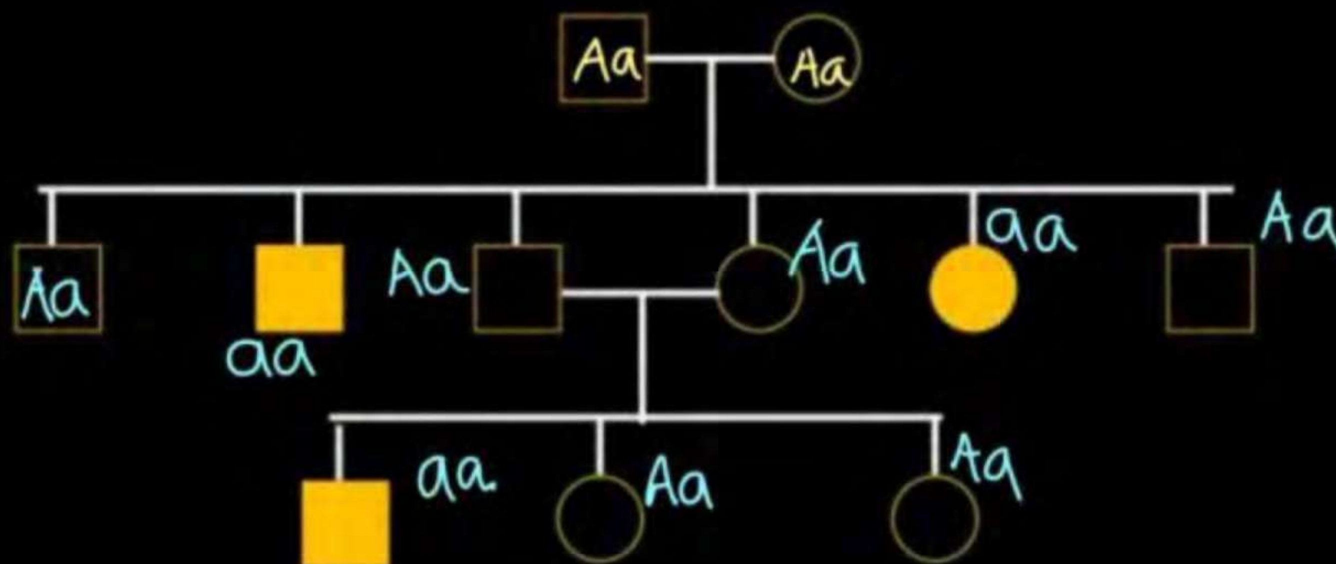
(2) Inheritance of a recessive sex-linked disease like haemophilia (X link Reces)

(3) Inheritance of ~~sex-linked~~ Auto Recessive inborn error of metabolism like phenylketonuria

(4) Pedigree chart is wrong as this is not possible

○/□ : Aa

●/■ : aa



Let us check for option b X linked Rec.

#Q. Study the pedigree chart. What does it show? (2009)

(1) Inheritance of a condition like phenylketonuria as an autosomal recessive trait

(2) Inheritance of a recessive sex-linked disease like haemophilia

(3) Inheritance of sex-linked inborn error of metabolism like phenylketonuria

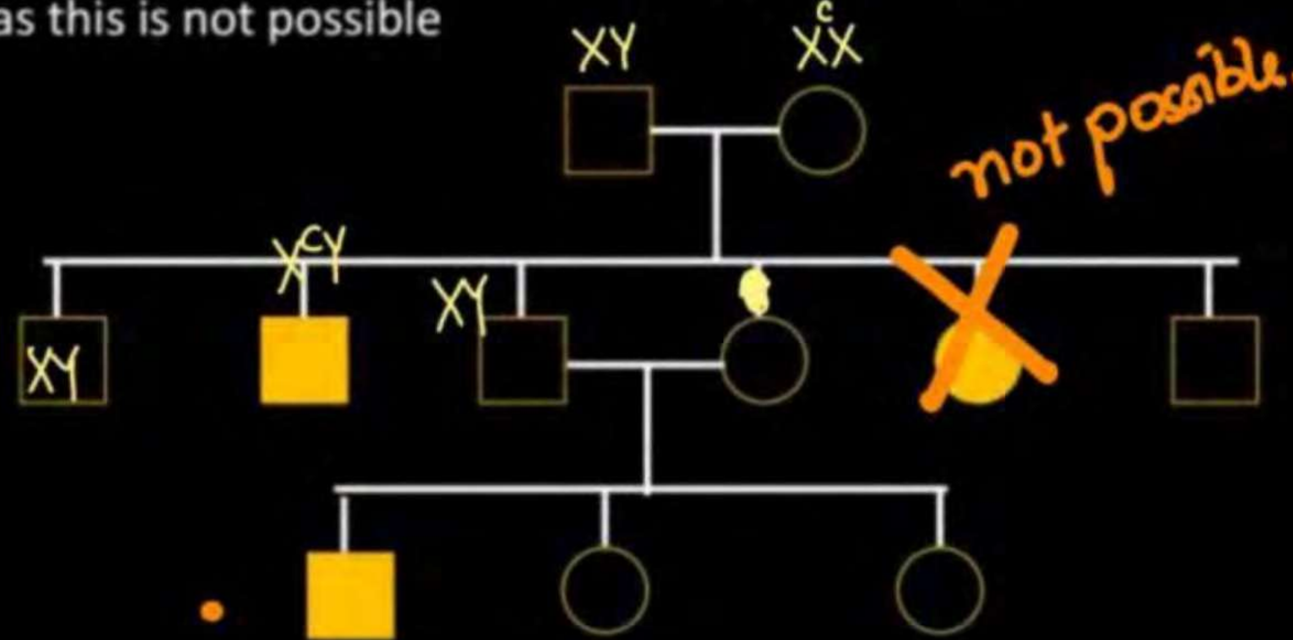
(4) Pedigree chart is wrong as this is not possible

X^cX : Normal / Car.

X^cY

XX

XY

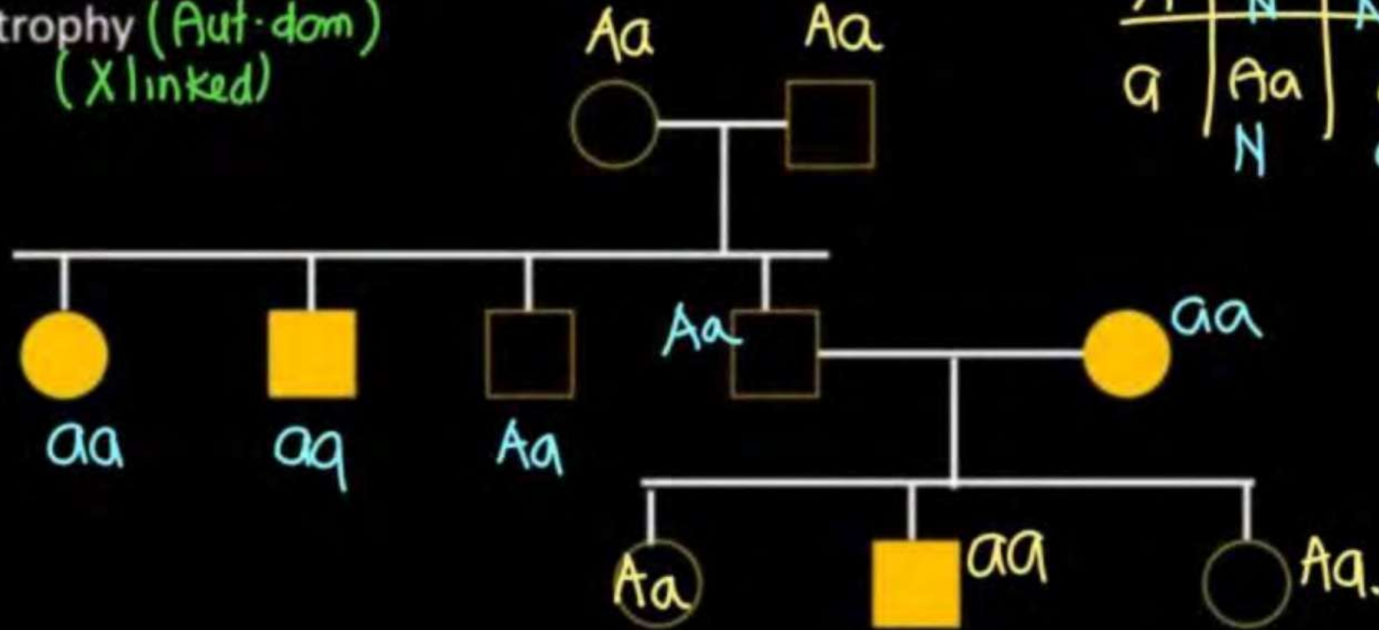


Let us
Check for
auto·Recessive.

#Q. The Pedigree chart given below depicts
(1) Cystic fibrosis (Aut·Recess)
(2) Myotonic dystrophy (Aut·dom)
(3) Haemophilia (X linked)

	A	a
A	AA N	Aa N
a	Aa N	aa aff

	A	a
a	Aa N	aa a
a	Aa N	aa a



Let us check for aut. dom

#Q. The Pedigree chart given below depicts

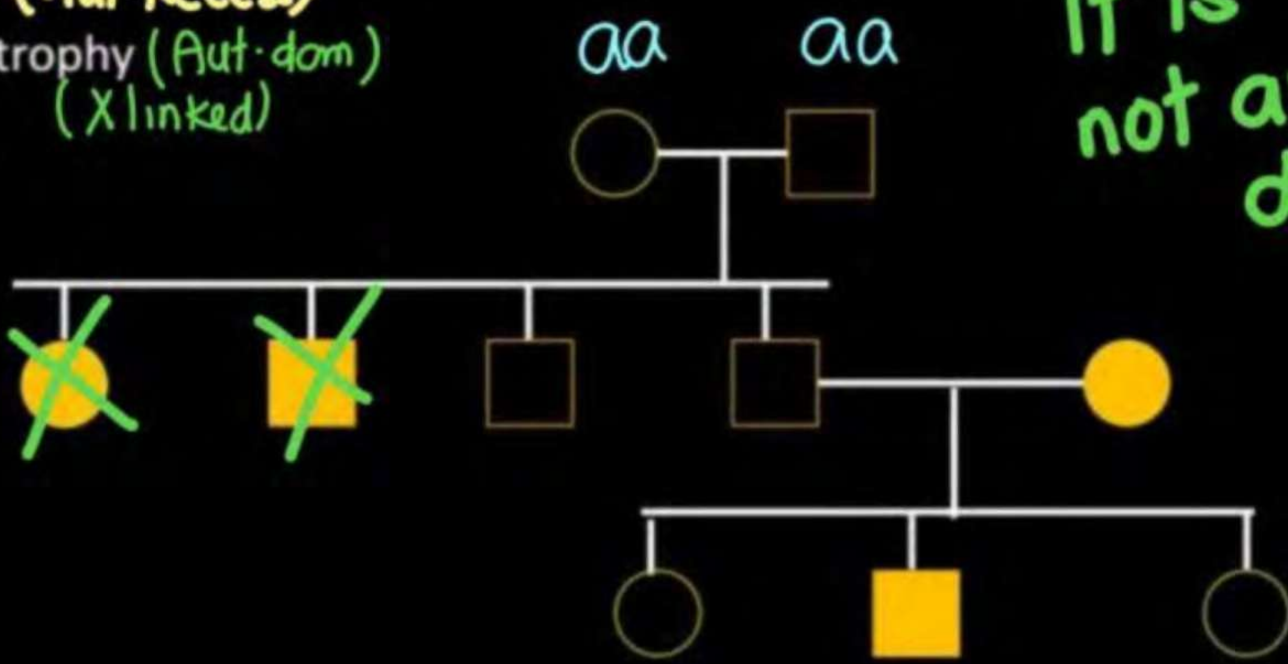
(1) Cystic fibrosis (Aut. Recess)

~~(2)~~ Myotonic dystrophy (Aut. dom)

(3) Haemophilia (X linked)

●/■ : Aa

○/□ : aa



It is not aut. dominant

X^aX : N/C

X^aY : aff

XX : Nor

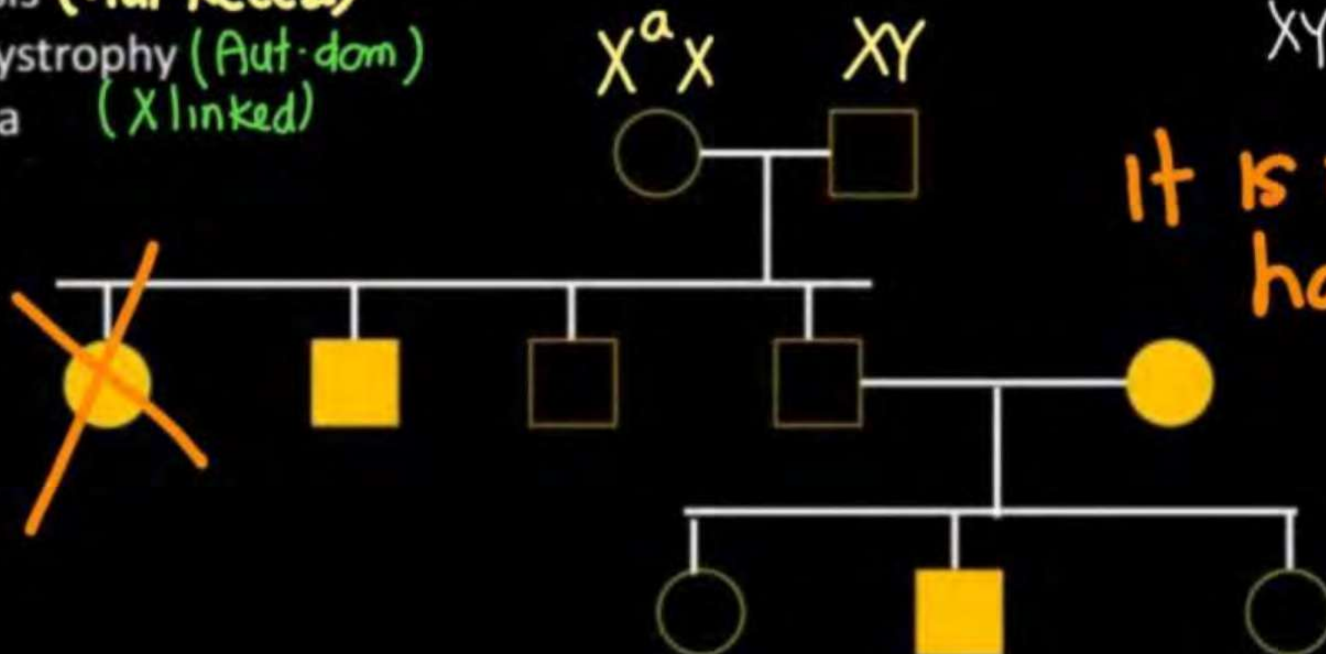
XY / Normal son.

#Q. The Pedigree chart given below depicts

(1) Cystic fibrosis (Aut·Recess)

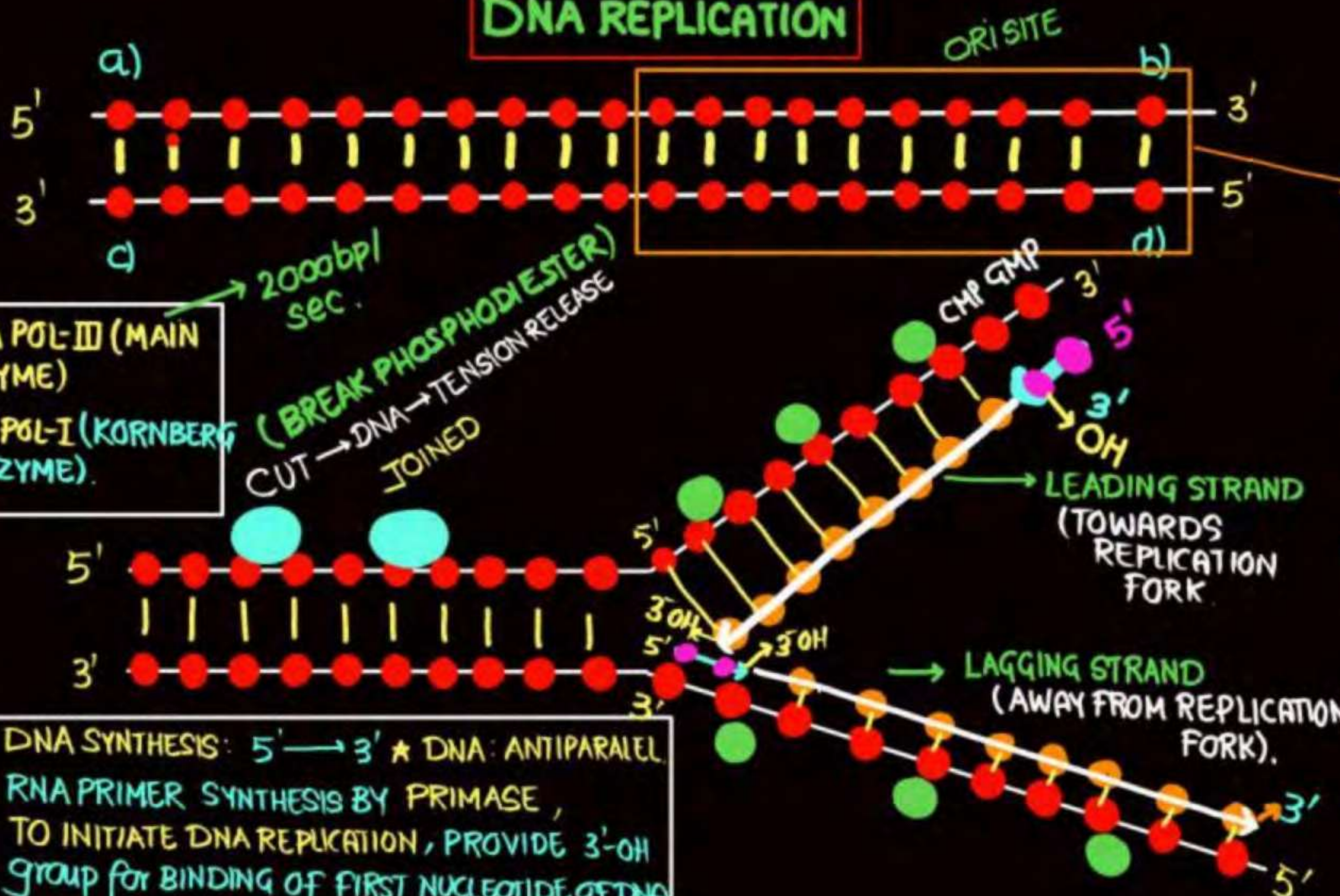
(2) Myotonic dystrophy (Aut·dom)

(3) Haemophilia (X linked)



It is not haemophilia

DNA REPLICATION

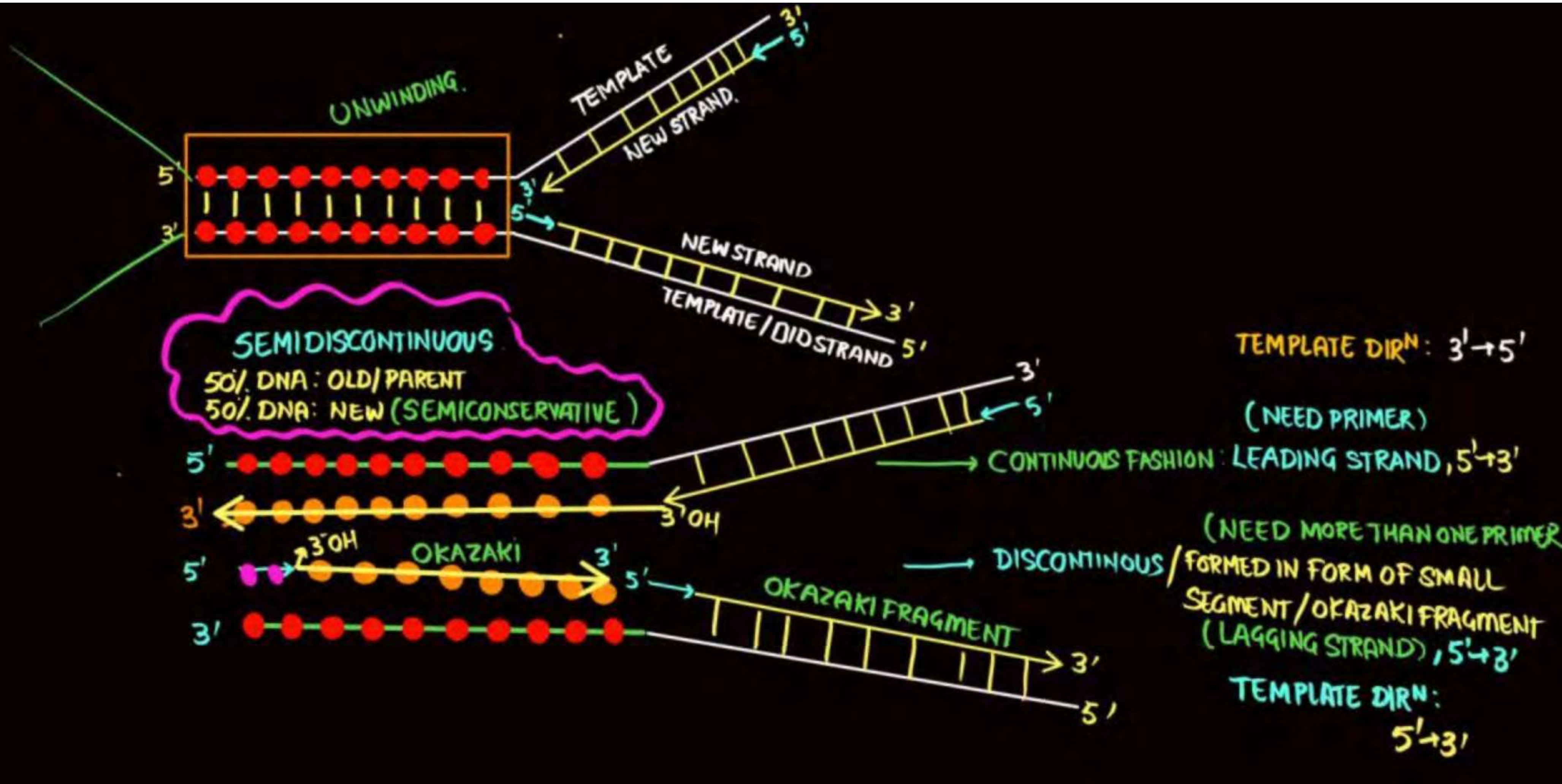


	FIRST	LAST
UPPER	a	b
LOWER	d	c

- ★ DNA POL-III (MAIN ENZYME)
- ★ DNA POL-I (KORNBERG ENZYME).

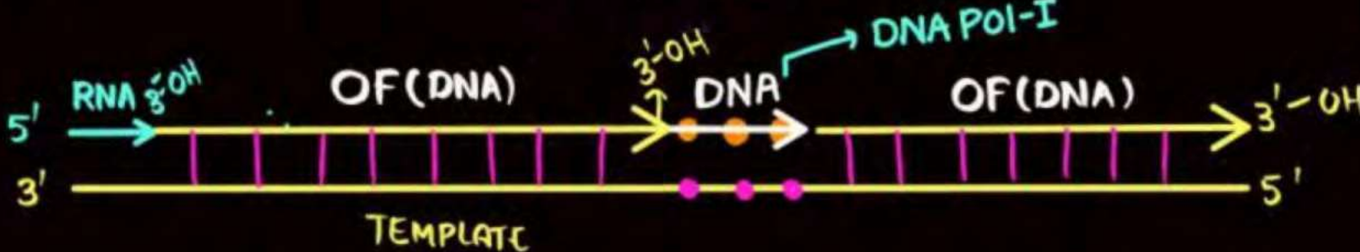
- ★ HELICASE / UNWINDASE : BREAK H_2 BOND (DENATURATION / UNWINDING OF DNA)
- ★ REPLICATION FORK.
- ★ ORI SITE : ORIGIN OF REPLICATION (A-T RICH) easy to BREAK DOUBLE BOND COMPARE TO TRIPLE BOND ($G \equiv C$)
- ★ DNA UNWIND OCCUR AT REGULAR INTERVAL OF TIME, AND NEVER UNWIND WHOLE DNA AT TIME
- ★ ● : SSB (SINGLE STRANDARD BINDING PROTEIN (PREVENT RENATURATION OF DNA
- ★ DUE TO HELICASE ACTIVITY SUPERCOILING OCCUR, PREVENTED BY TOPOISOMERASE / DNA GYRASE

- ★ DNA SYNTHESIS : 5' ⟶ 3' ★ DNA : ANTIPARALLEL
- ★ RNA PRIMER SYNTHESIS BY PRIMASE, TO INITIATE DNA REPLICATION, PROVIDE 3'-OH group for BINDING OF FIRST NUCLEOTIDE OF DNA
- ★ DNA POLYMERASE : DNA SYNTHESIS 5'→3' synthesis/Polymerisation activity
- ★ PROKARYOTE : DNA POl-I , DNA POL-II , DNA POL-III



UNWINDING.
TEMPLATE
NEW STRAND.
3'
5'
5'
3'
3'
5'
NEW STRAND
TEMPLATE/OLD STRAND
3'
5'
SEMIDISCONTINUOUS
50% DNA: OLD/PARENT
50% DNA: NEW (SEMICONSERVATIVE)
TEMPLATE DIRN: 3'→5'
(NEED PRIMER)
CONTINUOUS FASHION: LEADING STRAND, 5'→3'
3'OH
(NEED MORE THAN ONE PRIMER
DISCONTINOUS/FORMED IN FORM OF SMALL SEGMENT/OKAZAKI FRAGMENT
(LAGGING STRAND), 5'→3'
TEMPLATE DIRN:
5'→3'
OKAZAKI
OKAZAKI FRAGMENT

CLIMAX



★ REMOVAL OF PRIMER : DNA POl-I

★ GAP CREATED

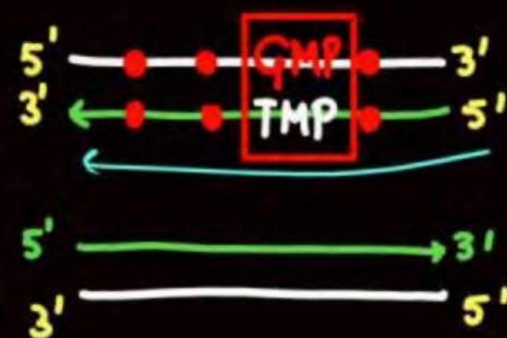
★ DNA SYNTHESIS BY DNA POl-I

★ SEALING OF STRAND: MOLECULAR GLUE/ DNA LIGASE.

EUKARYOTE: 5 TYPES OF DNA POl.

★ α, β, γ, delta, epsilon

	POLYMERISATION ACTIVITY (SYNTHESIS)	EXONUCLEASE ACTIVITY
DNA POl-I	5'→3'	5'→3' & 3'→5'
DNA POl-II	5'→3'	3'→5'
DNA POl-III (main)	5'→3'	3'→5'



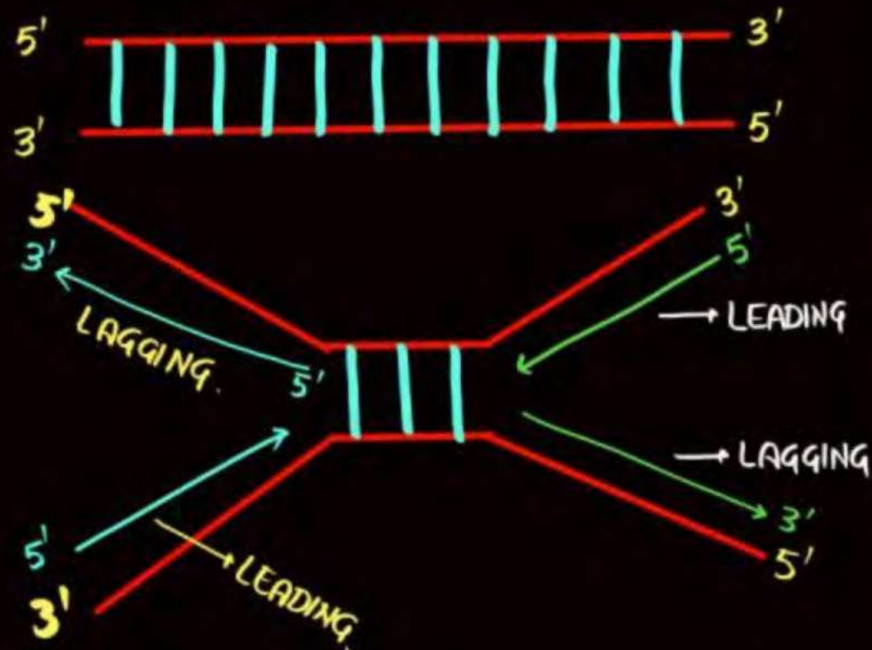
PROOF READING

★ DNA POl-III → WRONG BASE CUT → REMOVE (EXONUCLEASE ACTIVITY)

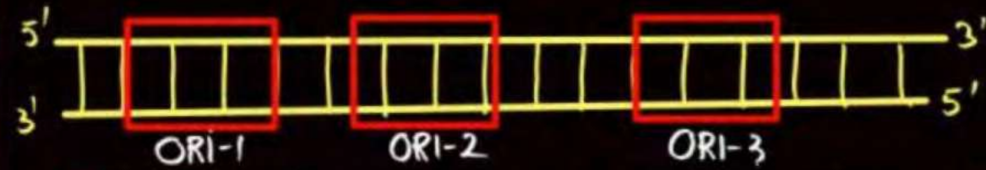
5'→3' exon. activity

3'→5' exonuclease activity

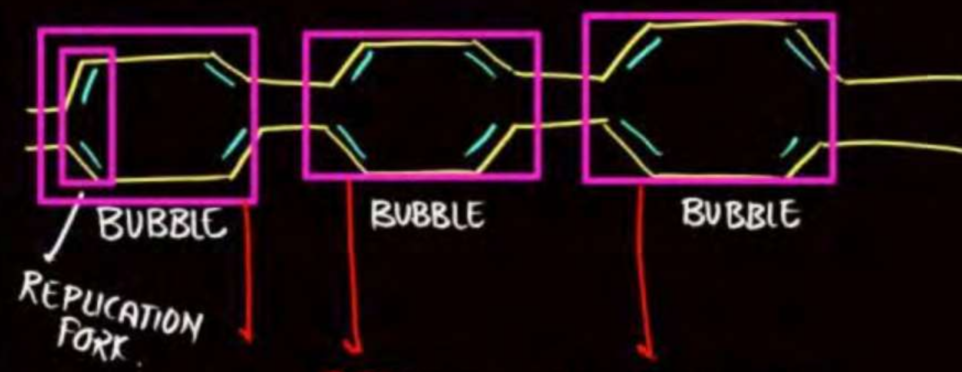
NOTE : DNA REPLICATION : BIDIRECTIONAL.



PROKARYOTE DNA : SINGLE ORI
(DNA REPL^{N} AT ONE POINT)

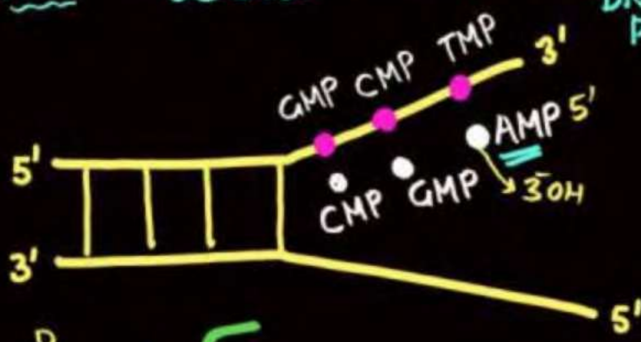


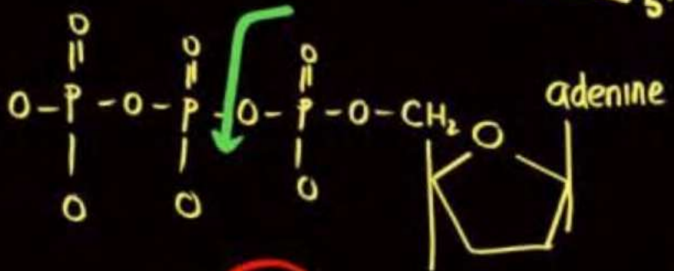
EUKARYOTE (DNA) : MANY (THOUSAND) ORI PRESENT (DNA REPL^{N} AT MANY POINT



REPLICON. SEGMENT OF DNA WHICH PARTICIPATE IN DNA REPLICATION.

NOTE : DNA POLYMERASE-III (DNA dependent DNA polymerase) ⇒ .





ATP ⟶ AMP + PPi

Pyrophosphate

GTP ⟶ GMP + PPi

CTP ⟶ CMP + PPi

NUCLEOTIDE : DUAL FUNCTION

- provide 3'-OH group for BINDING OF NEXT NUCLEOTIDE
- 2 Phosphate (energy) Release. FORM PHOSPHODIESTER BOND B/w TWO NUCLEOTIDE

PRIMASE : RNA SYNTHESIS (PRIMER)

DNA DEPENDENT RNA POLYMERASE

5.2.2 Properties of Genetic Material (DNA versus RNA)

From the foregoing discussion, it is clear that the debate between proteins versus DNA as the genetic material was unequivocally resolved from Hershey-Chase experiment. It became an established fact that it is DNA that acts as genetic material. However, it subsequently became clear that in some viruses, RNA is the genetic material (for example, Tobacco Mosaic viruses, QB bacteriophage, etc.). Answer to some of the questions such as, why DNA is the predominant genetic material? whereas RNA performs dynamic functions of messenger and adapter has to be found from the differences between chemical structures of the two nucleic acid molecules.

DNA $\xrightarrow{\text{TRANSCRIPTION}}$ mRNA (messenger)

SSRNA.

tRNA (eg).

adapter: amino acid ⟶ protein

SUPPLY (t-RNA) transfer RNA.

TRANSLATION

Can you recall the two chemical differences between DNA and RNA?

Deoxy Ribose Ribose

A molecule that can act as a genetic material must fulfill the following criteria:

Thymine URACIL

(i) It should be able to generate its replica (Replication). (DNA & RNA)

(ii) It should be stable chemically and structurally. (less Reactivity)

(iii) It should provide the scope for slow changes (mutation) that are required for evolution.

(iv) It should be able to express itself in the form of 'Mendelian Characters'. Pass from one genⁿ to another.

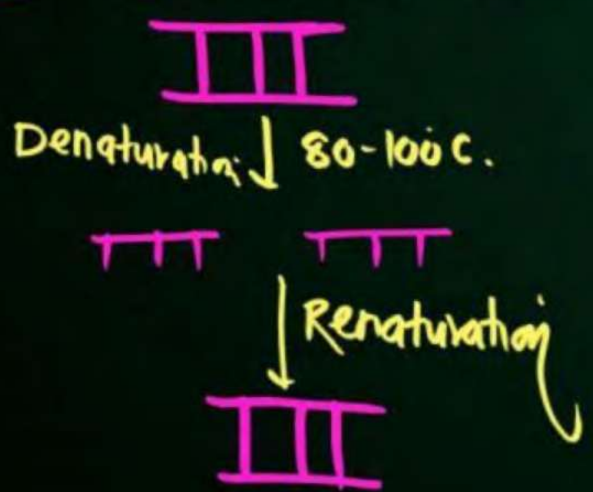
If one examines each requirement one by one, because of rule of base pairing and complementarity, both the nucleic acids (DNA and RNA) have the ability to direct their duplications. The other molecules in the living system, such as proteins fail to fulfill first criteria itself.

duplication
- DNA ⟶ DNA.
- RNA ⟶ RNA.

	DNA	RNA	PROTEIN
	1	1	0
Rep^n	✓	✓	×
Stab	1 ✓	× 0	

The genetic material should be stable enough not to change with different stages of life cycle, age or with change in physiology of the organism. Stability as one of the properties of genetic material was very evident in Griffith's 'transforming principle' itself that heat, which killed the bacteria, at least did not destroy some of the properties of genetic material. This now can easily be explained in light of the DNA that the two strands being complementary if separated by heating come together, when appropriate conditions are provided.

SOME VIRULENCY STILL THERE IN genetic material



Living S-III ← Living R-II ← enter

Further, 2′-OH group present at every nucleotide in RNA is a reactive group and makes RNA labile and easily degradable. RNA is also now known to be catalytic, hence reactive. Therefore, DNA chemically is less reactive and structurally more stable when compared to RNA. Therefore, among the two nucleic acids, the DNA is a better genetic material.

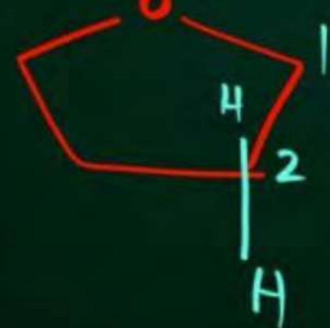
Reactivity more

more stability less.

TRANSLATION

RNA act as enzyme (RIBOZYME)

DeoxyRibose



In fact, the presence of thymine at the place of uracil also confers additional stability to DNA. (Detailed discussion about this requires understanding of the process of repair in DNA, and you will study these processes in higher classes.)

Both DNA and RNA are able to mutate. In fact, RNA being unstable, mutate at a faster rate. Consequently, viruses having RNA genome and having shorter life span mutate and evolve faster.

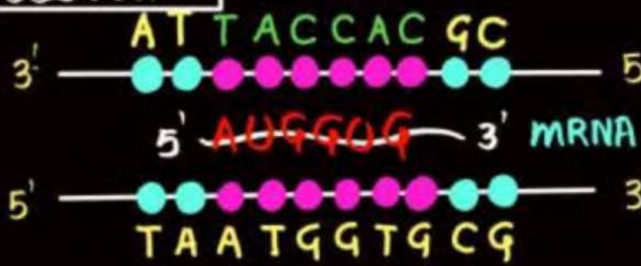
RNA can directly code for the synthesis of proteins, hence can easily express the characters. DNA, however, is dependent on RNA for synthesis of proteins. The protein synthesising machinery has evolved around RNA. The above discussion indicate that both RNA and DNA can function as genetic material, but DNA being more stable is preferred for storage of genetic information. For the transmission of genetic information, RNA is better.

DNA → mRNA → PROTEIN.

RNA → protein.

Transcription in PROKARYOTES

CONCEPT-①



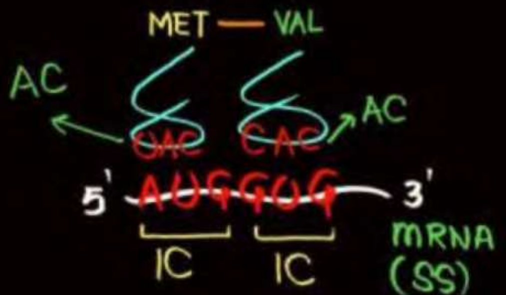
★ IC : CODON (3 BASE) / TRIPLET

★ tRNA CARRY AMINO ACID

★ AC : ANTICODON.

★ — : PEPTIDE BOND.

★ MET → VALINE (amino acid chain) ⟶ FORM PROTEIN.



★ mRNA & NON TEMPLATE SEQUENCE ARE SAME (EXCEPT URACIL)

★ mRNA & TEMPLATE : COMPLEMENTARY.

★ DNA ⟶ mRNA SYNTHESIS (5' ⟶ 3') ★ add^n of RIBONUCLEOTIDE OR RIBONUCLEOSIDE TRIPHOSPHATE (AMP, CMP, UMP, GMP) ★ PP$_i$ Released helps in PHOSPHODIESTER BOND. ★ RNA POLYMERASE (RNA SYNTHESIS) / DNA DEPENDENT RNA POLYMERASE → BREAKS H_2 BOND

★ ONLY ONE STRAND OF DNA PARTICIPATE BUT IN REPLICATION : BOTH STRAND PARTICIPATE ★ NO PRIMER REQUIRE AS IN DNA REPL^N.

★ ONLY A PART OF TEMPLATE PARTICIPATE ★ mRNA CODE FOR PROTEIN

★ AUG : METHIONINE ; GUG : VALINE

★ MESSENGER RNA CARRY MESSAGE FROM DNA IN FORM OF TRIPLET / CODON AND THIS CODON READ BY PARTICULAR tRNA WHICH CARRY AMINO ACID. SO HELPS IN PROTEIN FORMATION.

CONCEPT- 2

WHY BOTH STRAND DO NOT PARTICIPATE

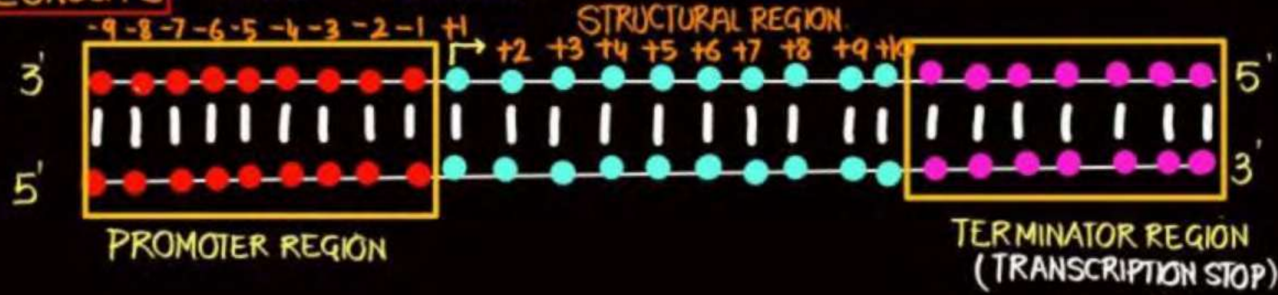
~~AUGGUG~~ (UPPER)

~~UACCAC~~ (LOWER)

→ BOTH mRNA SEQUENCE : COMPLEMENTARY SO THEY FORM H_2 BOND → mRNA BECOMES DOUBLE STRAND → SO NO tRNA BINDING → NO PROTEIN SYNTHESIS.

→ CODON OF BOTH RNA DIFFERENT SO THEY BRING DIFF. AMINO ACID SO TWO DIFFERENT TYPE OF PROTEIN, SO IT WILL COMPLICATE THE MACHINERY

CONCEPT-3 TRANSCRIPTIONAL UNIT.



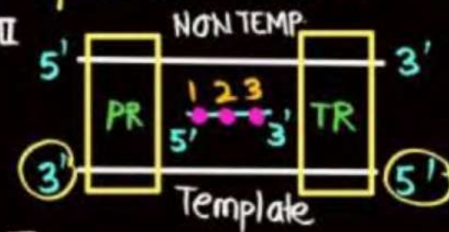
★ FORMATION OF m-RNA Start from STRUCURAL GENE/CISTRON.

Case-I

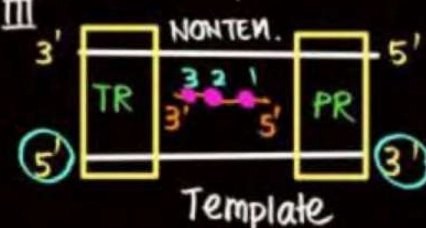
★ mRNA SHOW ANTIPARALLEL WITH DNA

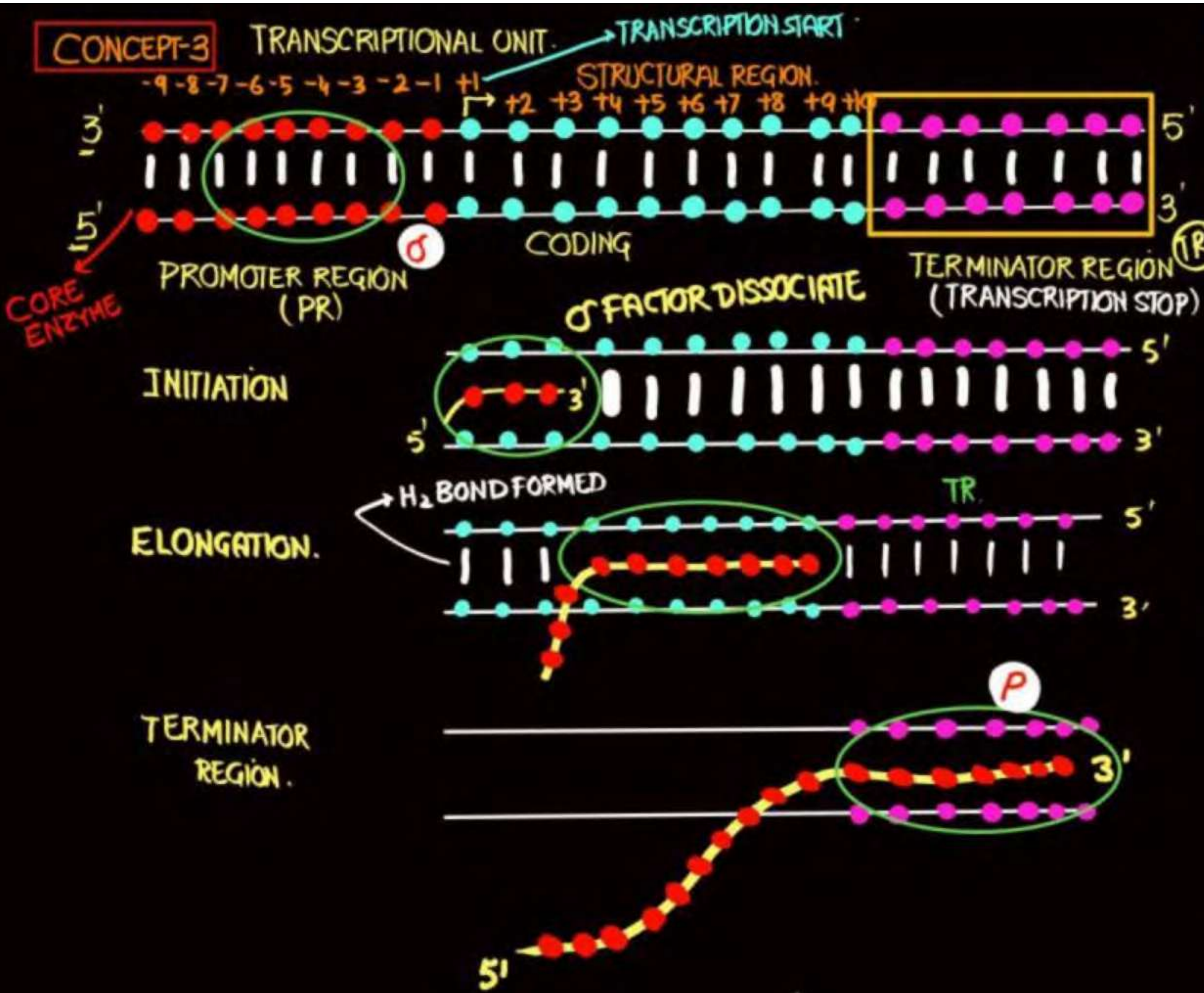
★ 3' end of mRNA TOWARDS TR.

Case-II



Case-III





RNA POLYMERASE
(CORE ENZYME)

★ α α' ω β β' + σ (SIGMA FACTOR) → RNA POLYMERASE (HOLOENZYME)

★ RNA POL (CORE ENZYME) BINDS TO PR WITH HELP OF 'σ' FACTOR/PROTEIN)

★ RNA POL BINDS TO PARTICULAR SEQ. IN PR CALLED CONSENSUS SEQUENCE (TATAAT → PRIBNOW BOX) & TTGACA

UPSTREAM ← +1 → DOWNSTREAM
PR, 5'end | TR, 3'end

★ If σ FACTOR ABSENT : TRANSCRIPTION OCCUR (NON-SPECIFIC)

★ RHO (P) PROTEIN BINDS TO CORE ENZYME AND RECOGNISE T.R

PROKARYOTES

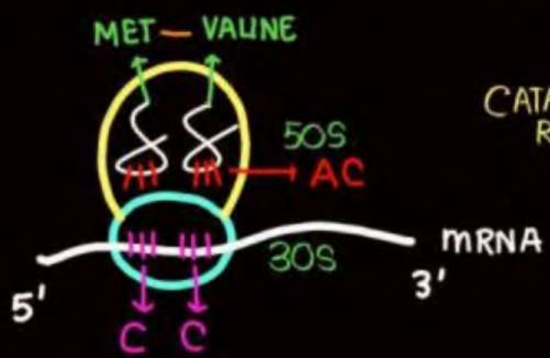
★ ONLY ONE TYPE OF RNA POLYMERASE → mRNA → PROVIDE CODON; tRNA → carry aminoacid; rRNA → IN RIBOSOME

All TYPE OF RNA NEED FOR PROTEIN SYNTHESIS (TRANSLATION)

rRNA → CATALYTIC ROLE; STRUCTURAL ROLE

⇛ IT HELPS IN BINDING OF mRNA TO RIBOSOME.

(HOW?)



★ C: CODON.

★ AC: ANTICODON

★ — : peptide BOND FORMED BY r-RNA (CATALYTIC ROLE)

↓

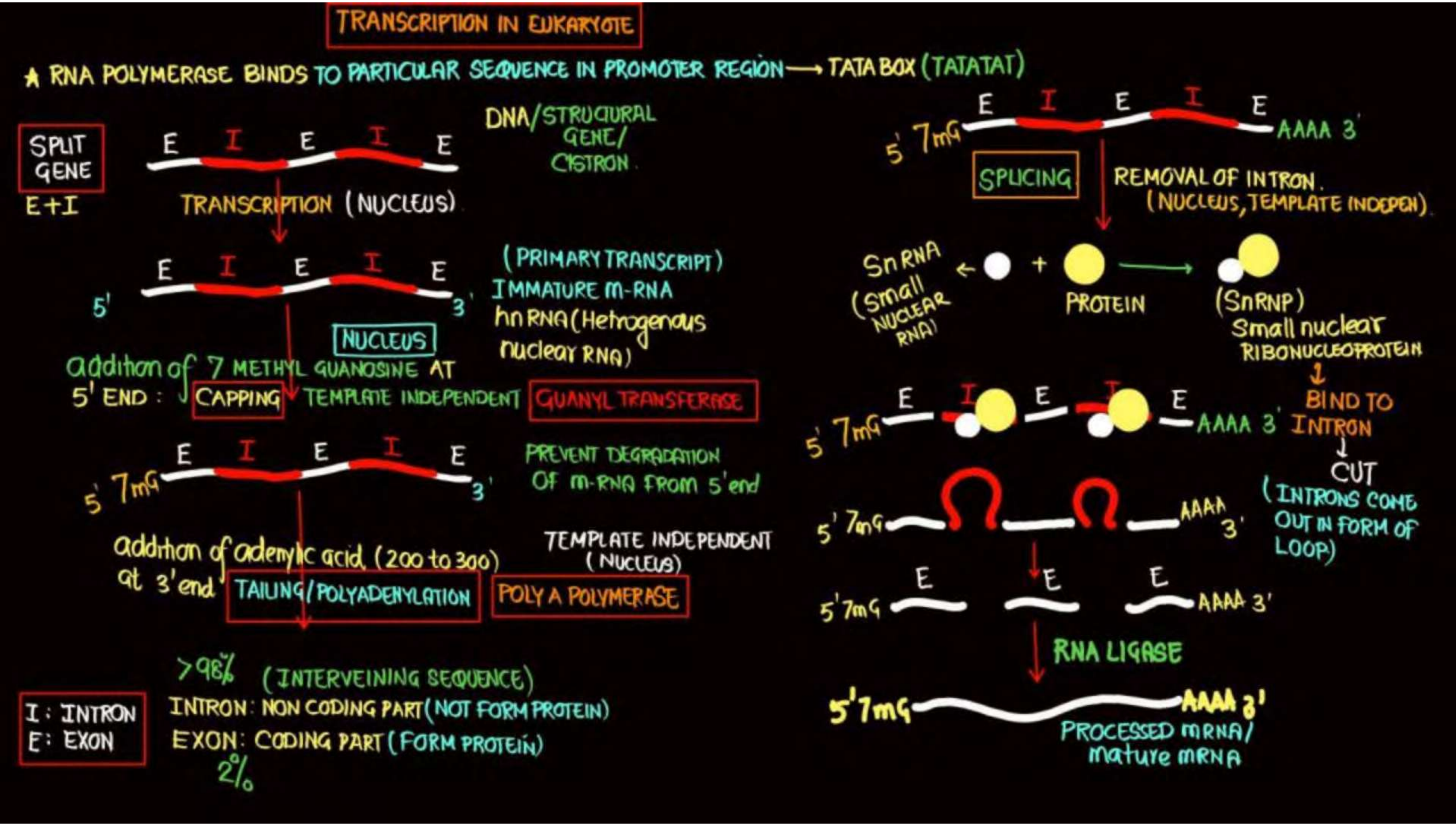
act as enzyme (RIBOZYME)

S.G/CISTRON

CISTRON

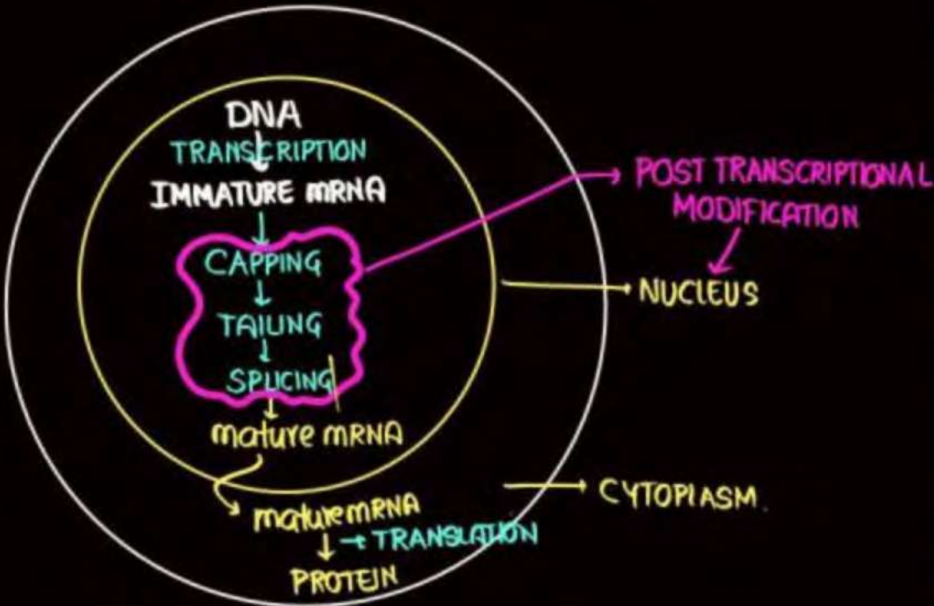
★ SEGMENT OF DNA Which CODE FOR PROTEIN/ CHAIN OF AMINOACID/ POLYPEPTIDE

★ DNA ⟶ mRNA ⟶ PROTEIN.



TRANSCRIPTION IN EUKARYOTE
* RNA POLYMERASE BINDS TO PARTICULAR SEQUENCE IN PROMOTER REGION → TATA BOX (TATATAT)
SPLIT GENE
E+I
E I E I E
DNA/STRUCTURAL GENE/ CISTRON
TRANSCRIPTION (NUCLEUS)
5' E I E I E 3'
(PRIMARY TRANSCRIPT)
IMMATURE m-RNA
hnRNA (Hetrogenous nuclear RNA)
NUCLEUS
addition of 7 METHYL GUANOSINE AT 5' END : CAPPING
TEMPLATE INDEPENDENT
GUANYL TRANSFERASE
5' 7mG E I E I E 3'
PREVENT DEGRADATION OF m-RNA FROM 5' end
addition of adenylic acid (200 to 300) at 3' end
TAILING/POLYADENYLATION
TEMPLATE INDEPENDENT (NUCLEUS)
POLY A POLYMERASE
>98% (INTERVEINING SEQUENCE)
I : INTRON
E : EXON
INTRON: NON CODING PART (NOT FORM PROTEIN)
EXON: CODING PART (FORM PROTEIN)
2%
5' 7mG E I E I E AAAA 3'
SPLICING
REMOVAL OF INTRON. (NUCLEUS, TEMPLATE INDEPEN)
SnRNA (Small NUCLEAR RNA)
PROTEIN
(SnRNP) Small nuclear RIBONUCLEOPROTEIN
BIND TO INTRON
CUT
(INTRONS COME OUT IN FORM OF LOOP)
5' 7mG E I E I E AAAA 3'
5' 7mG AAAA 3'
5' 7mG E E E AAAA 3'
RNA LIGASE
5' 7mG AAAA 3'
PROCESSED mRNA/ mature mRNA

SIMPLE VERSION (EUKARYOTES)

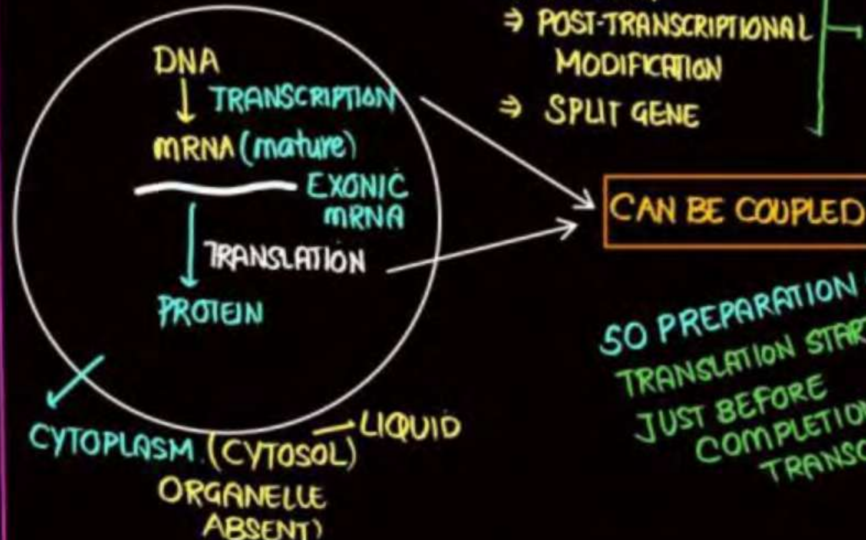


* TRANSCRIPTION & TRANSLATION: CANNOT BE COUPLED IN EUKARYOTE: HERE IMMATUR mRNA FIRST CONVERTS INTO mature mRNA

PROKARYOTES:

⇒ INTRONS
⇒ SPLICING
⇒ POST-TRANSCRIPTIONAL MODIFICATION
⇒ SPLIT GENE

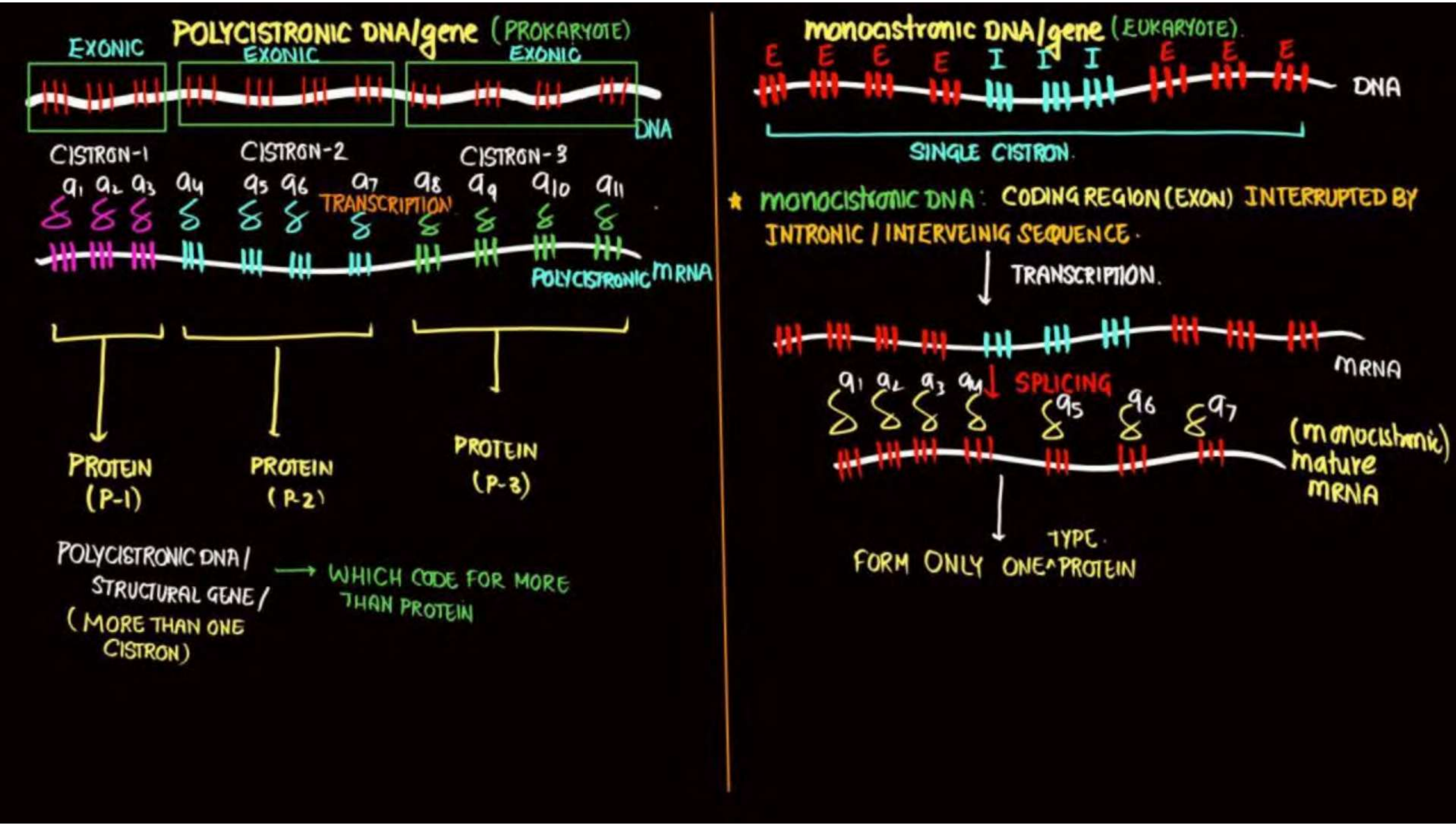
→ ABSENT



SO PREPARATION OF TRANSLATION START JUST BEFORE COMPLETION OF TRANSCRIPTION

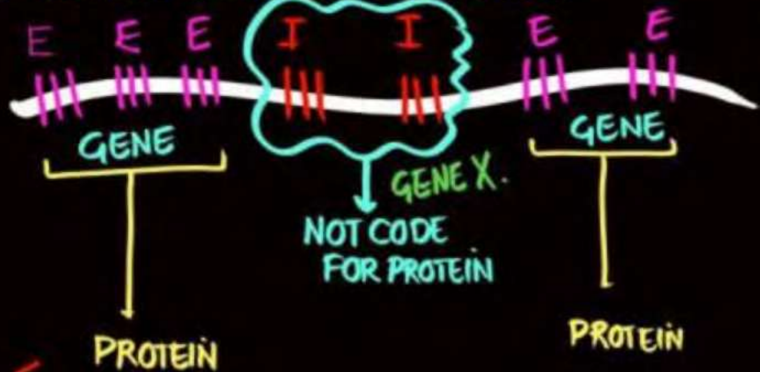
EUKARYOTE (THREE TYPES OF RNA POLYMERASE)

1. RNA POL-I : rRNA, 5·8S rRNA, 18S rRNA, 28S rRNA
2. RNA POL-II : mRNA / PRIMARY TRANSCRIPT / Hn RNA.
3. RNA POL-III : tRNA, Sn RNA, 5S rRNA


POLYCISTRONIC DNA/gene (PROKARYOTE)
EXONIC
EXONIC
EXONIC
DNA
CISTRON-1
CISTRON-2
CISTRON-3
a1 a2 a3 a4 a5 a6 a7 a8 a9 a10 a11
TRANSCRIPTION
POLYCISTRONIC mRNA
PROTEIN (P-1)
PROTEIN (P-2)
PROTEIN (P-3)
POLYCISTRONIC DNA / STRUCTURAL GENE / (MORE THAN ONE CISTRON)
→ WHICH CODE FOR MORE THAN PROTEIN
monocistronic DNA/gene (EUKARYOTE)
E E E E I I I E E E
DNA
SINGLE CISTRON.
★ monocistronic DNA: CODING REGION (EXON) INTERRUPTED BY INTRONIC / INTERVEINIG SEQUENCE.
TRANSCRIPTION.
mRNA
SPLICING
a1 a2 a3 a4 a5 a6 a7
(monocistronic) mature mRNA
FORM ONLY ONE TYPE PROTEIN

SPLIT GENE COMPLICATE DEFINITION OF GENE IN TERMS OF DNA → EUKARYOTE → BZ INTRON IS A PART OF DNA WHICH DO NOT CODE FOR PROTEIN SO IT IS NOT GENE

★ GENE : SEGMENT OF DNA WHICH FORM PROTEIN.



(monocistronic) DNA / STRUCTURAL GENE / CISTRON → WHICH FORM PROTEIN

SEGMENT OF DNA WHICH FORM ANY TYPE OF RNA (mRNA, rRNA, tRNA)

✓ CISTRON / ✓ Gene → mRNA

× CISTRON / ✓ Gene → tRNA

× CISTRON / ✓ Gene → rRNA

GENETIC CODE : RELATIONSHIP B/w NUCLEOTIDE SEQUENCE OF DNA, & mRNA → THIS mRNA BRINGS AMINOACID (PROTEIN)

① DNA ② mRNA ③ PROTEIN

3′ PR TAC AAA AAT ATT TR 5′

5′ PR ATG TTT TTA TAA TR 3′

Q: mRNA : 4 CODON.

4th : stop codon :

aminoacid : 4-1 ⇒ $\boxed{3}$

MET – Phe – Leu

NO tRNA

5′ AUG UUU UUA UAA 3′ mRNA.

initiation codon/start codon

TERMINATION/STOP CODON.

CODON : 4

NUCLEOTIDE : 4X3 : 12

UUU : PHENYLALANINE

UUA : LEUCINE

UAA, UAG, UGA :
NO tRNA
NO AMINO ACID

Gamow ← $\boxed{\text{GENETIC CODE IS TRIPLET}}$

* If genetic code is ~~Singlet~~
A, U, G, C = BASE IN RNA.

A — mRNA
U — mRNA
G — mRNA
C — mRNA

1 codon : 1 BASE

⇒ 4 CODON

(A.A)
TOTAL AMINO ACID: 20
1 CODON BRINGS 1 A.A
4 ⟶ 4 A.A
CODON ↓ A.A ↑
Shortage
16

⇒ 4^1 ⇒ 4

* If genetic code is ~~doublet~~
1 codon : 2 BASE

AU	AA
AG	UU
AC	GG
UG	CC
UA	
UC	
GA	
GU	
GC	
CA	
CU	
CG	

⇒ 4^2 ⇒ 16

16 CODON → 16 A.A.
CODON ↓
Shortage
4

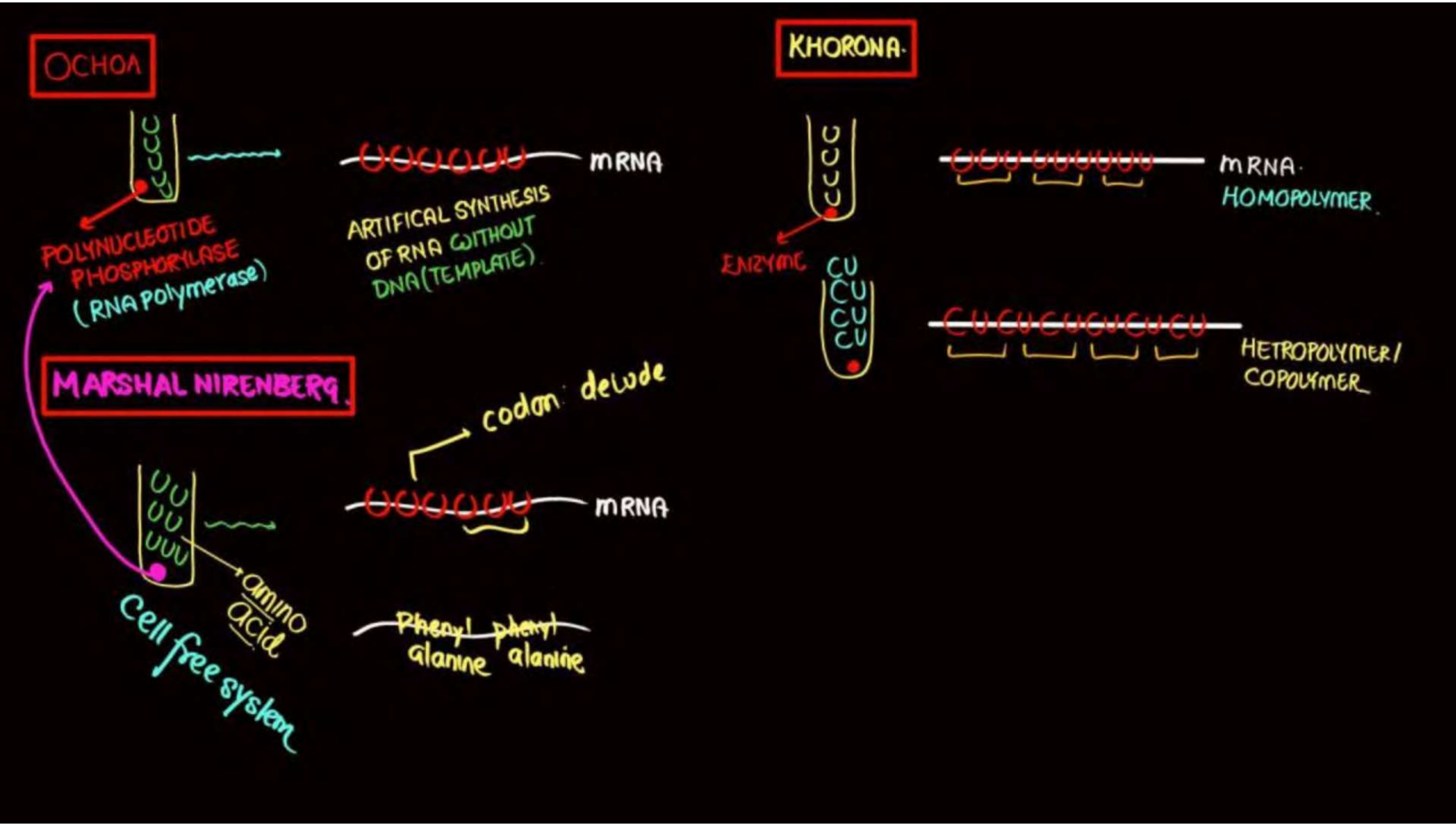
* If genetic code is TRIPLET.
4^3 ⇒ 64 CODON.
3 : STOP CODON.
64 − 3 ⇒ $\boxed{\text{61 C} \longrightarrow \text{20 A.A}}$

1 AMINO ACID CODED BY MORE THAN ONE CODON. (DEGENRACY OF GENETIC CODE)

REASON: ?

UGG : TRYPTOPHAN
AUG : METHIONINE
[EXCEPTION
NON DEGENERATE CODON.]

* IN MOST CASES, tRNA READS ONLY 1st & 2nd Base in codon to BRING PARTICULAR AMINO ACID. (WOOBLING)
3rd Base : WOBBLE BASE)



OCHOA
UUUUU
UUUUUU
mRNA
POLYNUCLEOTIDE PHOSPHORYLASE
(RNA polymerase)
ARTIFICAL SYNTHESIS OF RNA WITHOUT DNA (TEMPLATE).
KHORONA.
UUUU
UUU UUUUUU
mRNA.
HOMOPOLYMER.
ENZYME
CU CU CU CU
CUCUCUCUCUCU
HETROPOLYMER/ COPOLYMER
MARSHAL NIRENBERG.
codon: decode
UU UU UUU
UUUUUU
mRNA
amino acid
cell free system
Phenyl alanine phenyl alanine

Features of genetic code

a) Triplet code

Codon : Triplet
↓
3 Base present

g) stop codon

UAA : Ochre
UAG : amber
UGA : Opal

b) Non ambiguous

1 codon : 1 amino acid available

Exception : GUG

code for Two amino acid

ambiguous

~~III III GUG III~~ mRNA
Valine am. acid

(initiation)
~~GUG III III III~~ mRNA
↓
methionine

1 CODON DO NOT CODE FOR TWO DIFF. AMINO ACID

c) Commaless

GUGUUUCUG

No punctuation.

h) Non overlapping

GUG UCG

2 amino acid

d) Degeneracy of genetic code

1 amino acid Coded by more than one Codon.

Exception :

AUG ⇒ Methionine

UGG ⇒ Tryptophan

Non-Degenerate codon

e) nearly Universal

UUU code for phenylalanine in all organism

UGA : Stop codon (Nucleus)

UGA : Not stop codon (mitochondrial DNA)

f) Initiation Codon

AUG → methionine
AUG → initiation codon

Dual

III
AUG.
(protein synthesis : start)

MUTATION

⇒ Change in genotype / phenotype of organism

⇒ BASE/NUCLEOTIDE SEQUENCE IN DNA.
⇒ Chromosome Structure
⇒ Chromosome number
→ CHANGE

⇒ SUDDEN CHANGE
⇒ SOURCE OF DISCONTINOUS VARIATION.
⇒ CROSSING OVER: CONTINUOUS VARIATION.
⇒ CHEMICALS (NITROUS ACID, MUSTARD GAS)
RADIATION (α, β, γ, X Rays)
→ MUTAGENS ↓ CAUSE MUTATION.

⇒ SEGMENT OF DNA (MUTON) → UNDERGOES MUTATION.

TYPES

① GENE MUTATION

Change in nucleotides of DNA

a) SUBSTITUTION M

C$\boxed{T}$C → C$\boxed{A}$C

TRANSITION (4 TYPES)

★ PURINE REPLACE BY PURINE

A → G
G → A

★ PYRIMIDINE REPLACE BY PYRIMIDINE

C → T
T → C

$\boxed{\text{TRANSVERSION}}$ (8 TYPES).

★ PURINE REPLACE BY PYRIMIDINE OR PYRIMIDINE REPLACE BY PURINE

A → T
A → C
T → A
C → A
G → C
G → T
C → G
T → G.

(b) FRAMESHIFT M.

addition

deletion.

123 456 789
~~AUG AGG GUG~~ mRNA ⇒ (3) amino acid

If we add 'U' after 3rd Base

stop codon (TERMINATION

~~AUG UAG GGU G~~ ⇒ (1) amino acid

~~ABC DEF GHI~~

3rd Base delete

~~ABD EFG HI~~

→ diffⁿ codon → BRINGS DIFFERENT AMINO ACID.

Second letter

First letter	U	C	A	G	Third letter
U	UUU, UUC } Phe UUA, UUG } Leu	UCU, UCC, UCA, UCG } Ser	UAU, UAC } Tyr **UAA Stop** **UAG Stop**	UGU, UGC } Cys **UGA Stop** UGG Trp	U C A G
C	CUU, CUC, CUA, CUG } Leu	CCU, CCC, CCA, CCG } Pro	CAU, CAC } His CAA, CAG } Gln	CGU, CGC, CGA, CGG } Arg	U C A G
A	AUU, AUC, AUA } Ile AUG Met	ACU, ACC, ACA, ACG } Thr	AAU, AAC } Asn AAA, AAG } Lys	AGU, AGC } Ser AGA, AGG } Arg	U C A G
G	GUU, GUC, GUA, GUG } Val	GCU, GCC, GCA, GCG } Ala	GAU, GAC } Asp GAA, GAG } Glu	GGU, GGC, GGA, GGG } Gly	U C A G

Consider a statement that is made up of the following words each having three letters like genetic code.

B   BI   BIG

RAM HAS RED CAP

If we insert a letter B in between HAS and RED and rearrange the statement, it would read as follows:

addition

1 2 3 4 5 6

RAM HAS BRE DCA P codon change

diff amino acid

Similarly, if we now insert two letters at the same place, say BI'. Now it would read,

diff am. acid

RAM HAS BIR EDC AP

Now we insert three letters together, say BIG, the statement would read

RAM HAS BIG RED CAP

The same exercise can be repeated, by deleting the letters R, E and D, one by one and rearranging the statement to make a triplet word.

RAM HAS RED CAP

RAM HAS EDC AP R ✗

RAM HAS DCA P RE ✗ DELETION

RAM HAS CAP RED ✗

② CHROMOSOMAL ABERRATION.

- Change in structure of Chromosome ('C')
- OBSEVED IN CANCER CELL.

★ DELETION.

A B C D E F

loss of segment/gene

A B C D.

DUPLICATION

A B C D E F

segment of chromosome

DE

A BC DE DE F.

③ GENOMATIC MUTATION

- Change in NUMBER. of Chromosome

ANEUPLOIDY

loss of 'C'

monosomy

NULLISOMY

gain of 'C'

TRISOMY

TETRASOMY.

EUPLOIDY

HAPLOIDY

$2n = 10$

$\boxed{n = 5.}$

POLYPLOIDY

$2n : 10$

$\boxed{3n : 15.}$

$\boxed{4n : 20}$

TRANSLATION mRNA ⟶ PROTEIN INITIATION, ELONGATION, TERMINATION

AMINOACYLATION OF tRNA / Charging of tRNA

a) ACTIVATION OF AMINO ACID

AMINOACID + ATP ⟶ AMINOACYL AMP + PP_i

(INACTIVE) ACTIVE FORM.

b) CHARGING OF tRNA

AMINOACYL AMP + tRNA ⟶ AMINO ACYL tRNA + AMP

CHARGED tRNA

This Reactions Catalysed By Amino acyl tRNA synthetase.

INITIATION

① mRNA BINDS TO SMALLER SUBUNIT OF RIBOSOME

dissociated state

30S/40S
↓ ↓
PRO EUK.

(a)

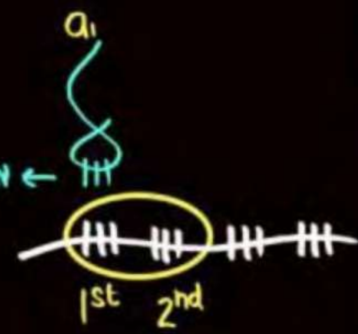
1 : INITIATION C (AUG)

4 : TERMINATION C

② 1st t-RNA (initiator) carry 1st amino acid

P : FORMYLMETHIONINE

E : METHIONINE



(b)

NOTE: SOME PROTEINS (INITIATION FACTORS) INVOLVED

PROK : 3 → IF-1, IF-2, IF-3.

EUK : 9

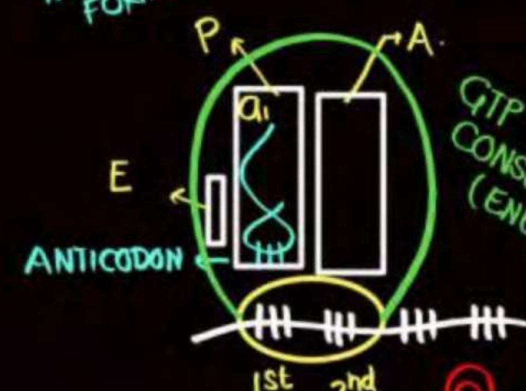
③ BINDING OF LARGER SUBUNIT OF RIBOSOME (50S/60S) to smaller SUBUNIT

PRO EUK.

3 SITE

E (EXIT) P (PEPTIDYL) A (AMINO ACYL)

association (COMPLETE RIBOSOME FORMED)

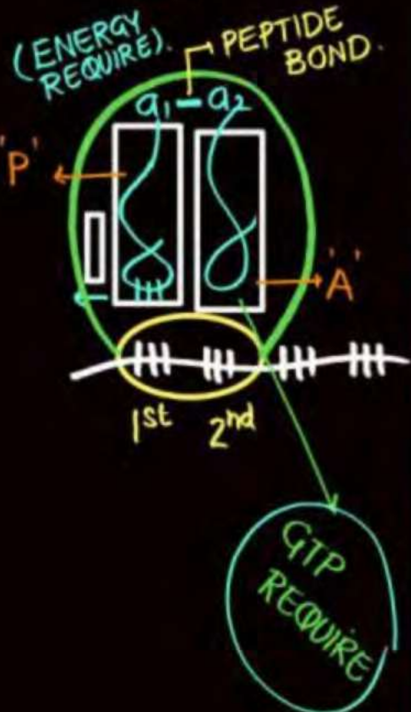


GTP CONSUMED (ENERGY)

(c)

ELONGATION

⇒ BINDING OF 2^{ND} tRNA at 'A' site.



⇒ PEPTIDE BOND FORMATION. B/ω TWO AMINO ACID

$$NH_2-\underset{R}{\overset{H}{C}}-COOH + H_2N-\underset{R}{\overset{H}{C}}-COOH \xrightarrow{-H_2O}$$

1st

$$NH_2-\underset{R}{\overset{H}{C}}-\boxed{CO-NH}-\underset{R}{\overset{H}{C}}-COOH$$

↓

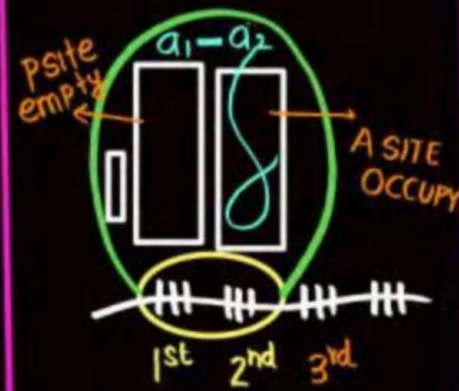
PEPTIDE BOND

(PEPTIDYL TRANSFERASE ENZYMES)

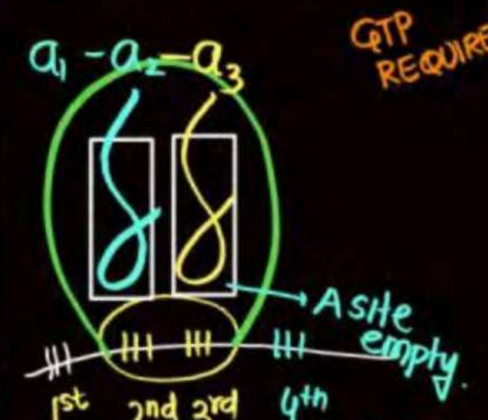
23S rRNA	28S rRNA
(PROK)	(EUK)
(50S)	(60S)

$\boxed{\text{RIBOZYME}}$ → RNA ACT AS ENZYME (CATALYST)

⇒ tRNA at P SITE DEGRADED & MOVES OUT THROUGH EXIT



⇒ movement/SLIDING of RIBOSOME ON mRNA.
RUN → 1 CODON/3 BASE



1 ATP
2 GTP

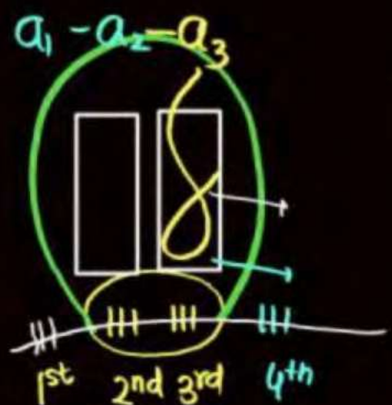
NOTE : ELONGATION FACTOR.

PRO : EF-TU, EF-TS, EF-G

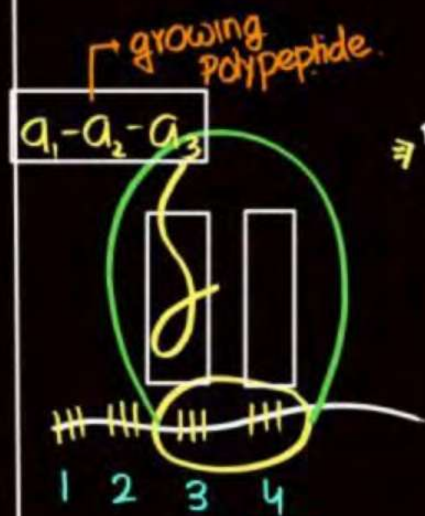
EUK : eEF-1 , eEF-2

TERMINATION

tRNA OF 'P' SITE DEGRADE & MOVES OUT THROUGH 'E' SITE



RIBOSOME AGAIN MOVE



UAA (stop codon: no tRNA).

⇒ PROTEIN SYNTHESIS STOP.

LAST AMINO ACID/ growing polypeptide chain at 'P' site

RELEASING FACTOR (PROTEIN) → SEPERATE POLYPEPTIDE CHAIN FROM tRNA.

RF-1

RF-2

GTP CONSUMED

★ 1 ATP: activation of amino acid

★ 1 GTP: SLIDING.

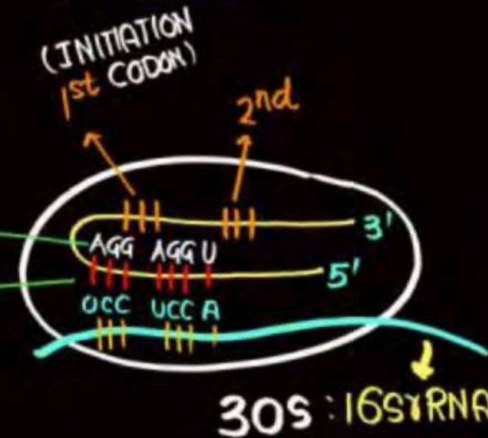
★ 1 GTP: tRNA BIND AT A SITE

MRNA

UTR: UNTRANSLATED REGION IN mRNA BEFORE IC & after TC

: PROTEIN NOT FORMED BUT THEY MAKES TRANSLATION EFFICIENT.

PROKARYOTES

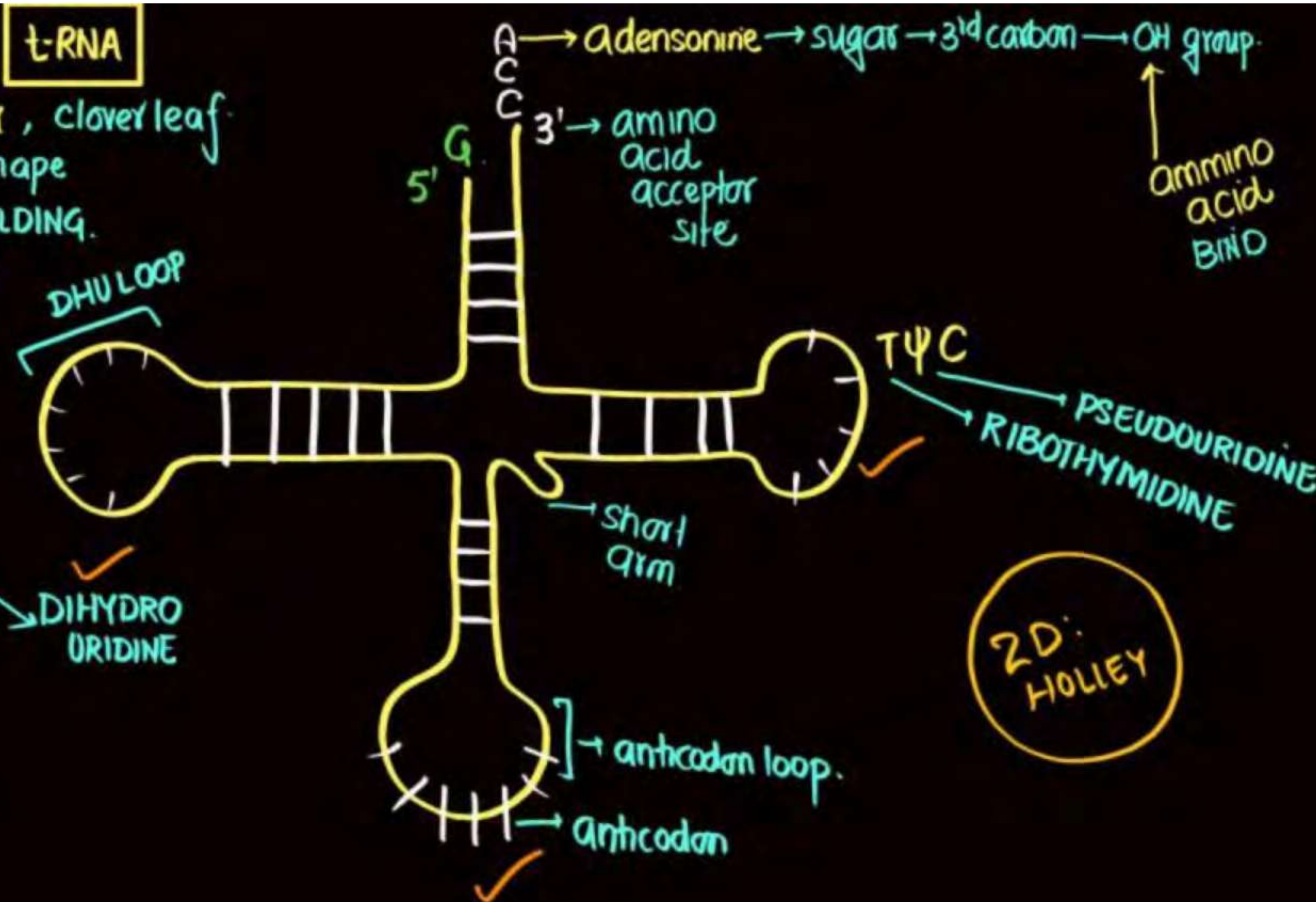


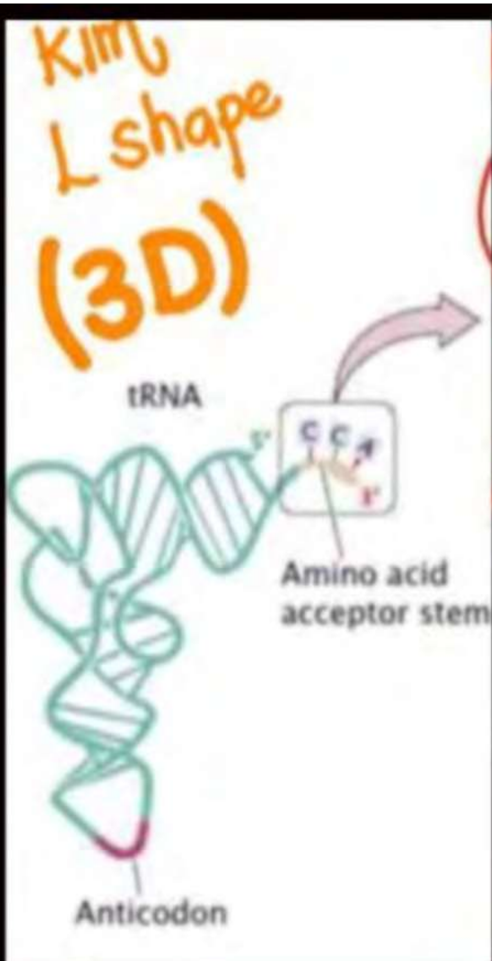
UTR

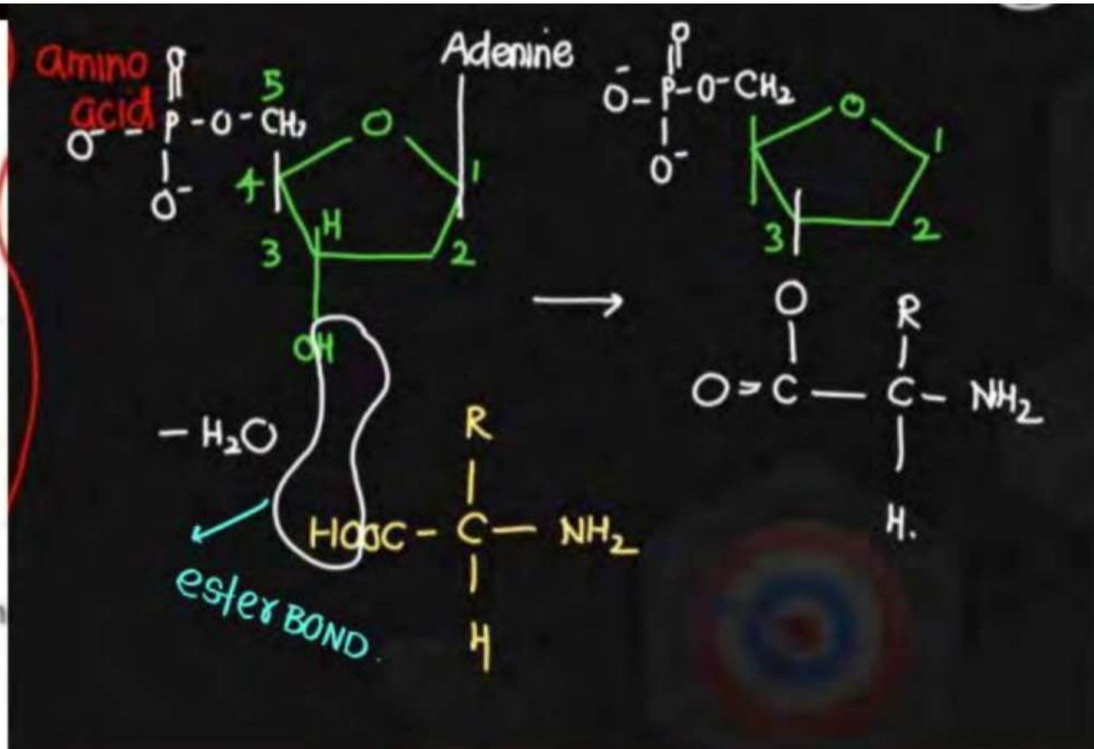
SHINE-DELGERNO SEQUENCE (SD SEQUENCE)

t-RNA

- ⇒ 2D / SECONDARY ST : HOLLEY , Clover leaf.
- ⇒ 3D : KIM. , Inverted L Shape
- ⇒ single strandard : BUT FOLDING.
  so it appear as double strand.
- ⇒ 5' end : GUANINE.
- ⇒ 3'end : CCA sequence.
- ⇒ Some abnormal Base present
  Pairing NOT POSSIBLE : LOOP ARE FORMED




Kim
L shape
(3D)
tRNA
Amino acid acceptor stem
Anticodon


amino acid
Adenine
− H2O
ester BOND

	mRNA	tRNA	rRNA
Synthesis	RNA POL-II	RNA POL-III	RNA POL-I
Location	NUCLEUS	NUCLEUS	NUCLEOLUS.
Adapter RNA	×	adapter b/w amino acid & codon. ✓ a_1 mRNA	×
Soluble RNA	×	codon SOLUBLE IN NACL. ✓	×
Size	small	smallest	Largest
Percentage	1- 5%	10-15%	50-80%

REGULATION
OF $\boxed{\text{GENE EXPRESSION}}$

DNA ⟶ PROTEIN

EUKARYOTES

* DNA ⟶ Immature mRNA (PRIMARY TRANSCRIPT)
* Immature mRNA $\xrightarrow[\text{SPLICING}]{\text{PROCESSING/}}$ mature mRNA
* mature mRNA (NUCLEUS) $\xrightarrow{\text{MOVE}}$ mature mRNA (CYTOPLASM)
* mature mRNA $\xrightarrow{\text{TRANSLATION}}$ PROTEIN

PROKARYOTES

⇒ DOMINANT SITE :

INITIATION OF TRANSCRIPTION

$\boxed{\text{WAIT}}$

LAC OPERON. (PROKARYOTES). → BACTERIA.

⇒ METABOLISM OF LACTOSE (CATABOLISM).
(BREAKDOWN) DISSACHARIDE.

⇒ SEGMENT OF DNA. WHICH CONSIST OF

GENE

* REGULATOR
* PROMOTER
* OPERATOR
* STRUCTURAL

→ CONTROL

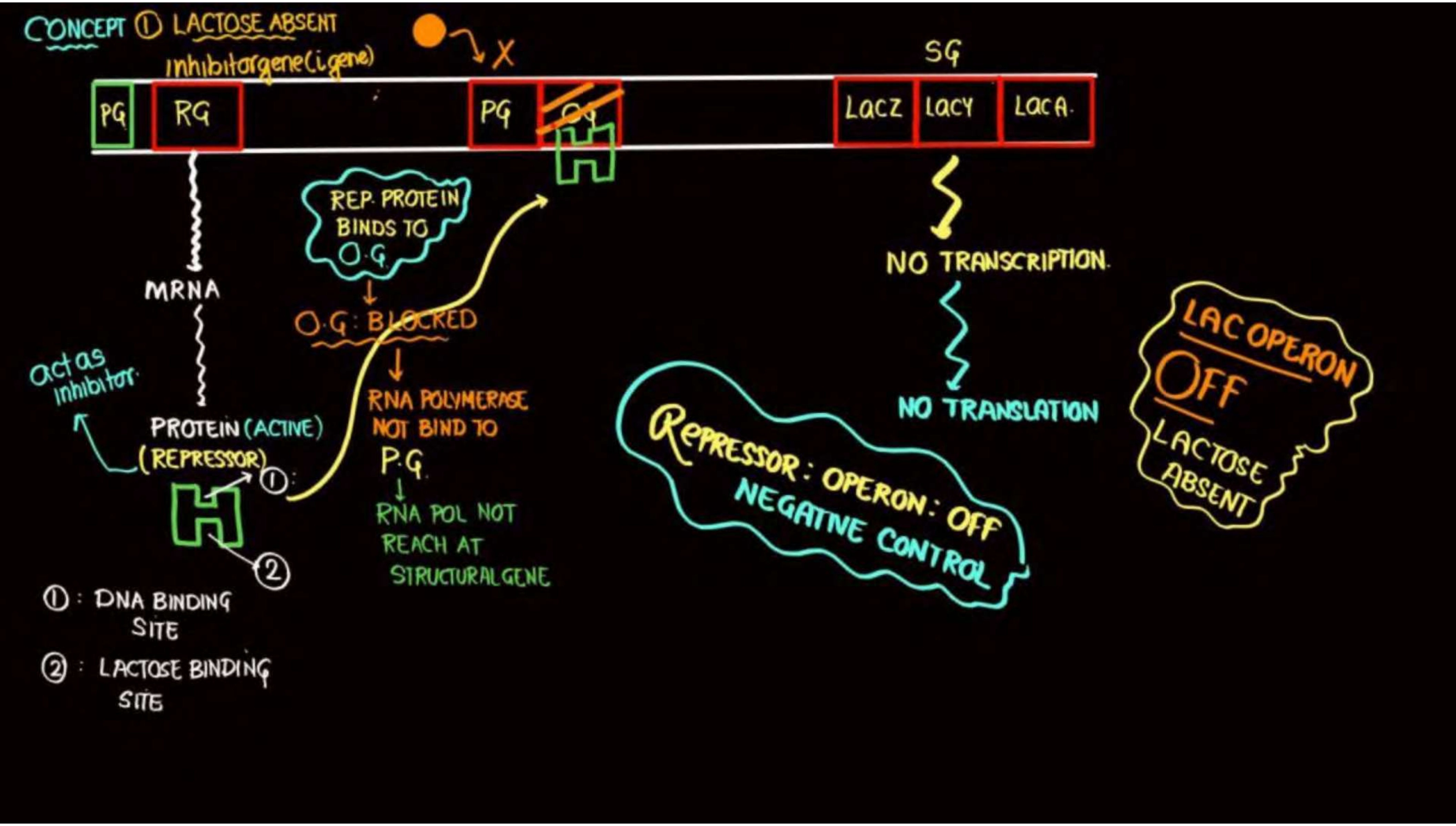
Jacob

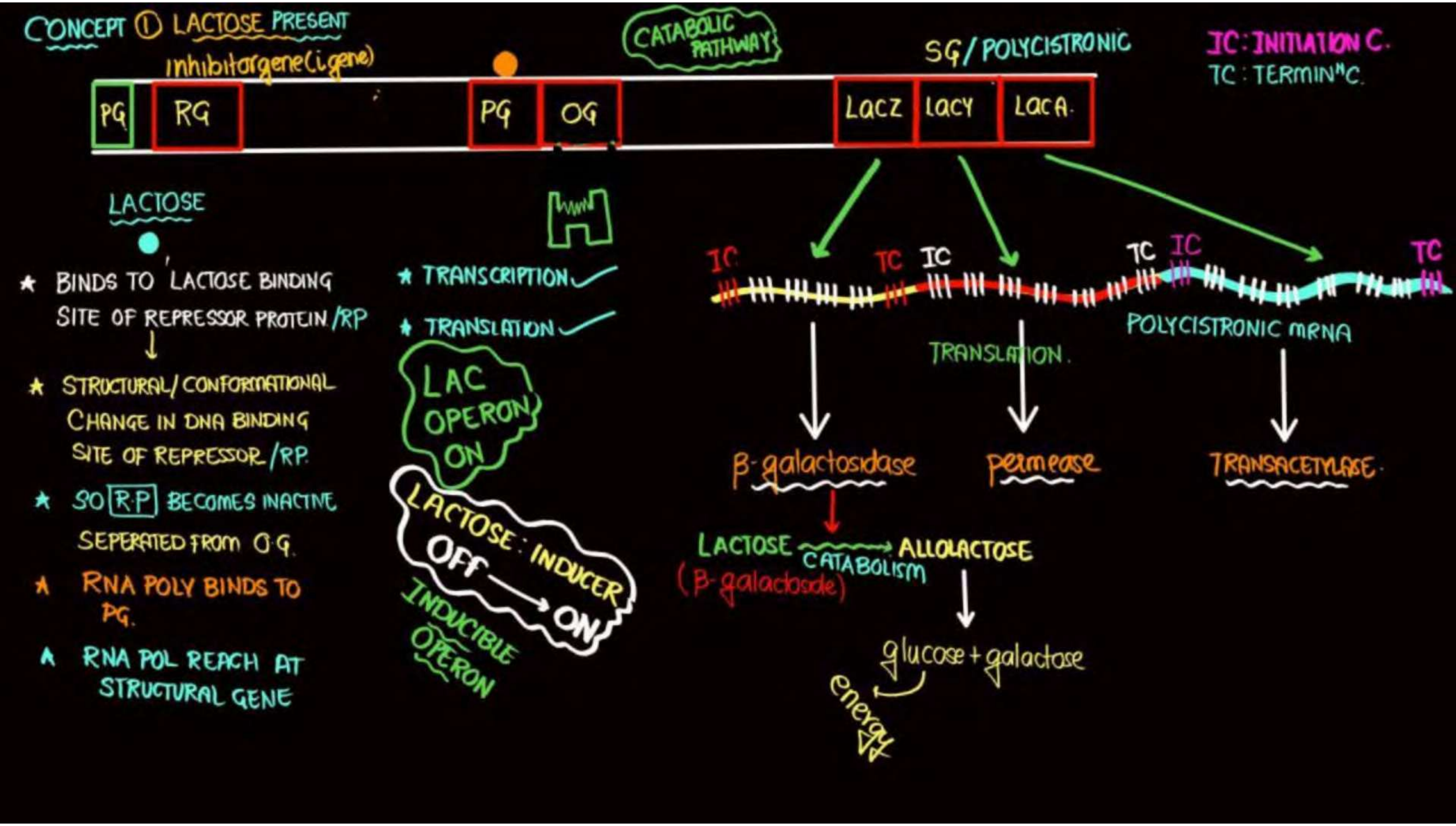
MONOD

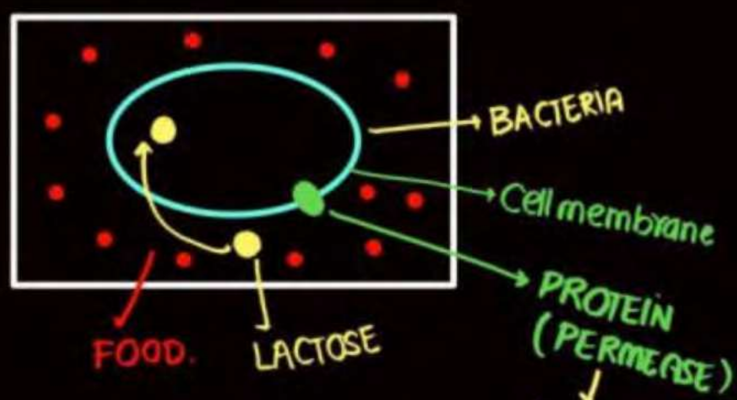
ENERGY.

↑

* LACTOSE ⟶ $\boxed{\text{glucose}}$ + galactose


CONCEPT ① LACTOSE ABSENT
Inhibitorgene(i gene)
X
SG
PG
RG
PG
OG
Lacz
Lacy
Laca.
REP. PROTEIN BINDS TO O.G.
O.G: BLOCKED
RNA POLYMERASE NOT BIND TO P.G.
RNA POL NOT REACH AT STRUCTURALGENE
MRNA
act as inhibitor.
PROTEIN (ACTIVE)
(REPRESSOR)
①
②
① : DNA BINDING SITE
② : LACTOSE BINDING SITE
NO TRANSCRIPTION.
NO TRANSLATION
REPRESSOR : OPERON : OFF
NEGATIVE CONTROL
LAC OPERON
OFF
LACTOSE ABSENT


CONCEPT ① LACTOSE PRESENT
inhibitorgene(i gene)
CATABOLIC PATHWAY
SG/POLYCISTRONIC
IC: INITIATION C.
TC: TERMINⁿC.
PG
RG
PG
OG
Lacz
lacy
LacA.
LACTOSE
★ BINDS TO LACTOSE BINDING SITE OF REPRESSOR PROTEIN/RP
★ STRUCTURAL/CONFORMATIONAL CHANGE IN DNA BINDING SITE OF REPRESSOR/RP.
★ SO R.P BECOMES INACTIVE SEPERATED FROM O.G.
★ RNA POLY BINDS TO PG.
★ RNA POL REACH AT STRUCTURAL GENE
★ TRANSCRIPTION
★ TRANSLATION
LAC OPERON ON
LACTOSE: INDUCER
OFF → ON
INDUCIBLE OPERON
IC
TC
IC
TC
IC
TC
POLYCISTRONIC mRNA
TRANSLATION.
β-galactosidase
permease
TRANSACETYLASE.
LACTOSE
(β-galactoside)
CATABOLISM
ALLOLACTOSE
glucose + galactose
energy



↓

entry of LACTOSE INO BACTERIA.

(ACTIVE TRANSPORT).

⇒ SOME TOXIC SUBSTANCE CAN ENTER INTO CELL

DETOXIFICATION

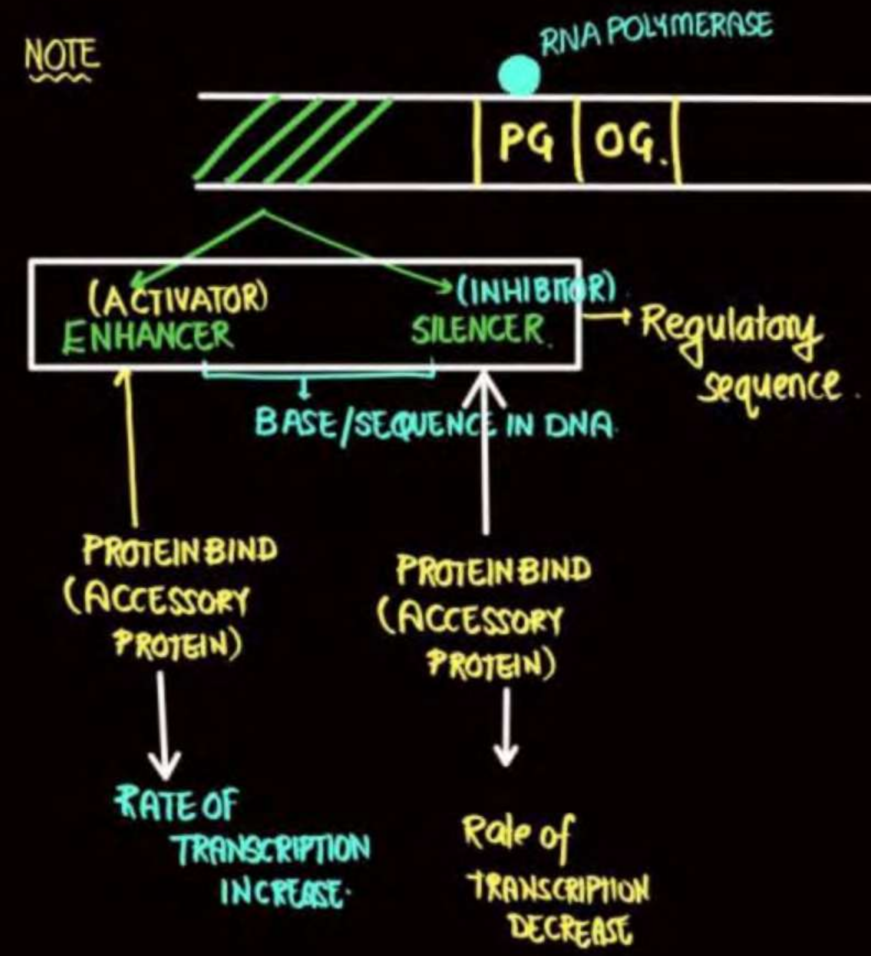
(TRANSACETYLASE).

SECRET

⇒ LACTOSE : ENTER → LAC OPERON ON → PERMEASE बनेगा.

पहले   बाद मे.

⇒ very very low Level of enzymes present in Bacteria.
Otherwise lactose will NOT ENTER INTO CELL.


NOTE
RNA POLYMERASE
S.G.
PG
OG.
(ACTIVATOR)
ENHANCER
(INHIBITOR)
SILENCER
Regulatory sequence.
BASE/SEQUENCE IN DNA
PROTEIN BIND (ACCESSORY PROTEIN)
PROTEIN BIND (ACCESSORY PROTEIN)
RATE OF TRANSCRIPTION INCREASE.
Rate of TRANSCRIPTION DECREASE

POSITIVE CONTROL OF LAC OPERON

glucose absent
Lactose present

↓ FORMED

$\boxed{\text{CAMP}}$ ●

└→ BIND

CATABOLIC ACTIVATOR PROTEIN ● (CAP)

→ RNA POLYMERASE BINDS TO P.G.

↓

TRANSCRIPTION START.

glucose present, LACTOSE ABSENT

- NO cAMP
- NO COMPLEX FORMED.
- NO BINDING TO CAP SITE
- RNA polymerase not able to BIND AT P.G.
- SO NO TRANSCRIPTION

Q. If BOTH GLUCOSE &
LACTOSE GIVEN TO
BACTERIA

BACTERIA FIRST
UTILISE 'GLUCOSE' (Lac op. OFF)

ONCE glucose FINISHED

then: operon: ON.
(Lactose)

Catabolic
Repression

Q. If NON SENSE MUTATION OCCUR IN (NON-SENSE/
LacY gene STOP CODON.

WHICH ENZYME FORMED

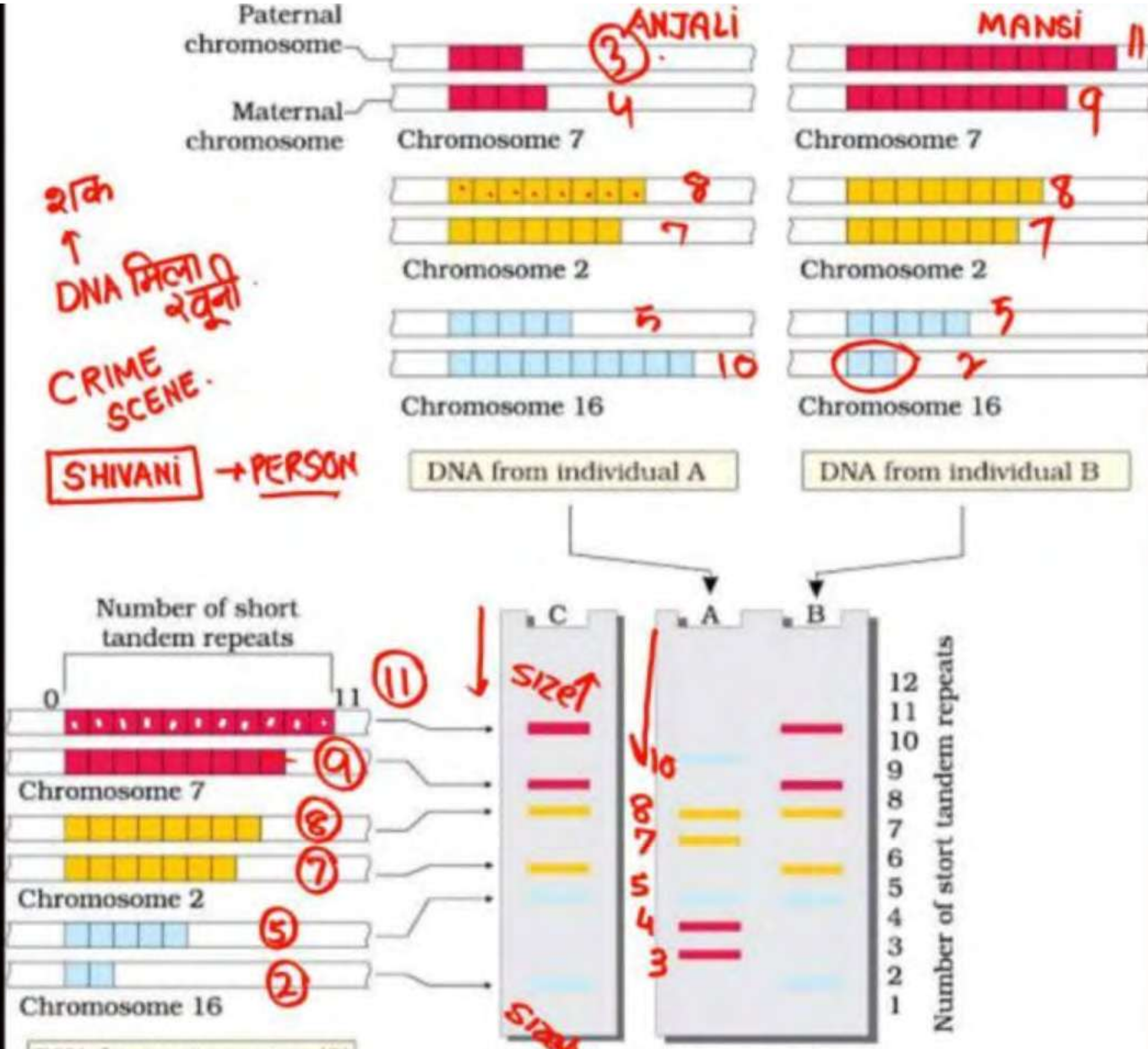
a) β-galacto
b) permease
c) Transacetylase
d) Both (a) & (c)

Q CONSTITUTIVE GENE

eg: Regulator gene
↓
Continously express
↓
Repressor protein

NON-CONSTITUTIVE GENE

eg structural gene
⇒ express if Lactose present



Amplified repeats,separated by size on a gel, give a DNA fingerprint

1 BOX : ATG

DNA fingerprinting / DNA profiling

⇒ Human genome (Haploid set of chromosome : Length : 3.3×10^9 bp : Haploid

⇒ Diploid : length : 6.6×10^9 bp.

⇒ All Human : 99.9% DNA same

⇒ All Human : 0.1% DNA show differences/variation/polymorphism

⇒ Study : 0.1% DNA

⇒ $\dfrac{3.3 \times 10^9 \text{ bp} \times 0.1}{100}$

⇒ $\boxed{3.3 \times 10^6 \text{ bp}}$: variation

0.1% DNA

- Repeat after Regular interval of Time
- Satellite DNA
- Repetitive DNA
- Intronic DNA
- Not code for protein
- $\boxed{3.3 \times 10^6 \text{ bp.}}$

Q All intronic DNA are satellite DNA

a) True b) False

Q All satellite DNA are Intronic DNA

a) True b) False

Satellite DNA

	10^{-6} Microsatellite (Short Tendam Repeat)	10^{-3} Minisatellite / VNTR
	S S S S ATG CAT ATG TAC ATG ATG GAC	GCCGATCGTG TA GCCGATCGTG AT GCCGATCGTG
⇒ No. of Repeating Unit:	Four	Three
⇒ No. of Basepair in one unit	Three Base pair	10bp
⇒ Rich in	AT Rich	GC Rich
⇒ length	Short	Long
⇒ Length of Satellite	1-6 bp	10 bp- 60 bp

Variable Number of Tendam Repeat

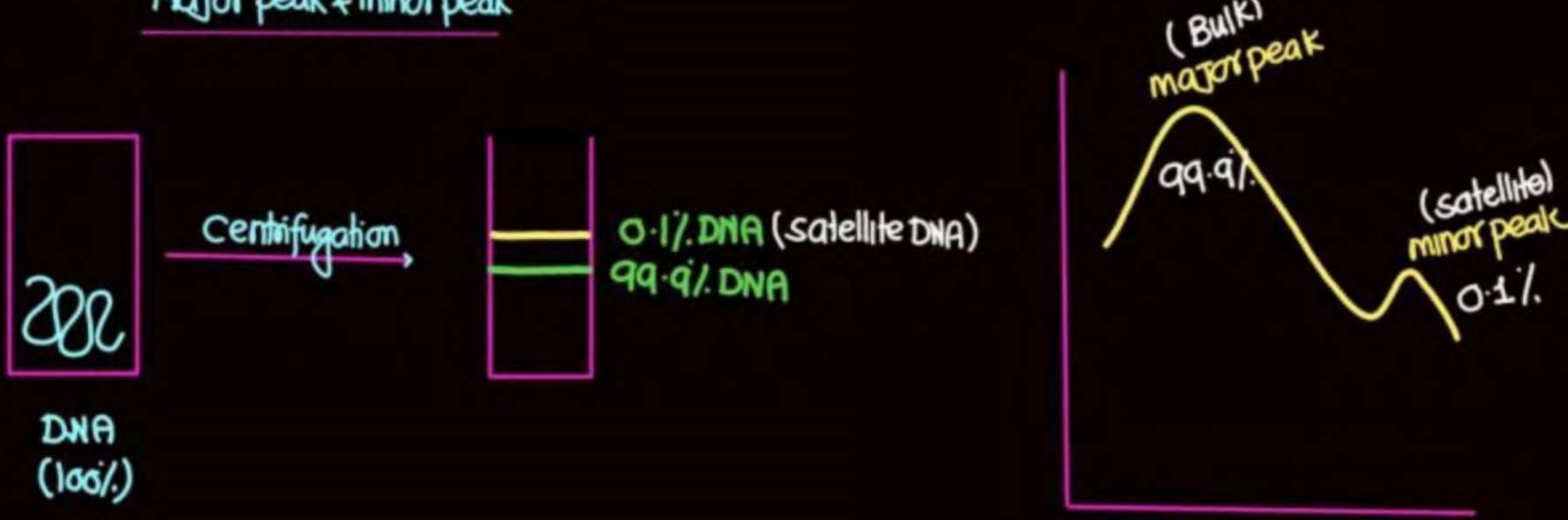
wait

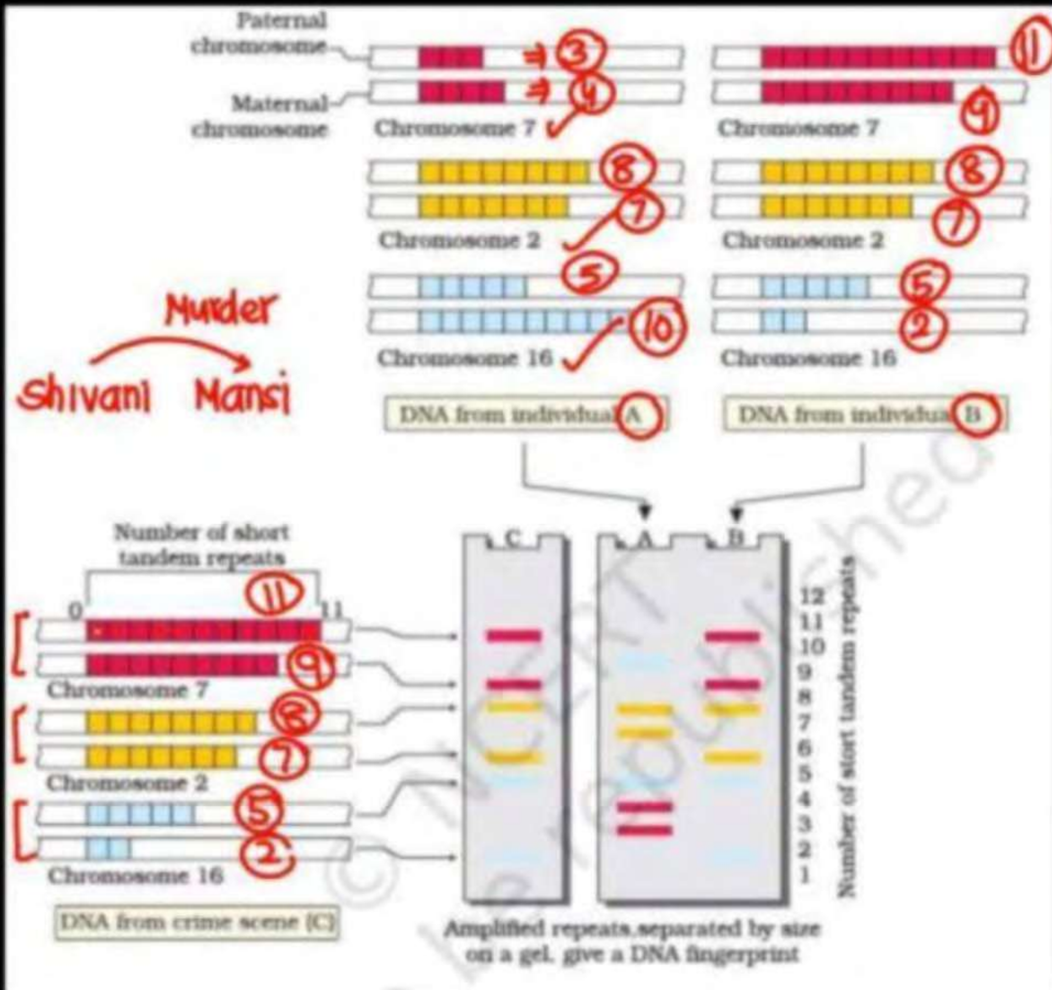
			no. of Repeating unit
Rahul	ATG ATG ATG ATG	Restriction Fragment	4
pinky	ATG ATG ATG ATG ATG ATG ATG	Rest Frag	7
Anjali	ATG ATG ATG ATG ATG ATG ATG ATG	Rest. Frag	8

Restriction endonuclease

Restriction
Fragment
length
Polymorphism (variation)
(RFLP)

Major peak & minor peak





Chrom 7 → 11 Red. / 9 Red

Chrom 2 → 8 yellow / 7 ⇒ yellow

Chrom 16 → 5 ⇒ Blue / 2 ⇒ Blue

STR

1 Box : 1 Repeat : ATG : 3 bp : Microsatellite/

Slide 189

Tandem repeats

4 repeats

Genome 1 CTAGAGATAGATAGATAGATACTAGAC 4

Genome 3 CTAGAGATAGATAGATAGATAGATACT 5

5 repeats

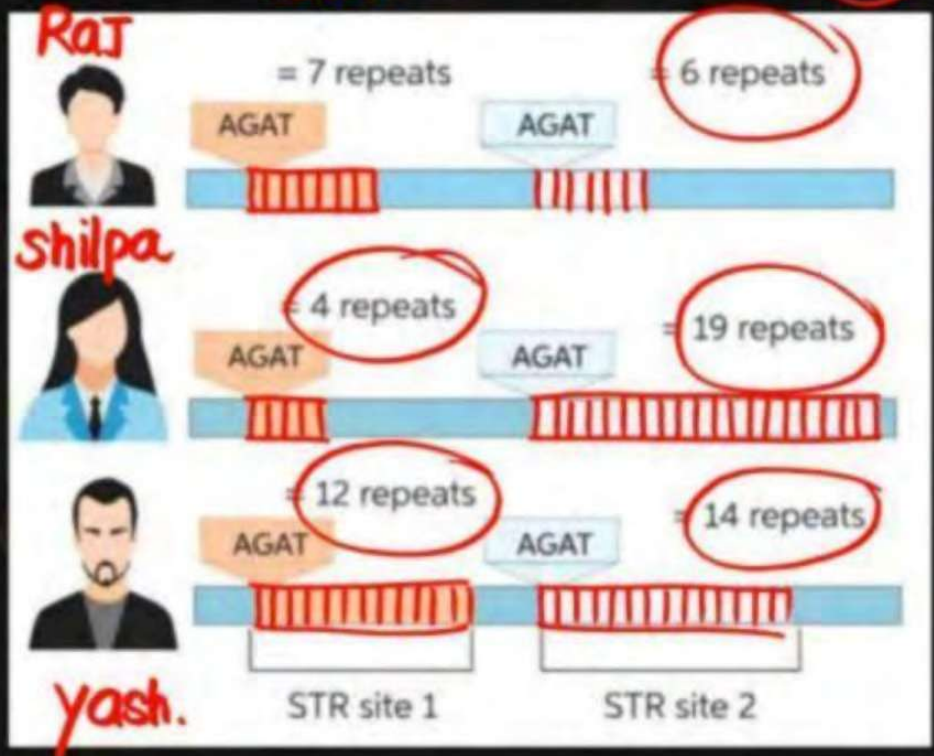
don't write

Short Tandem
Repeats

Sample 1 CTAGAGATAGATAGATAGATAGATAGATAGATACTAGACTAGACTAG - 7
Sample 2 CTAGAGATAGATAGATAGATAGATAGATAGATAGATACTAGACTAGA - 8
Sample 3 CTAGAGATAGATAGATAGATAGATAGATAGATAGATAGATACTAGAC - 9

Slide 10

Chromosome = 7 = 13



1 Repeat ⇒ AGAT (4 bp) : STR/Microsatellite

AGAT AGAT AGAT AGAT AGAT AGAT AGAT

person : 1 ⇒ AGAT ⇒ 7+6 ⇒ 13

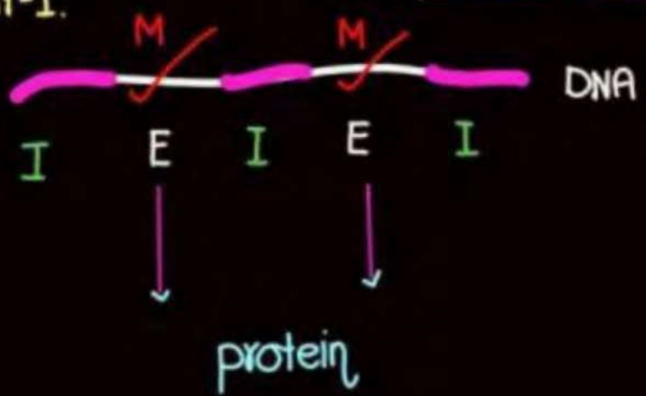
person 2 ⇒ AGAT ⇒ 4+19 ⇒ 23

person 3 ⇒ AGAT ⇒ 12+14 = 26

Repeating unit vary in all individual.

Part-1.

Why 0.1% Region show variation



⇒ If Mutation occur in exonic part then these changes express immediately in form of Normal / abnormal protein, (mostly)

↓

Effect Reproductive capacity

so mutation Not Transmit to Next gen^n

↓

That mutation will disappear after Death.

★ I : Intron

★ E : Exon

★ M : Mutation

part ②

if Mut^n occur in intronic part of DNA

↓

It won't express immediately Bz intron Not form protein,

↓

But it modify the sequence a Bases in DNA

↓

These changes inherit from one gen^n to another gen^n is the Basis of DNA fingerprinting.

Technique

Chromosome: 6

⇒ Crime:	Hair/sperm/Blood(WBC) (Isolate DNA)	Person A (Mansi)	Person B (shivani)
a) DNA isolation		ATATATGCA 3 Repeat (satellite)	CGCGCGATA 3 Repeat (satellite)
b) Restriction endonuclease Digestion (got satellite DNA)		ATATAT	CGCGCG
c) Gel electrophoresis (Towards anode)		ATATAT (DNA on gel)	CGCGCG (DNA on gel)

Double strand DNA

d) Southern Blotting

ATATAT
(DNA on gel)

Treated with chemical

CGCGCG
(DNA on gel)

DNA Becomes single strand.

Transfer of DNA from Gel to Nylon / Nitrocellulose membrane
Called Southern Blotting

ATATAT

CGCGCG

Nylon memb

e) probe Hybridisation

⇒ Artifically DNA synthesis (singlestrand)

TATATA

Radioactive substance

(F) AutoRadiography (X Rays)

CRIME SCENE

DNA

↓

Study

↓

Find Base sequence of that DNA

ATATAT

(satellite)

TATATA
ATATAT

Mansi

Complem. Base pairing हुआ

(probe present)

Flurescence show ✓

TATATA
GCGCG

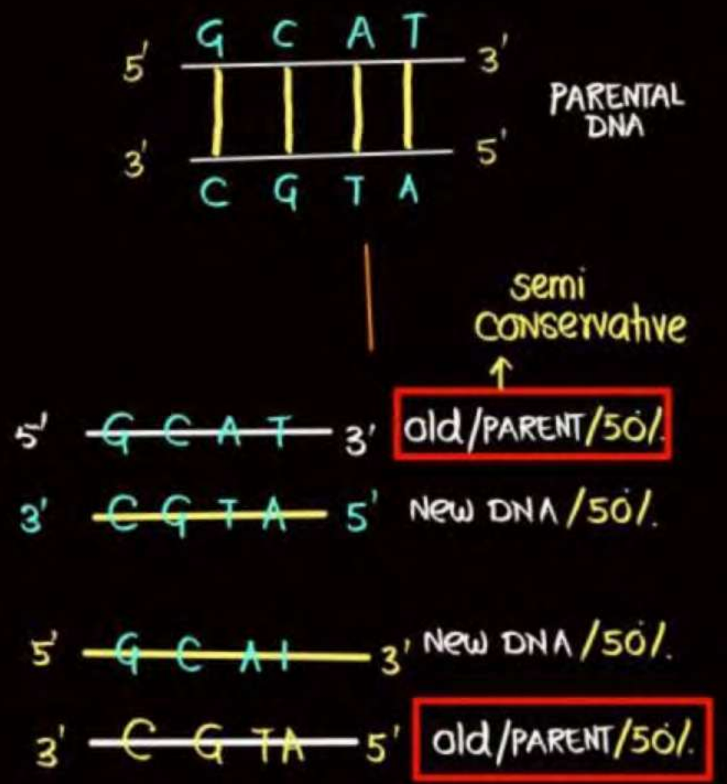
Nylon memb

Shivani

No pairing probe wash out

No flurescence.

SEMICONSERVATIVE MODE OF REPLICATION



1st Time: study: E. Coli (Bacteria)

Plants (vicia faba/Beans)
Human cells
} → HIGHER ORGANISM.

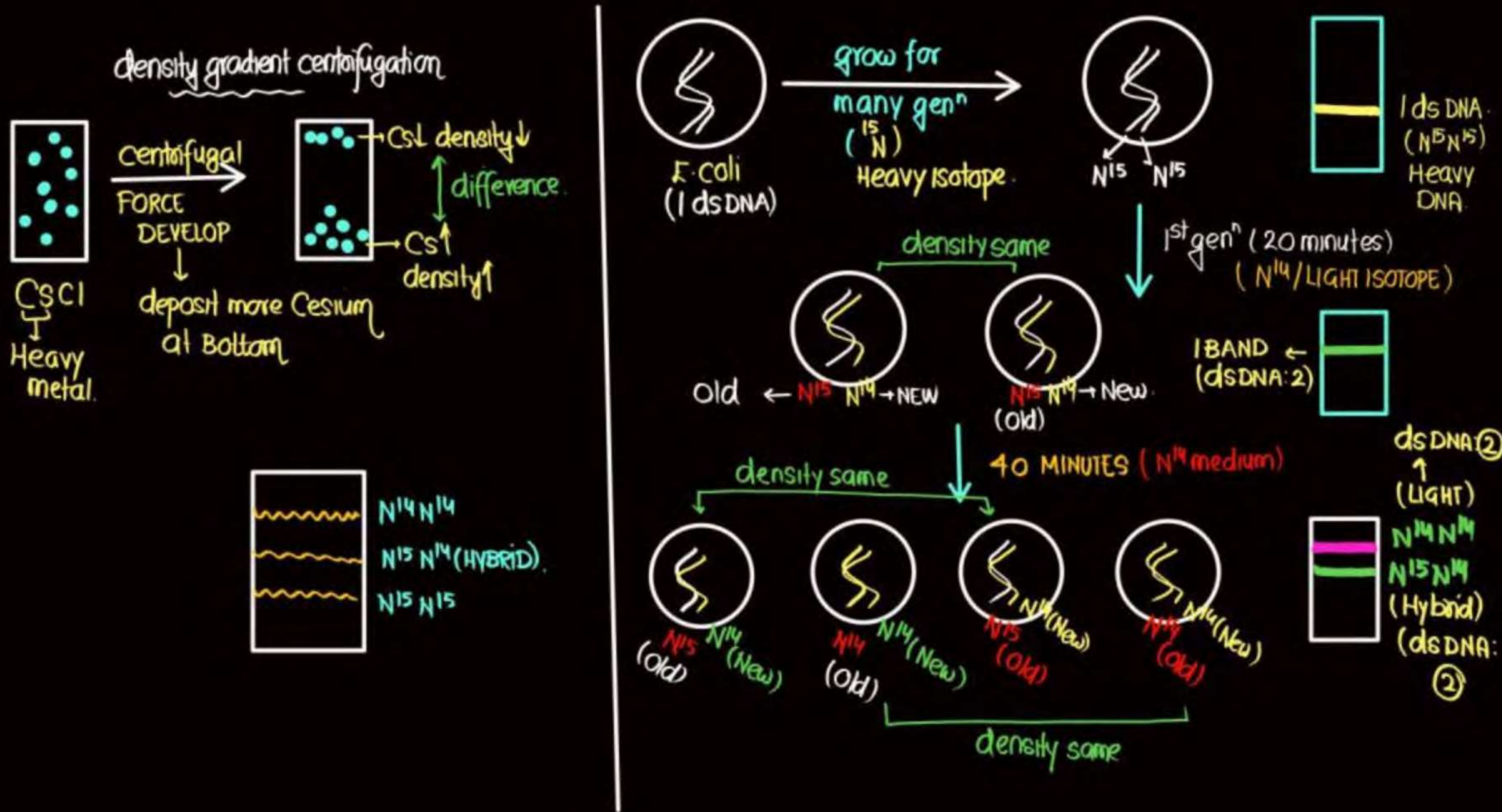
① MATTHEW MESSELSON & FRANKLIN STAHL

1958, E. Coli, (PROKARYOTE).

Heavy Isotope: $^{15}NH_4Cl \Rightarrow \boxed{^{15}N}$

Light Isotope: $^{14}NH_4Cl \Rightarrow \boxed{^{14}N}$

density gradient centrifugation Technique.
(CsCl)


density gradient centrifugation
centrifugal FORCE DEVELOP
deposit more Cesium at Bottom
CsCl
Heavy metal
CsCl density↓
difference
Cs↑ density↑
N14 N14
N15 N14 (HYBRID)
N15 N15
E. coli (1 ds DNA)
grow for many genn (15N) Heavy isotope
N15 N15
1 ds DNA (N15 N15) Heavy DNA
1st genn (20 minutes) (N14/LIGHT ISOTOPE)
density same
Old ← N15 N14 → NEW
N15 N14 → New (Old)
1 BAND ← (dsDNA: 2)
40 MINUTES (N14 medium)
density same
N15 (Old) N14 (New)
N14 (Old) N14 (New)
N15 (Old) N14 (New)
N14 (Old) N14 (New)
density same
dsDNA: 2 (LIGHT)
N14 N14
N15 N14 (Hybrid) (dsDNA: 2)

generation	Time (minutes)	Heavy DNA ($N^{15}N^{15}$)	Hybrid DNA ($N^{15}N^{14}$)	Light DNA ($N^{14}N^{14}$)
1st	20	0	2	0
2nd	40	0	2	0 + 2 = 2
3rd	60	0	2	2 + 4 = 6
4th	80	0	2	6 + 8 = 14

SHORT CUT

$N^{15}N^{15}$

$\downarrow N^{14}$ (1^{st} gen^n)

$N^{15}N^{14}$ $\quad$ $N^{15}N^{14}$

$\downarrow N^{14}$ (2^{nd} gen^n).

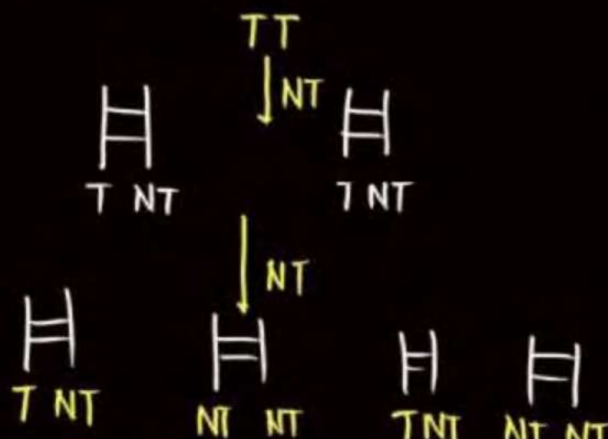
$N^{15}N^{14}$ $\quad$ $N^{14}N^{14}$ $\quad$ $N^{15}N^{14}$ $\quad$ $N^{14}N^{14}$.

② Taylor.

Beans / vicia faba, (EUKARYOTE).

Radioactive Thymidine

Q Both strand of Bactena have Thymidine grow for Two gen^n in NON-Radioactive Thymidine

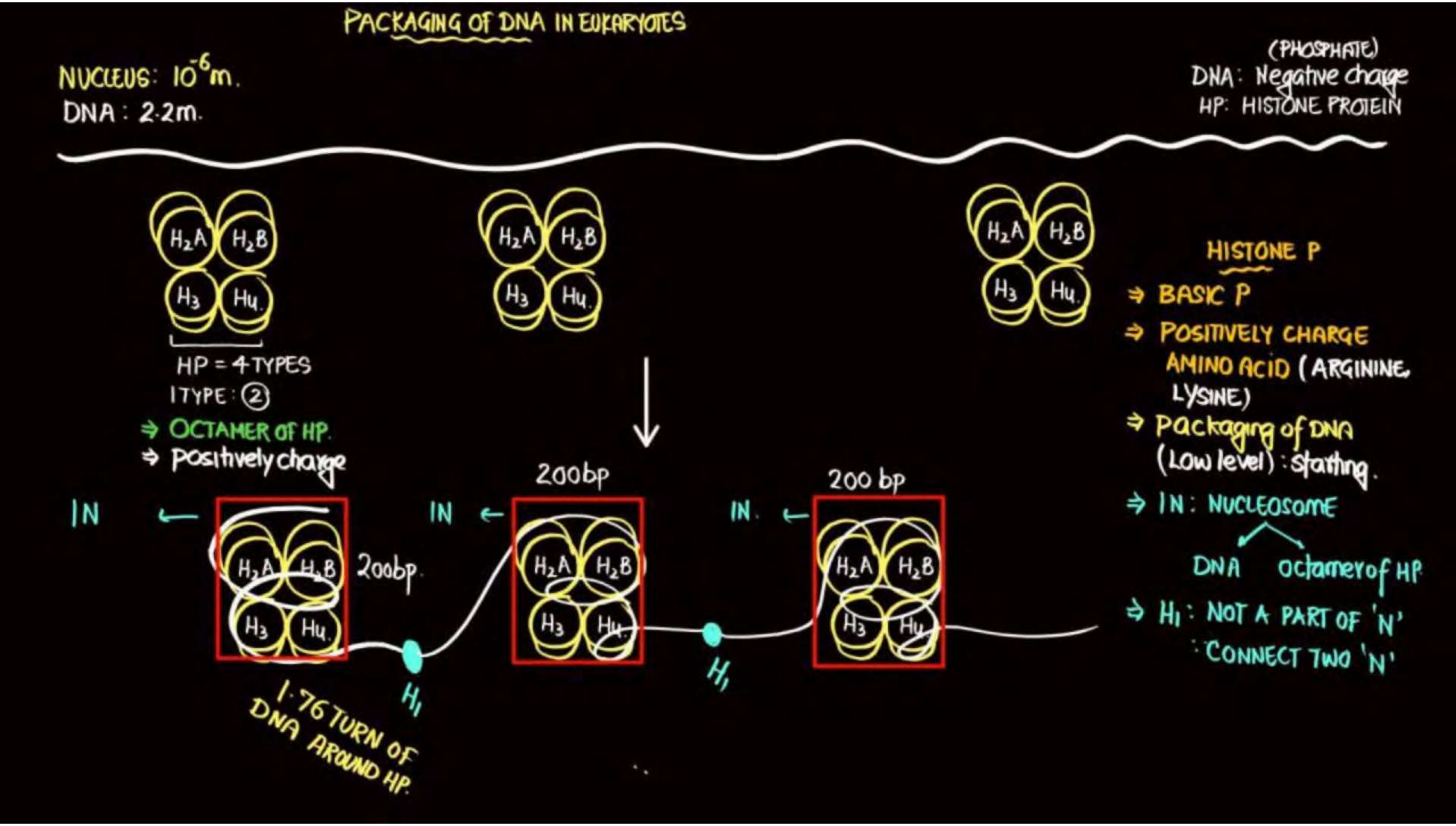


③ CAIRNS

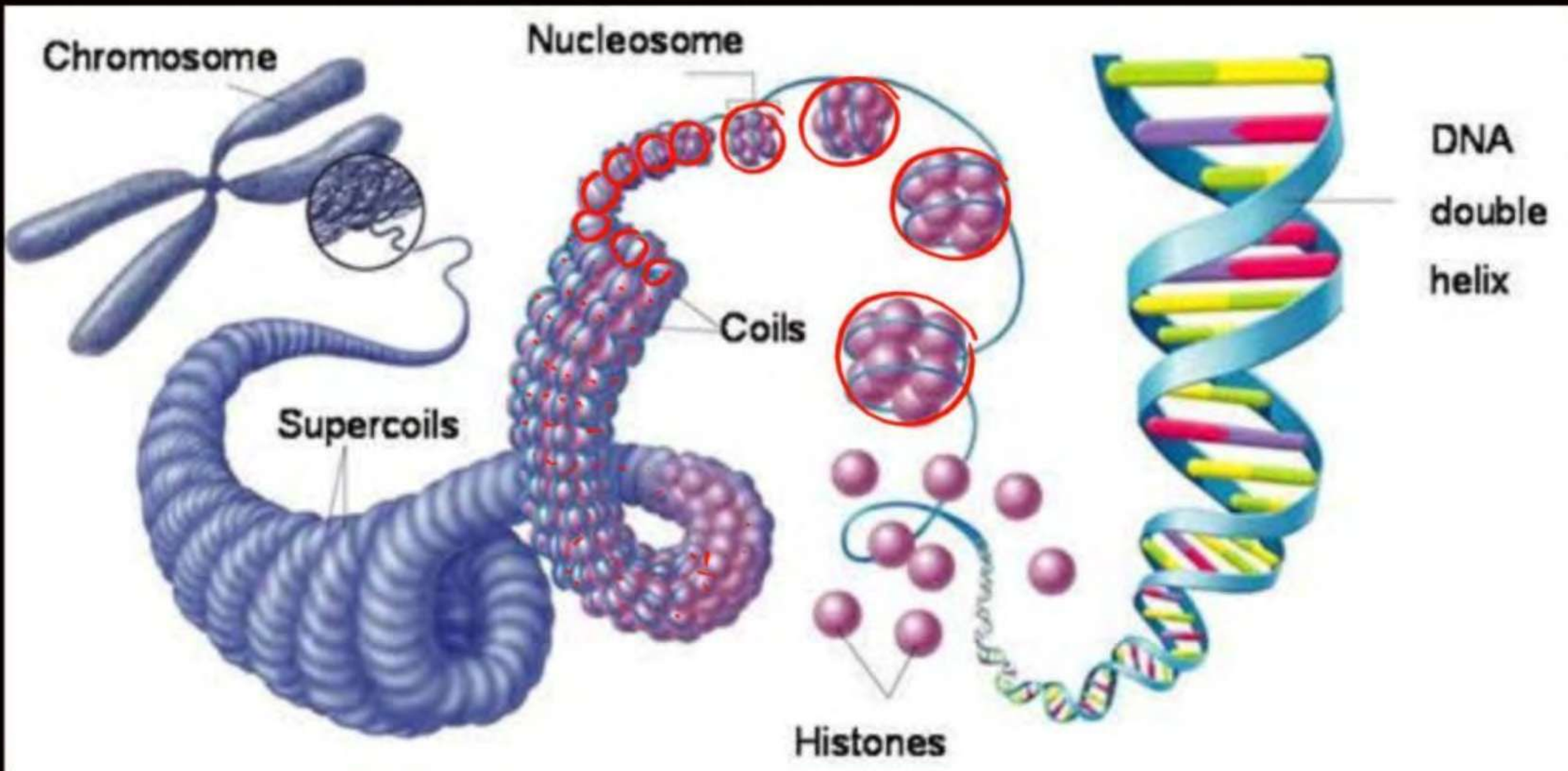
Radioactive Thymidine

E. coli

(PROKARYOTE)


PACKAGING OF DNA IN EUKARYOTES
NUCLEUS: 10^{-6}m.
DNA: 2.2m.
(PHOSPHATE)
DNA: Negative charge
HP: HISTONE PROTEIN
H_2A H_2B H_3 H_4
HP = 4 TYPES
1 TYPE: 2
⇒ OCTAMER OF HP.
⇒ Positively charge
IN
200bp.
H_1
1.76 TURN OF DNA AROUND HP.
200bp
200 bp
HISTONE P
⇒ BASIC P
⇒ POSITIVELY CHARGE AMINO ACID (ARGININE, LYSINE)
⇒ Packaging of DNA (Low level): starting.
⇒ IN: NUCLEOSOME
DNA
octamer of HP
⇒ H_1: NOT A PART OF 'N'
: CONNECT TWO 'N'

PACKAGING OF DNA IN EUKARYOTES



(SCAFFOLD PROTEIN)

A DNA + HP ⟶ NUCLEOSOME ⟶ MORE PACKAGING + NON HIST. PROTEIN ⟶ Chromatin

(BASIC)

↓

LOW LEVEL

MORE NUCLEOSOME

(ACIDIC)/

HIGH LEVEL

(INTERPHASE)

↓

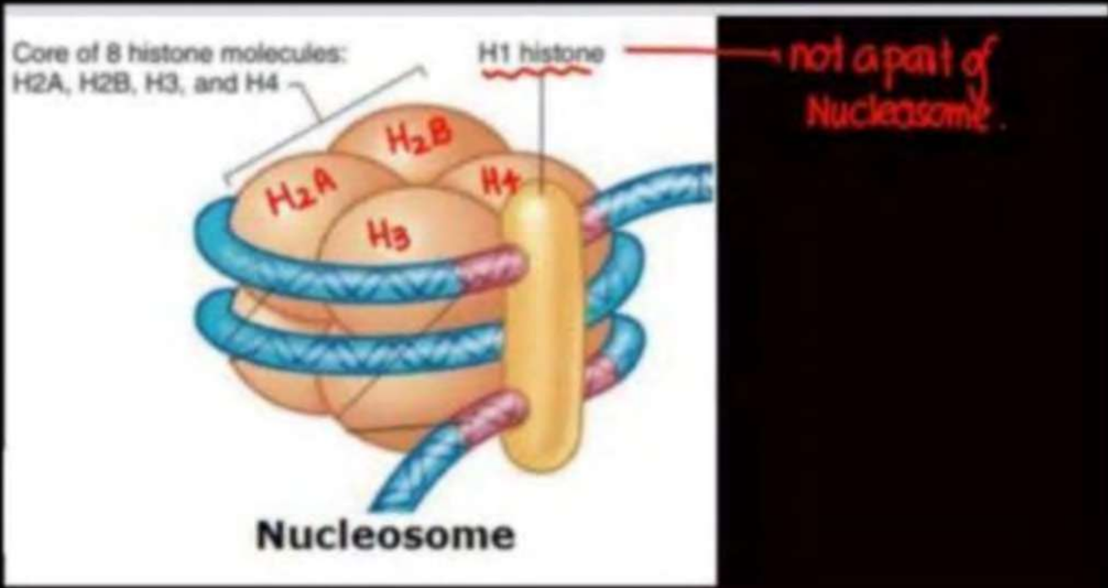
Chromatin

Condensed chromosome

↓

COND. CHROMOSOME

(METAPHASE)


Core of 8 histone molecules:
H2A, H2B, H3, and H4
H1 histone
not a part of Nucleosome.
H2B
H2A
H4
H3
Nucleosome

Slide 43

Q: How many Beads (Nucleasome) in eukaryotic DNA.

No. of Nucleasome : $\dfrac{6.6 \times 10^9\ bp}{200\ bp}$

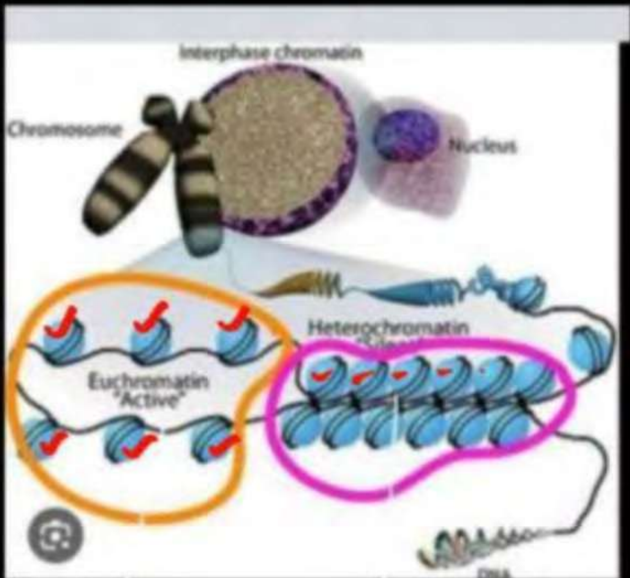
$\Rightarrow \boxed{3.3 \times 10^7}$

Q If length of E. coli : 1.36 mm
Can you calculate no. of Base pair in E. coli

$\Rightarrow$ length = no. of Bp x distance B/w bp

$\Rightarrow \dfrac{1.36 \times 10^{-3}\ m}{0.34 \times 10^{-9}\ m}$: no. of Base

$\Rightarrow \boxed{4 \times 10^6\ bp}$

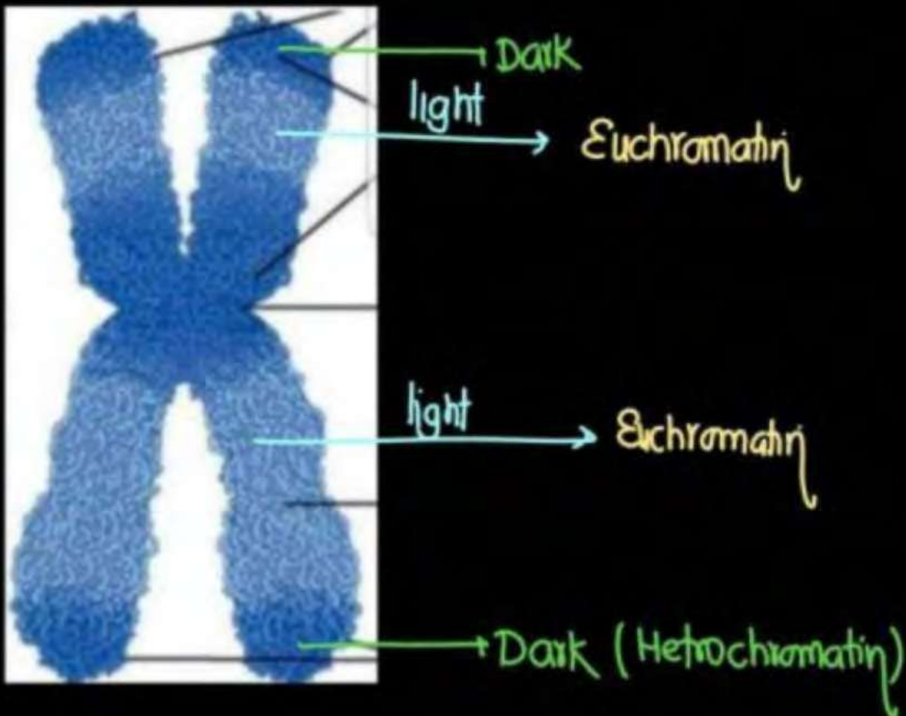


Unwound Wound

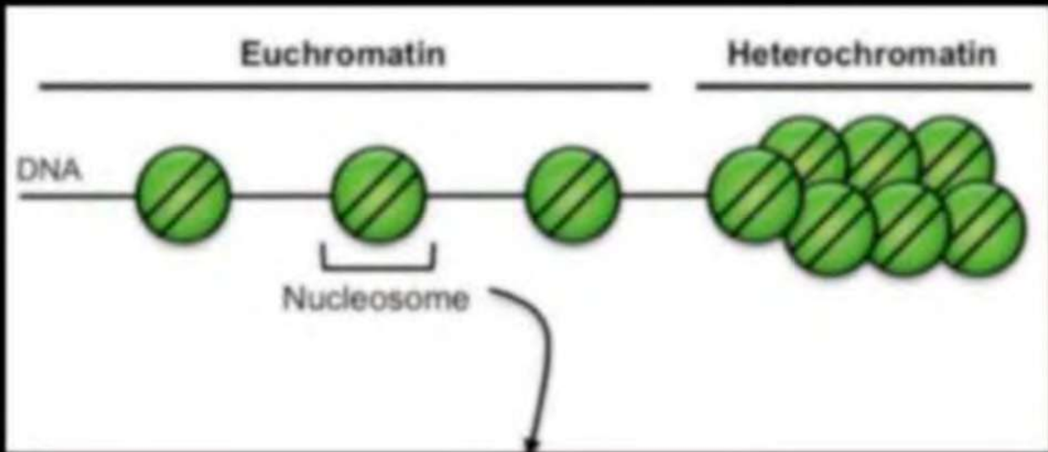
Chromatin

Euchromatin	Hetrochromatin
⇒ loosely packed.	⇒ TIGHTLY PACKED.
⇒ LIGHTLY STAIN	⇒ DARKLY STAIN.
DNA (TRANSCRIPTIONALLY ACTIVE)	DNA (TRANSCRIPTIONALLY INACTIVE).
↓	↓
mRNA	NO mRNA

Slide 42


Dark
light
Euchromatin
light
Euchromatin
Dark (Hetrochromatin)

Slide 45



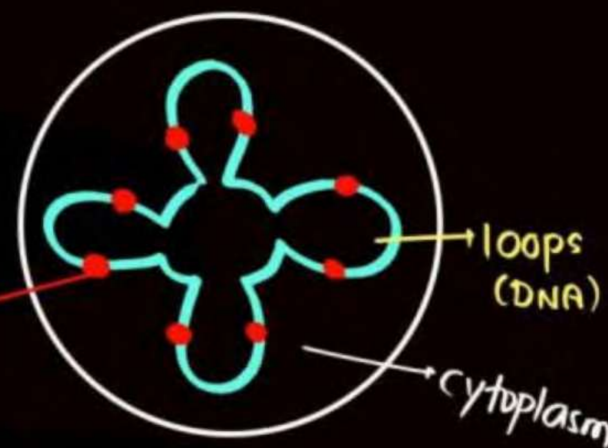
Slide 44

packaging in prokaryotes

⇒ Well defined NUCLEUS ABSENT

⇒ HISTONE PROTEIN: ABSENT
IT DOESN'T MEAN NUCLEUS SCATTERED IN CYTOPLASM.

⇒ PACKAGING: NON HISTONE PROTEIN/POLYAMINE (BASIC)



Topic : NCERT BOOSTER

5.9 Human Genome Project

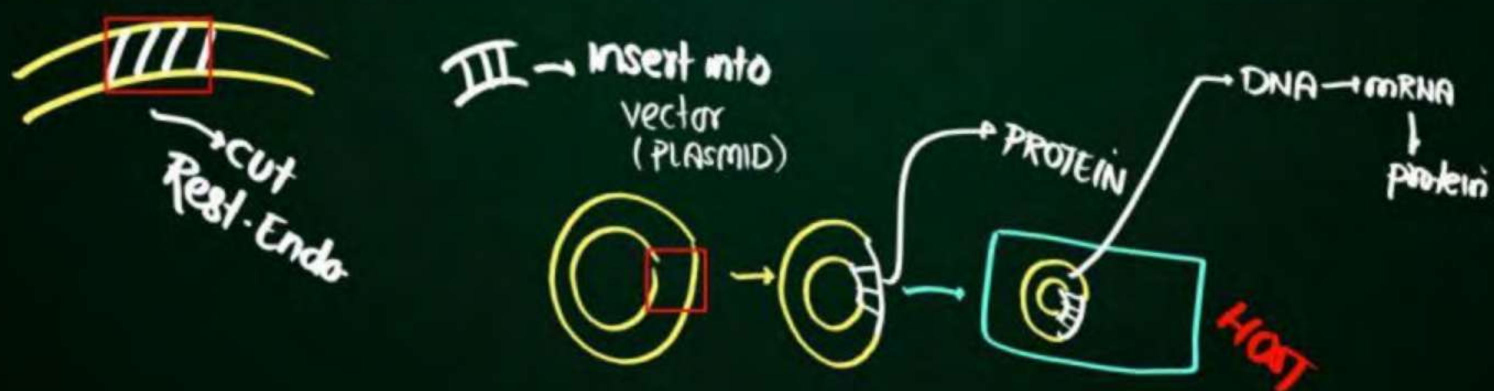
information

DNA (seq^n) $\longrightarrow$ mRNA $\longrightarrow$ PROTEIN

In the preceding sections you have learnt that it is the sequence of bases in DNA that determines the genetic information of a given organism. In other words, genetic make-up of an organism or an individual lies in the DNA sequences. If two individuals differ, then their DNA sequences should also be different, at least at some places. 0.1% = differ.

These assumptions led to the quest of finding out the complete DNA sequence of human genome. With the establishment of genetic engineering techniques where it was possible to isolate and clone any piece of DNA and availability of simple and fast techniques for determining DNA sequences, a very ambitious project of sequencing human genome was launched in the year 1990.

Human Genome Project (HGP) was called a mega project. You can imagine the magnitude and the requirements for the project if we simply define the aims of the project as follows:



haploid

Human genome is said to have approximately $\boxed{3 \times 10^9 \text{ bp}}$ and if the cost of sequencing required is US $ 3 per bp (the estimated cost in the beginning), the total estimated cost of the project would be approximately 9 billion US dollars. Further, if the obtained sequences were to be stored in typed form in books, and if each page of the book contained 1000 letters and each book contained 1000 pages, then 3300 such books would be required to store the information of DNA sequence from a single human cell. The enormous amount of data expected to be generated also necessitated the use of high speed computational devices for data storage and retrieval, and analysis. HGP was closely associated with the rapid development of a new area in biology called **Bioinformatics.**

Goals of HGP

Some of the important goals of HGP were as follows:

(i) Identify all the approximately 20,000-25,000 genes in human DNA;

(ii) Determine the sequences of the 3 billion chemical base pairs that make up human DNA;

(iiii) Store this information in databases;

(iv) Improve tools for data analysis;

(v) Transfer related technologies to other sectors, such as industries;

(vi) Address the ethical, legal, and social issues (ELSI) that may arise from the project.

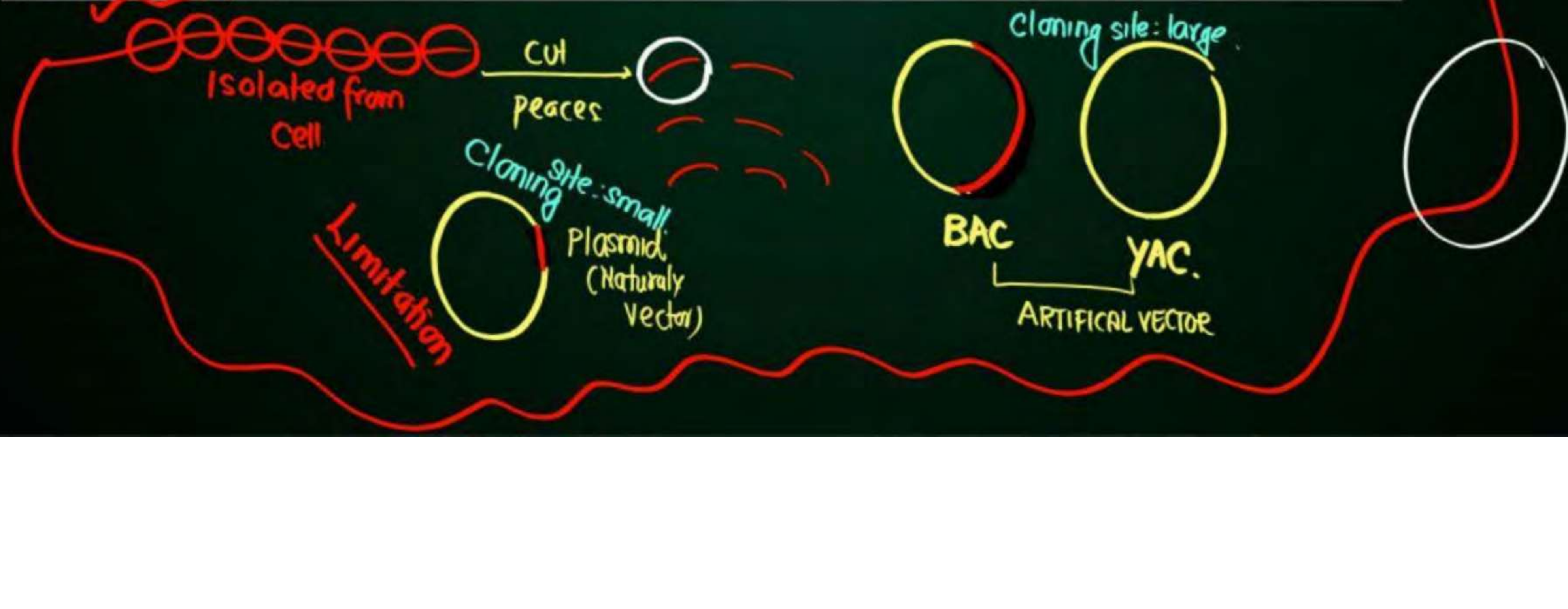
The Human Genome Project was a 13-year project coordinated by the U.S. Department of Energy and the National Institute of Health. During the early years of the HGP, the Wellcome Trust (U.K.) became a major partner; additional contributions came from Japan, France, Germany, China and others. The project was completed in 2003. Knowledge about the effects of DNA variations among individuals can lead to revolutionary new ways to diagnose, treat and someday prevent the thousands of disorders that affect human beings.

Besides providing clues to understanding human biology, learning about non-human organisms DNA sequences can lead to an understanding of their natural capabilities that can be applied toward solving challenges in health care, agriculture, energy production, environmental remediation. Many non-human model organisms, such as bacteria, yeast, *Caenorhabditis elegans* (a free living non-pathogenic nematode), *Drosophila* (the fruit fly), plants (rice and *Arabidopsis*), etc., have also been sequenced.

Methodologies : The methods involved two major approaches. One approach focused on identifying all the genes that are expressed as RNA (referred to as **Expressed Sequence Tags** (ESTs). The other took the blind approach of simply sequencing the whole set of genome that contained all the coding and non-coding sequence, and later assigning different regions in the sequence with functions (a term referred to as **Sequence Annotation**).

For sequencing, the total DNA from a cell is isolated and converted into random fragments of relatively smaller sizes (recall DNA is a very long polymer, and there are technical limitations in sequencing very long pieces of DNA) and cloned in suitable host using specialised vectors. The cloning resulted into amplification of each piece of DNA fragment so that it subsequently could be sequenced with ease. The commonly used hosts were bacteria and yeast, and the vectors were called as **BAC** (bacterial artificial chromosomes), and **YAC** (yeast artificial chromosomes).

BACTERIA



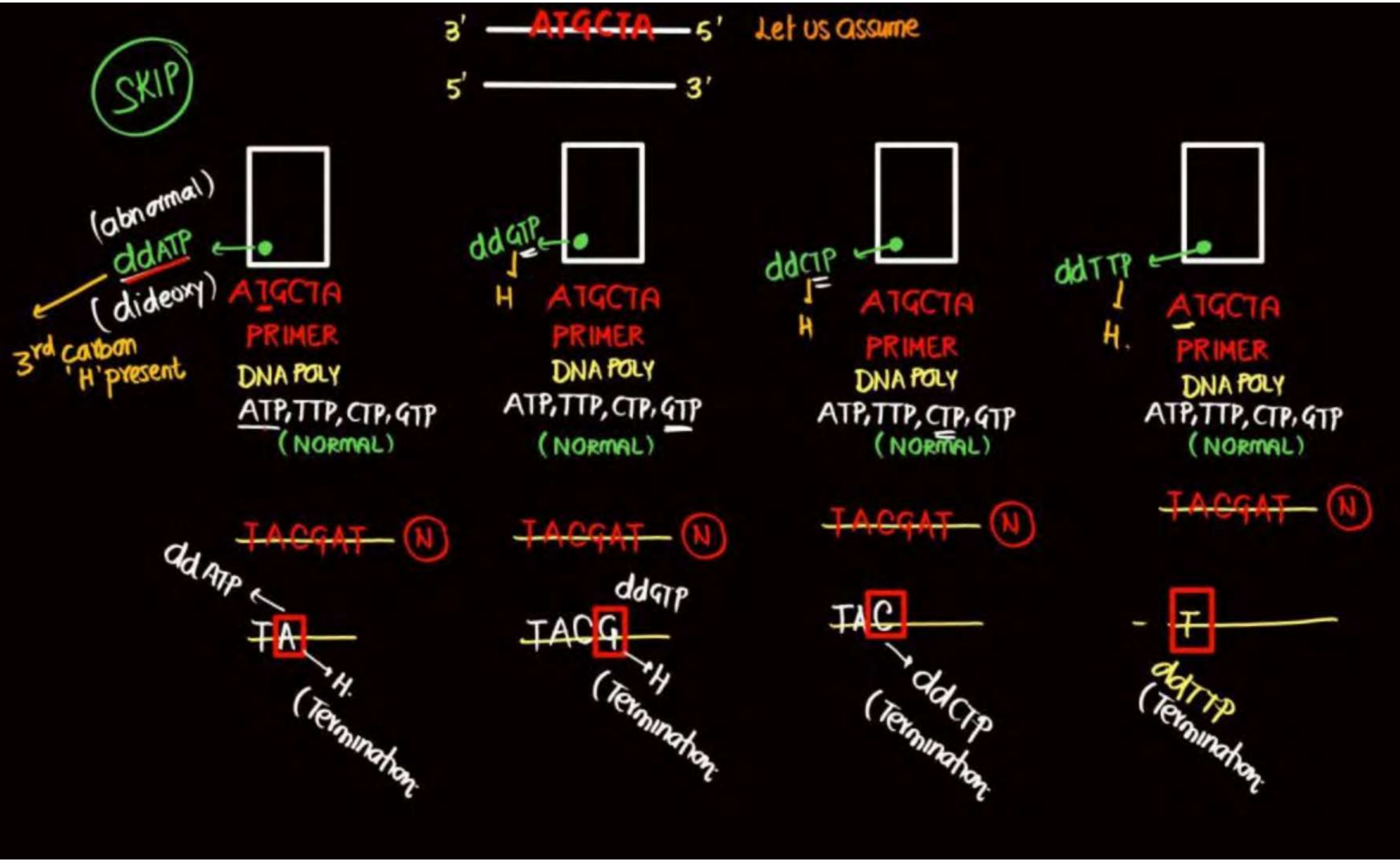
The fragments were sequenced using automated DNA sequencers that worked on the principle of a method developed by Frederick Sanger. (Remember, Sanger is also credited for developing method for determination of amino acid sequences in proteins). These sequences were then arranged based on some overlapping regions present in them.

Last

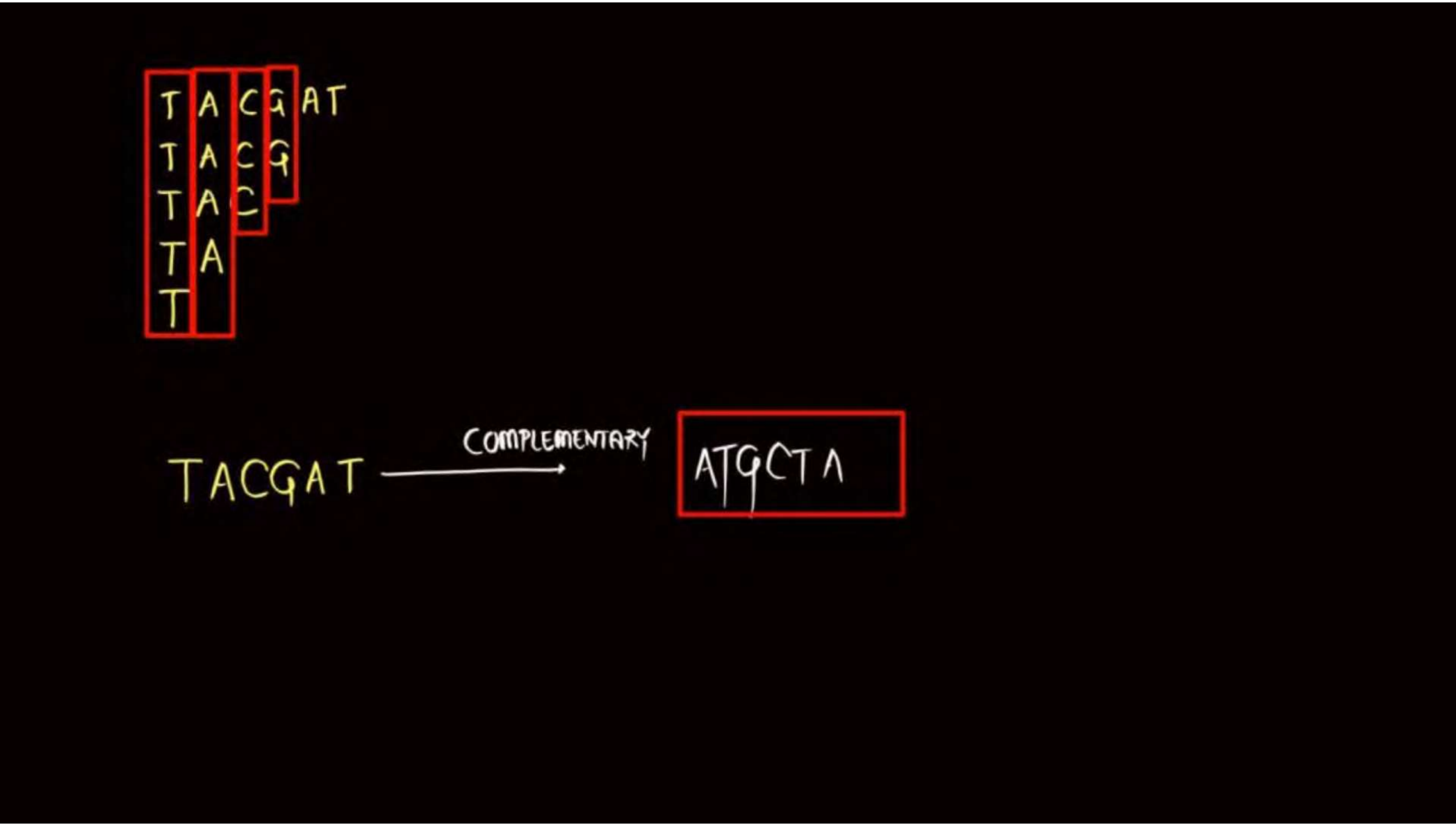
This required generation of overlapping fragments for sequencing. Alignment of these sequences was humanly not possible. Therefore, specialised computer based programs were developed (Figure 5.15). These sequences were subsequently annotated and were assigned to each chromosome.

Last.

Expl^n: out of NCERT.



3' ATGCTA 5' Let us assume
5' 3'
SKIP
(abnormal)
ddATP
(dideoxy)
3rd carbon 'H' present
ATGCTA
PRIMER
DNA POLY
ATP, TTP, CTP, GTP
(NORMAL)
TACGAT N
ddATP
TA
H
(Termination)
ddGTP
H
ATGCTA
PRIMER
DNA POLY
ATP, TTP, CTP, GTP
(NORMAL)
TACGAT N
ddGTP
TACG
H
(Termination)
ddCTP
H
ATGCTA
PRIMER
DNA POLY
ATP, TTP, CTP, GTP
(NORMAL)
TACGAT N
TAC
ddCTP
(Termination)
ddTTP
H.
ATGCTA
PRIMER
DNA POLY
ATP, TTP, CTP, GTP
(NORMAL)
TACGAT N
T
ddTTP
(Termination)


TACGAT
TACG
TAC
TA
T
TACGAT
COMPLEMENTARY
ATGCTA

The sequence of chromosome 1 was completed only in May 2006 (this was the last of the 24 human chromosomes – 22 autosomes and X and Y – to be sequenced). Another challenging task was assigning the genetic and physical maps on the genome. This was generated using information on polymorphism of restriction endonuclease recognition sites, and some repetitive DNA sequences known as microsatellites (one of the applications of polymorphism in repetitive DNA sequences shall be explained in next section of DNA fingerprinting).

⇒ position of gene on chromosome. ⇒ dist^n B/w Two gene.

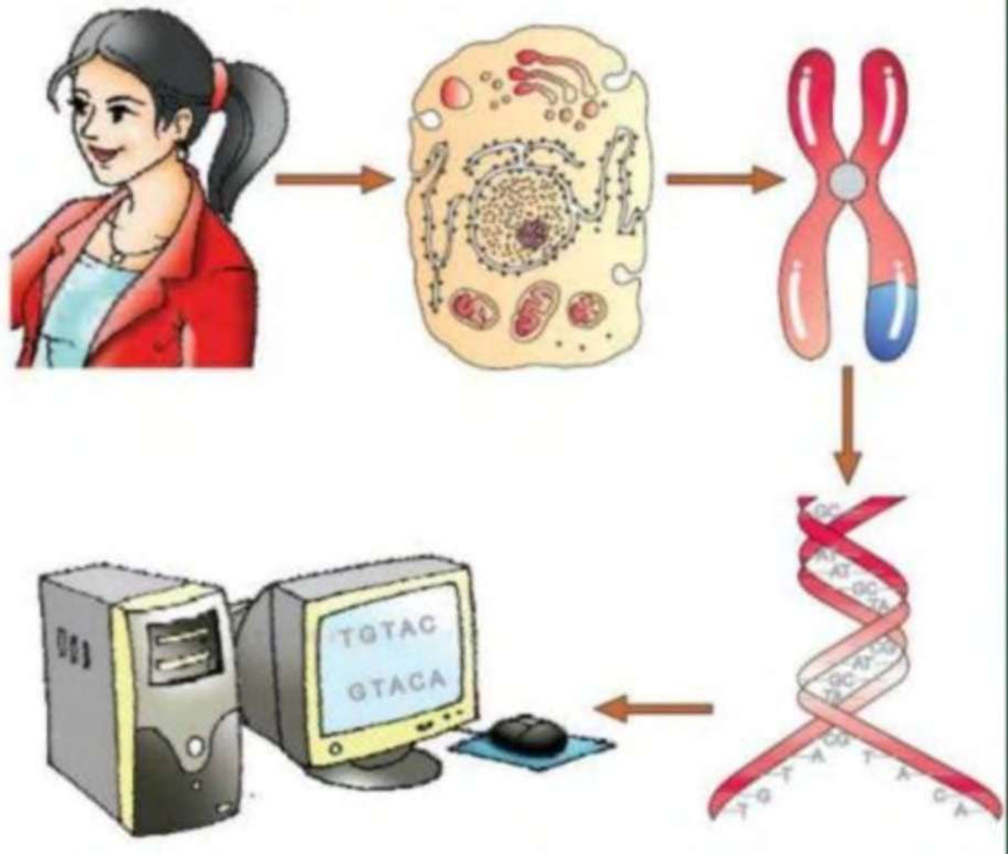


Figure 5.15 A representative diagram of human genome project

5.9.1 Salient Features of Human Genome

Some of the salient observations drawn from human genome project are as follows:

(i) The human genome contains 3164.7 million bp.

(ii) The average gene consists of $\boxed{\text{3000 bases}}$ but sizes vary greatly, with the largest known human gene being dystrophin at 2.4 million bases.

Largest gene → dystrophin protein

(2.4 million Base)

(iii) The total number of genes is estimated at 30,000–much lower than previous estimates of 80,000 to 1,40,000 genes. Almost all (99.9 per cent) nucleotide bases are exactly the same in all people.

(iv) The functions are unknown for over 50 per cent of the discovered genes.

(v) Less than 2 per cent of the genome codes for proteins. (Exon)

(vi) Repeated sequences make up very large portion of the human genome.

(Intron) Rep. DNA

(vii) Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times. They are thought to have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution. no protein.

(viii) Chromosome 1 has most genes (2968), and the Y has the fewest (231).

(ix) Scientists have identified about 1.4 million locations where single-base DNA differences (**SNPs – single nucleotide polymorphism**, pronounced as 'snips') occur in humans. This information promises to revolutionise the processes of finding chromosomal locations for disease-associated sequences and tracing human history.

DNA IS A GENETIC MATERIAL

F. GRIFFITH EXPERIMENT, 1928

★ STREPTOCOCCUS PNEUMONIAE

★ R-II strain / S-III strain → ② FORM

CAPSULE (Polysaccharides) → SUGAR.

R-II S-III

	R-II	S-III
colony/cell	ROUGH (NOT SHINING)	SMOOTH APPEARENCE (SHINING)
CAPSULE	ABSENT	PRESENT
	NON-PATHOGENIC/ NON VIRULENT	PATHOGENIC/ VIRULENT
PNEUMONIA	NO	YES

MICE + R-II (GOOD) $\xrightarrow{\text{NO PNEUMONIA}}$ NO DEATH.

MICE + S-III (BAD) $\xrightarrow{\text{PNEUMONIA}}$ DEATH.

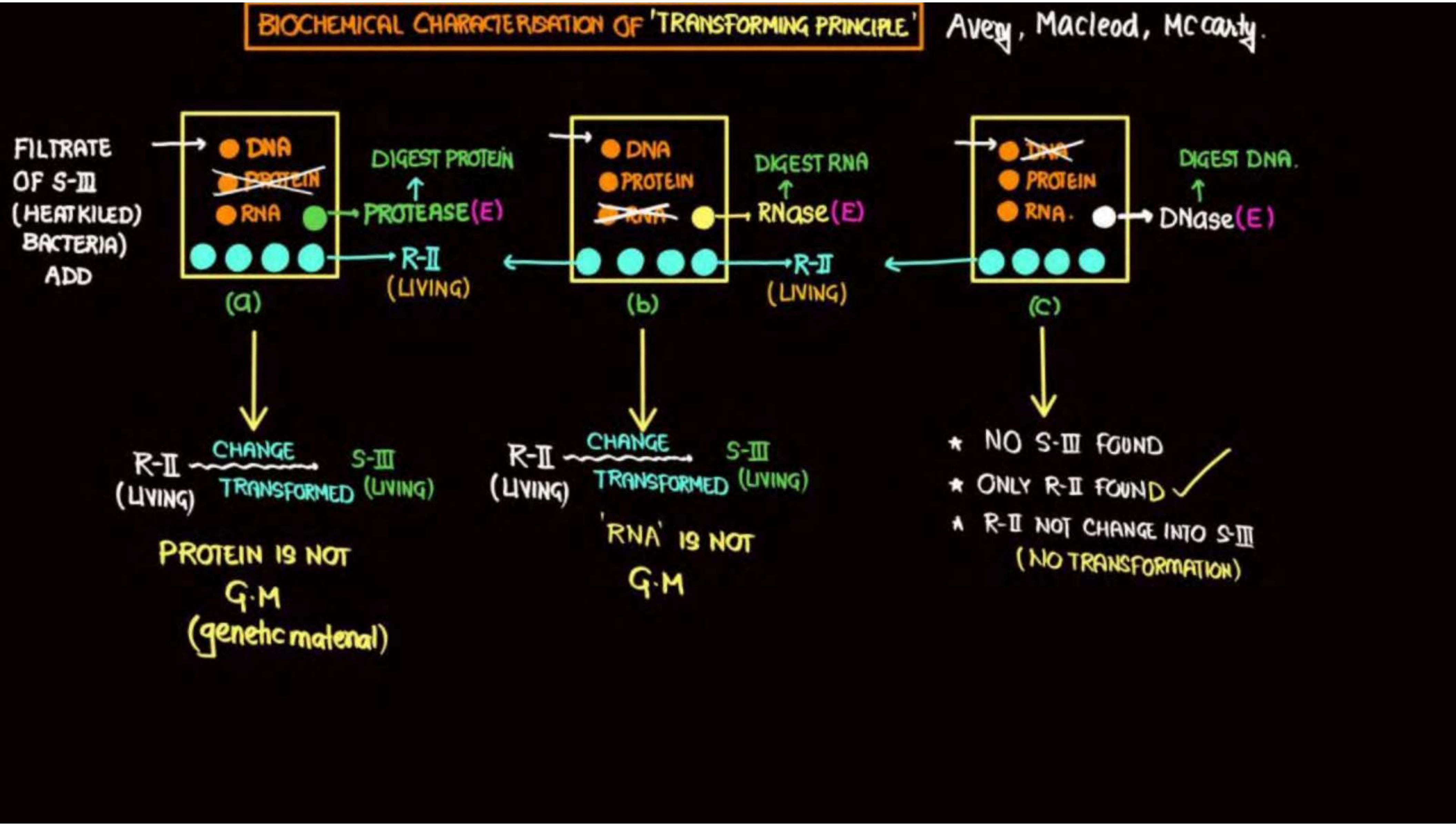
MICE + S-III (HEAT KILLED) $\xrightarrow{\text{NO PNEUMONIA}}$ NO DEATH.

MICE + R-II (GOOD) + S-III (HEAT KILLED) ⟶ DEATH.

HE WAS EXPECTING 'NO DEATH' BUT MICE DIED

GRIFFITH SAID: SOMETHING (TRANSFORMING PRINCIPLE/ GENETIC MATERIAL) TRANSFER FROM HEAT KILLED S-III BACTERIA TO LIVING R-II BACTERIA SO R-II DEVELOP CAPSULE AND CHANGE INTO LIVING S-III BACTERIA WHICH KILLED MICE.

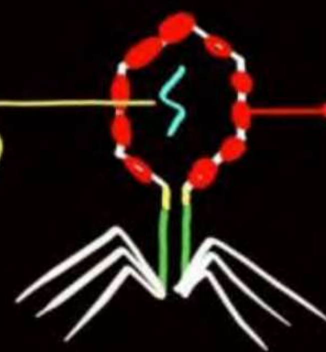
★ WHAT IS 'BIOCHEMICAL COMPOSITION OF 'SOMETHING' NOT EXPLAINED BY GRIFFITH.


BIOCHEMICAL CHARACTERISATION OF 'TRANSFORMING PRINCIPLE'
Avery, Macleod, MC carty.
FILTRATE OF S-III (HEAT KILLED) BACTERIA) ADD
DNA
~~PROTEIN~~
RNA
DIGEST PROTEIN
PROTEASE (E)
R-II (LIVING)
(a)
DNA
PROTEIN
~~RNA~~
DIGEST RNA
RNase (E)
R-II (LIVING)
(b)
~~DNA~~
PROTEIN
RNA.
DIGEST DNA.
DNase (E)
(c)
R-II (LIVING)
CHANGE
TRANSFORMED
S-III (LIVING)
PROTEIN IS NOT G.M (genetic material)
R-II (LIVING)
CHANGE
TRANSFORMED
S-III (LIVING)
'RNA' IS NOT G.M
* NO S-III FOUND
* ONLY R-II FOUND
* R-II NOT CHANGE INTO S-III (NO TRANSFORMATION)

HERSHEY AND CHASE EXP: 1952

- UNEQUIVOCAL PROOF: DNA IS GENETIC MATERIAL
- VIRUS: T_2 ⟶ infection BACTERIA (BACTERIOPHAGE), ds DNA
- E. COLI

DNA ⟵
(phosphorus)
AMP
GMP
CMP
TMP



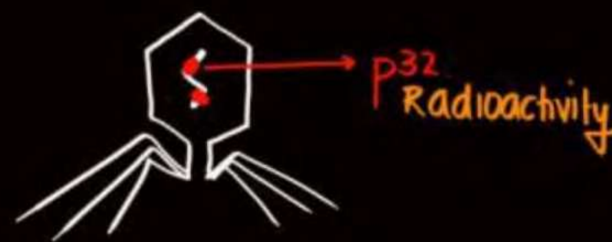
⟶ HEAD / PROTEIN COAT / CAPSID
↓
amino acid
(methionine, cysteine)
↓
SULPHUR PRESENT

- CONCLUSION: 'P': DNA
  'S': PROTEIN COAT

★ SOME T-2 VIRUS GROW IN A MEDIUM CONTAINING.
RADIOACTIVE S^{35} → ENTER INTO PROTEIN COAT

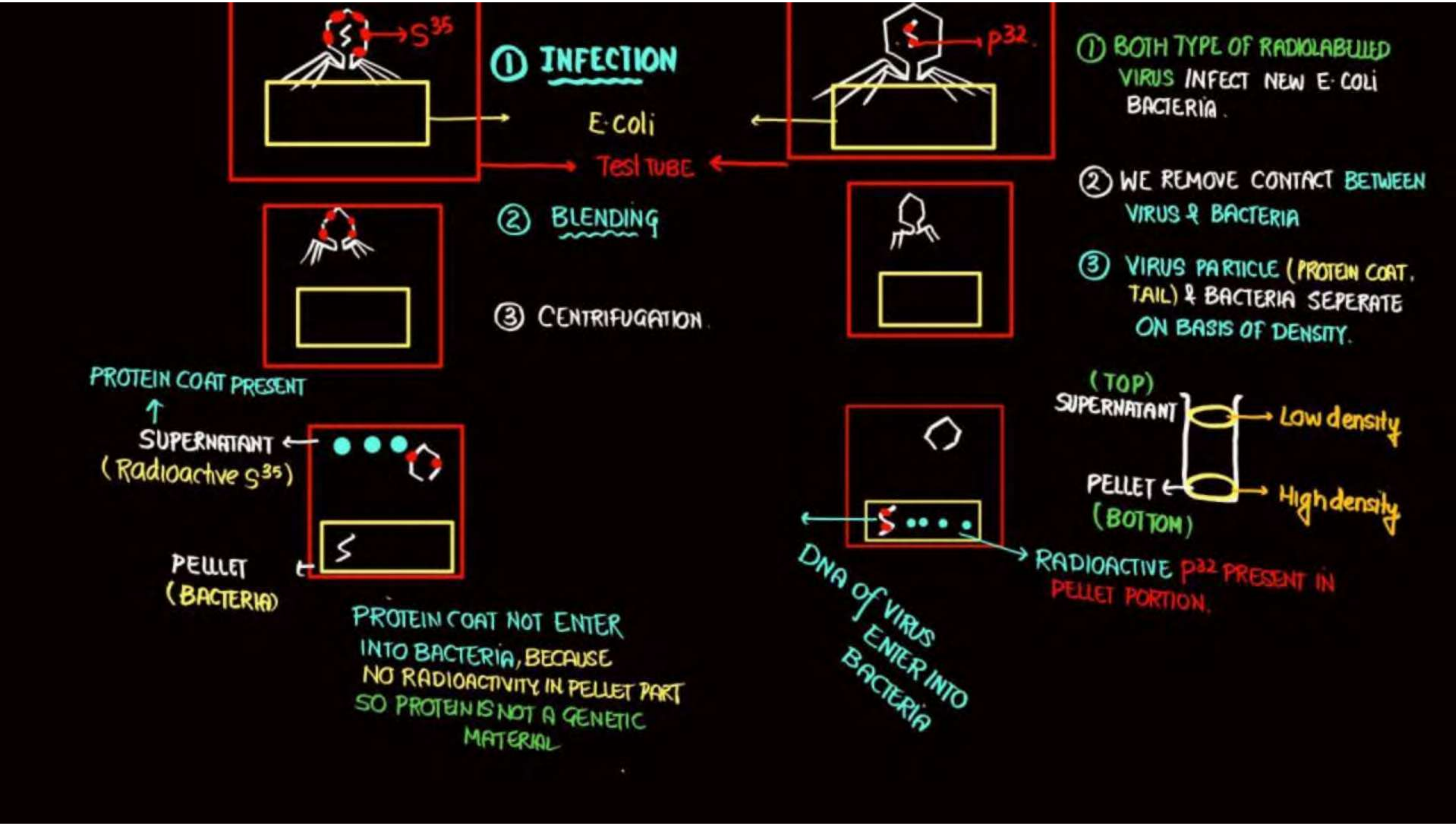
RADIOLABELLED VIRUS.

★ SOME T-2 VIRUS GROW IN A MEDIUM CONTAINING.
RADIOACTIVE P^{32}



EXPERIMENT

① INFECTION
② BLENDING
③ CENTRIFUGATION



S^{35}
① INFECTION
E·coli
Test TUBE
② BLENDING
③ CENTRIFUGATION.
P^{32}.
① BOTH TYPE OF RADIOLABELLED VIRUS INFECT NEW E·COLI BACTERIA.
② WE REMOVE CONTACT BETWEEN VIRUS & BACTERIA
③ VIRUS PARTICLE (PROTEIN COAT, TAIL) & BACTERIA SEPERATE ON BASIS OF DENSITY.
PROTEIN COAT PRESENT
SUPERNATANT
(Radioactive S^{35})
PELLET
(BACTERIA)
PROTEIN COAT NOT ENTER INTO BACTERIA, BECAUSE NO RADIOACTIVITY IN PELLET PART
SO PROTEIN IS NOT A GENETIC MATERIAL
(TOP)
SUPERNATANT
Low density
PELLET
(BOTTOM)
High density
DNA of VIRUS ENTER INTO BACTERIA
RADIOACTIVE P^{32} PRESENT IN PELLET PORTION.

DNA

(PHOSPHATE)

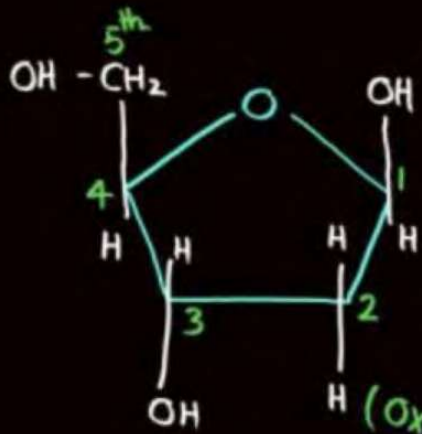
★ ACIDIC SUBSTANCE : IDENTIFIED: FRIEDRICH MEISCHER : IN NUCLEUS, 1869.

★ DNA → NUCLEIC ACID → MADE UP OF MANY NUCLEOTIDE

- NITROGENOUS BASE
  - PYRIMIDINE
    - CYTOSINE (DNA, RNA)
    - THYMINE (ONLY DNA)
    - URACIL (ONLY RNA)
  - PURINE
    - ADENINE
    - GUANINE

    ADENINE, GUANINE → DNA & RNA
- SUGAR
- PHOSPHATE

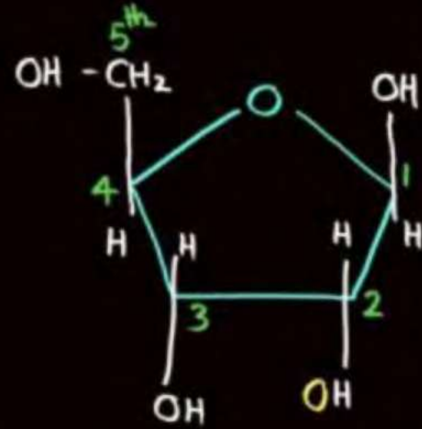
SUGAR



(oxygen absent)

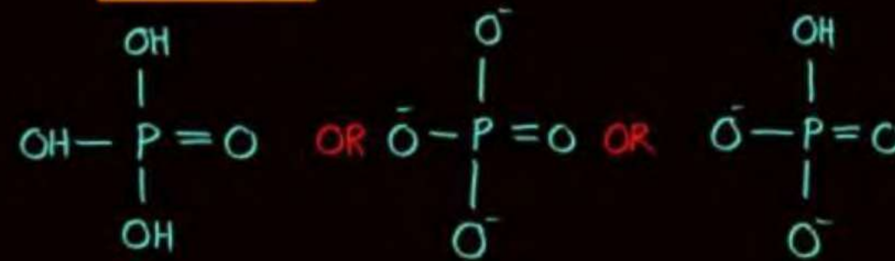
DEOXYRIBOSE
(DNA)

without OXYGEN.



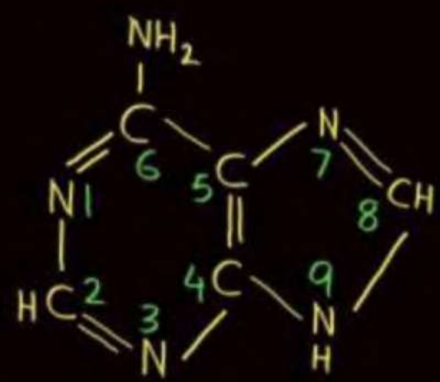
RIBOSE
(RNA)

PHOSPHATE

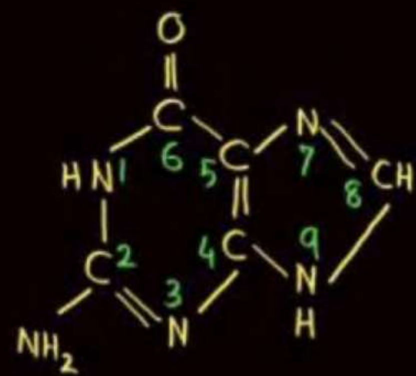


N₂ BASE

PURINE



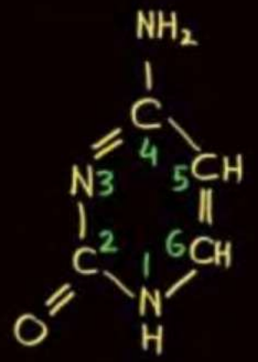
ADENINE



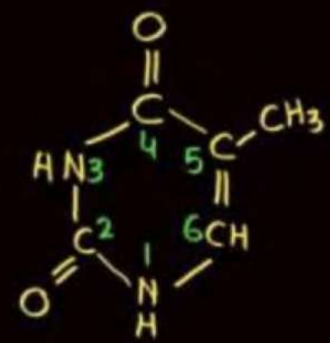
GUANINE

* HETROCYCLIC COMPOUND
* DOUBLE RING
* NITROGEN POSITION: 1, 3, 7, 9.

PYRIMIDINE

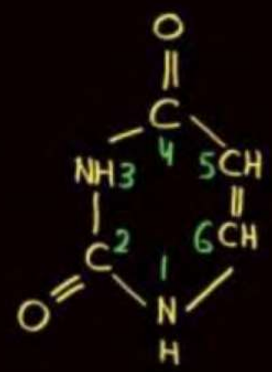


Cytosine



Thymine

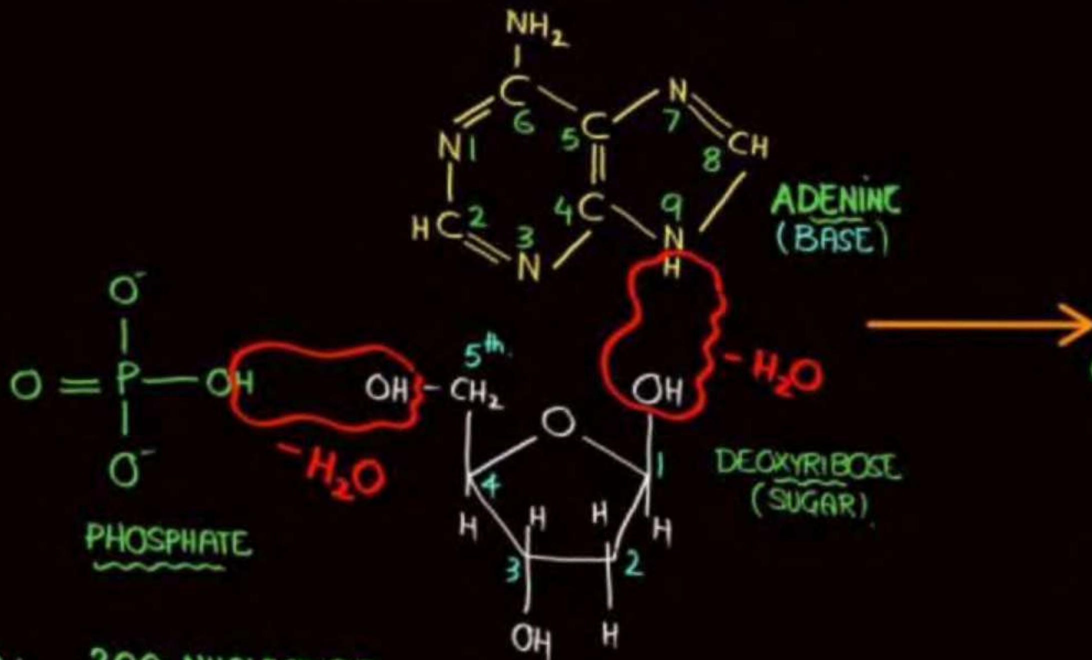
(5-METHYL URACIL)

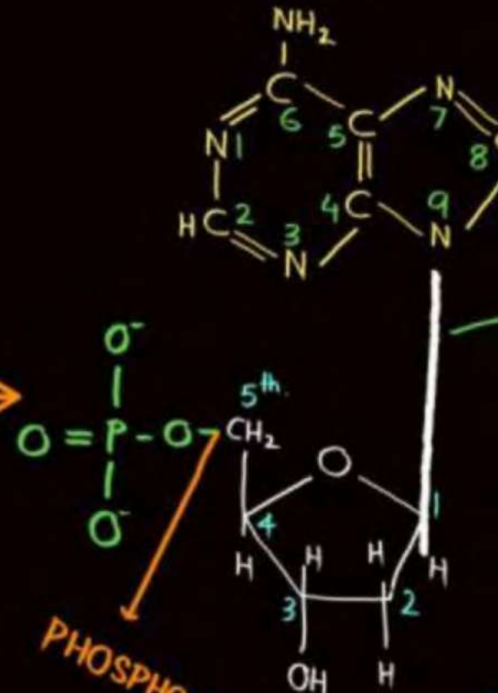


URACIL

- ★ HETROCYCLIC COMPOUND
- ★ SINGLE RING
- ★ 'N' : 1^{st}, 3^{rd}.

NUCLEOTIDE AND BONDING (ADENINE / GUANINE) (PURINE).





PHOSPHOMONOESTER BOND.

N-glycosidic BOND (SUGAR (1st carbon) & BASE (9th).

(1→9th).

5th carbon : PHOSPHATE (SUGAR) 5'

3rd carbon : OH group 3'

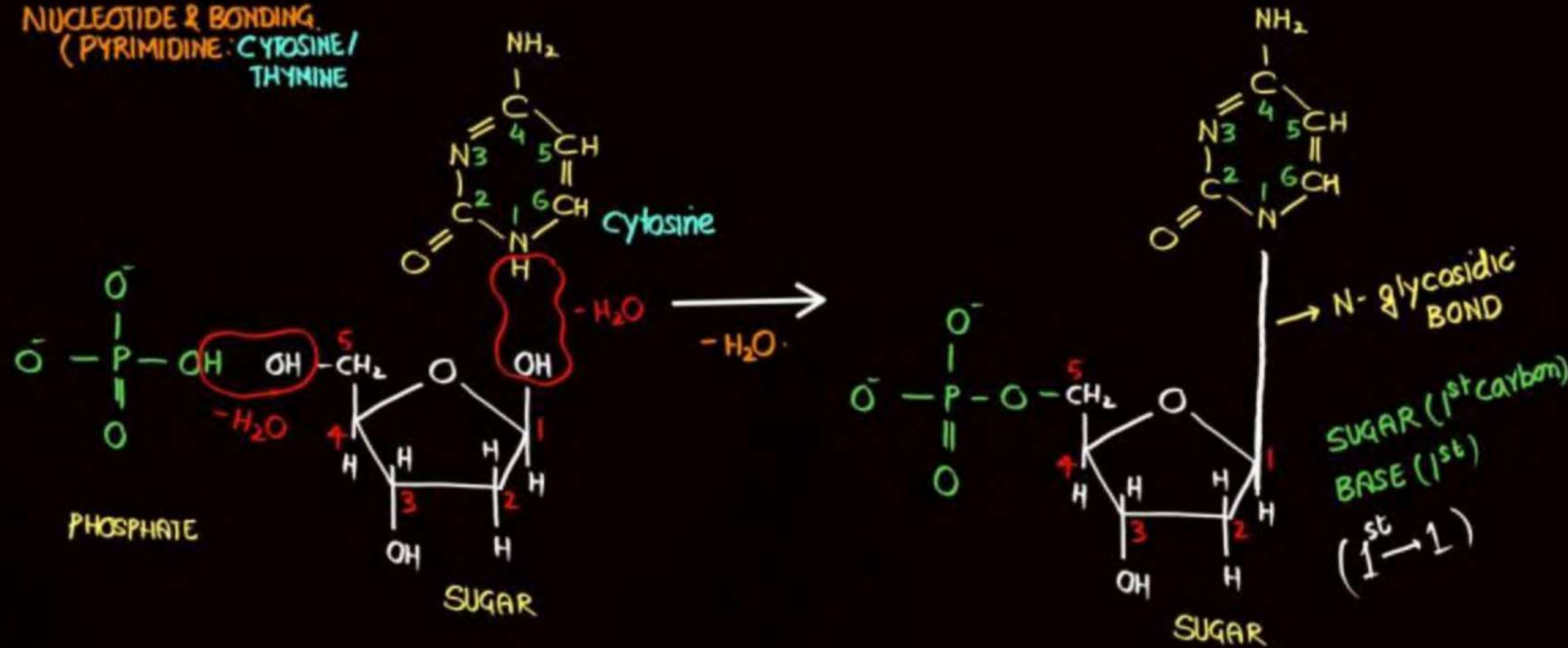
Q: 200 NUCLEOTIDE

BASE: 200

PHOSPHATE: 200

GLYCOSIDIC BOND: 200

NUCLEOTIDE & BONDING
(PYRIMIDINE: CYTOSINE/
THYMINE

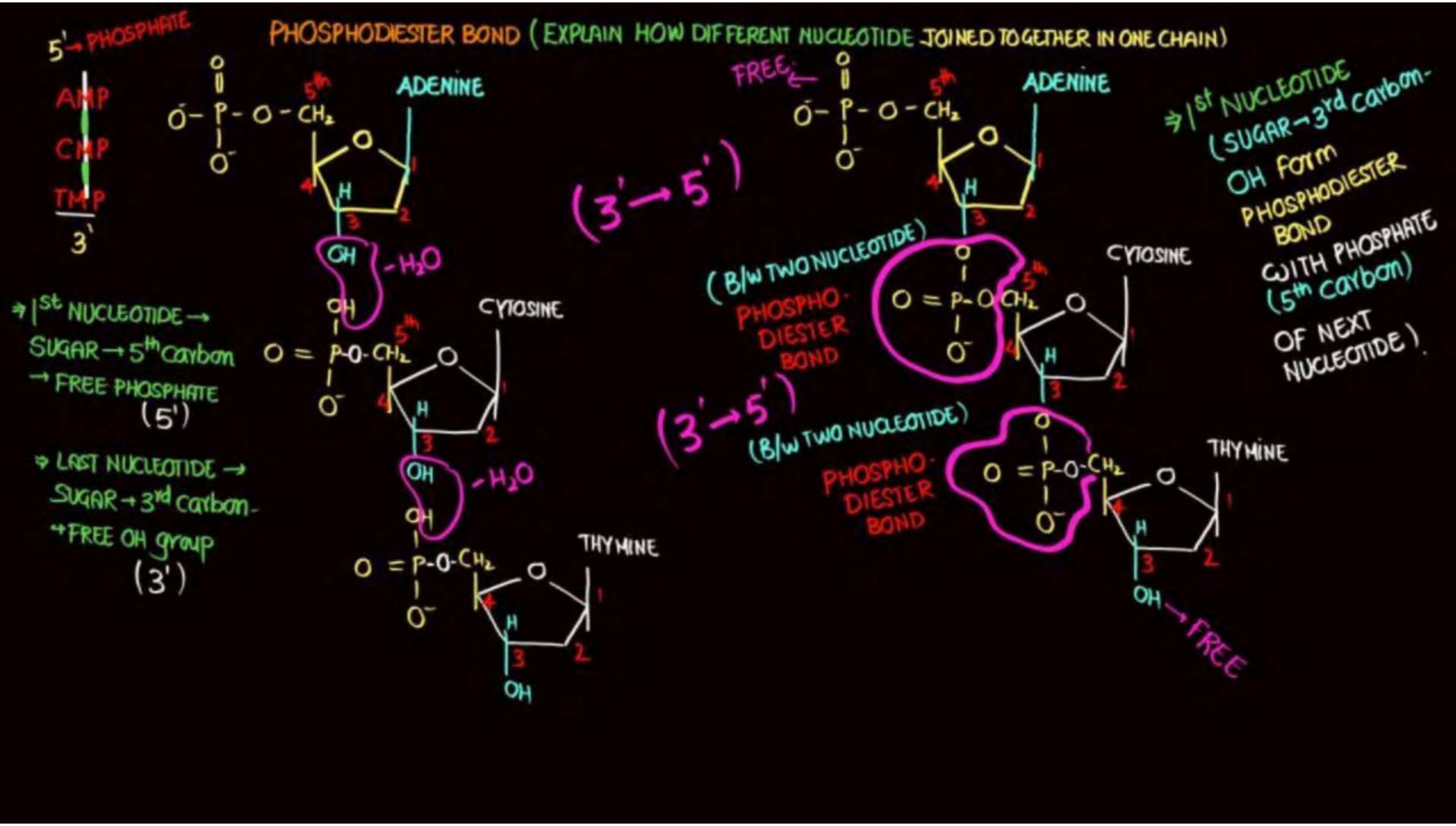


DNA

BASE		SUGAR		NUCLEOSIDE		PHOSPHATE		NUCLEOTIDE
ADENINE	+	DEOXYRIBOSE	→	DEOXYADENOSINE		PHOSPHATE		DEOXYADENOSINE MONOPHOSPHATE / DEOXYADENYLIC ACID (AMP)
GUANINE	+	DEOXYRIBOSE	→	DEOXYGUANOSINE		PHOSPHATE		DEOXYGUANOSINE MONOPHOSPHATE / DEOXYGUANYLIC ACID (GMP)
THYMINE	+	DEOXYRIBOSE	→	DEOXYTHYMIDINE		PHOSPHATE		DEOXYTHYMIDINE MONOPHOSPHATE / DEOXYTHYMIDYLIC ACID (TMP)
CYTOSINE	+	DEOXYRIBOSE	→	DEOXYCYTIDINE		PHOSPHATE		DEOXYCYTIDINE MONOPHOSPHATE / DEOXYCYTIDYLIC ACID (CMP)

RNA

ADENINE	+	RIBOSE	→	ADENOSINE		PHOSPHATE	→	ADENOSINE PHOSPHATE
GUANINE	+	RIBOSE	→	GUANOSINE		PHOSPHATE	→	GUANOSINE PHOSPHATE
URACIL	+	RIBOSE	→	URIDINE		PHOSPHATE	→	URIDINE PHOSPHATE
CYTOSINE	+	RIBOSE	→	CYTIDINE		PHOSPHATE		CYTIDINE PHOSPHATE



PHOSPHODIESTER BOND (EXPLAIN HOW DIFFERENT NUCLEOTIDE JOINED TOGETHER IN ONE CHAIN)
5' → PHOSPHATE
AMP
CMP
TMP
3'
ADENINE
CYTOSINE
THYMINE
5th
OH
-H2O
(3' → 5')
⇒ 1st NUCLEOTIDE → SUGAR → 5th carbon → FREE PHOSPHATE (5')
⇒ LAST NUCLEOTIDE → SUGAR → 3rd carbon → FREE OH group (3')
FREE
(B/W TWO NUCLEOTIDE)
PHOSPHO-DIESTER BOND
OH → FREE
⇒ 1st NUCLEOTIDE (SUGAR → 3rd carbon-OH form PHOSPHODIESTER BOND WITH PHOSPHATE (5th carbon) OF NEXT NUCLEOTIDE).

QUESTION.

AMP = TMP
TMP = AMP
CMP ≡ GMP

H_2 BOND.

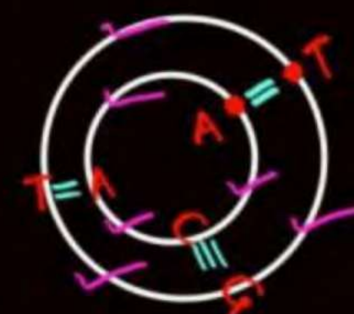
A = T (2) DOUBLE
T = A (2) DOUBLE
G ≡ C (3) TRIPLE
C ≡ G (3) TRIPLE

★ COMPLEMENTARY BASE PAIRING.

★ NUCLEOTIDE : 6
BASE : 6
BASE PAIR : BASE/2 ⇒ $6/2$ ⇒ 3.
GLYCOSIDIC BOND : 6 (equal to number of NUCLEOTIDE)
PHOSPHODIESTER BOND : NO. OF BASE − 2
(LINEAR DNA) : 6 − 2 ⇒ $\boxed{4}$
HYDROGEN BOND : SEVEN.

Q: 2000 Base pair :
PHOSP. DIESTER BOND, If DNA is LINEAR.
⇒ 4000 Base
⇒ 4000 − 2
⇒ $\boxed{3998}$

Q. If 3 Base pair present,
Phosp. BOND ?
If DNA IS CIRCULAR (PSEUDOMONAS).



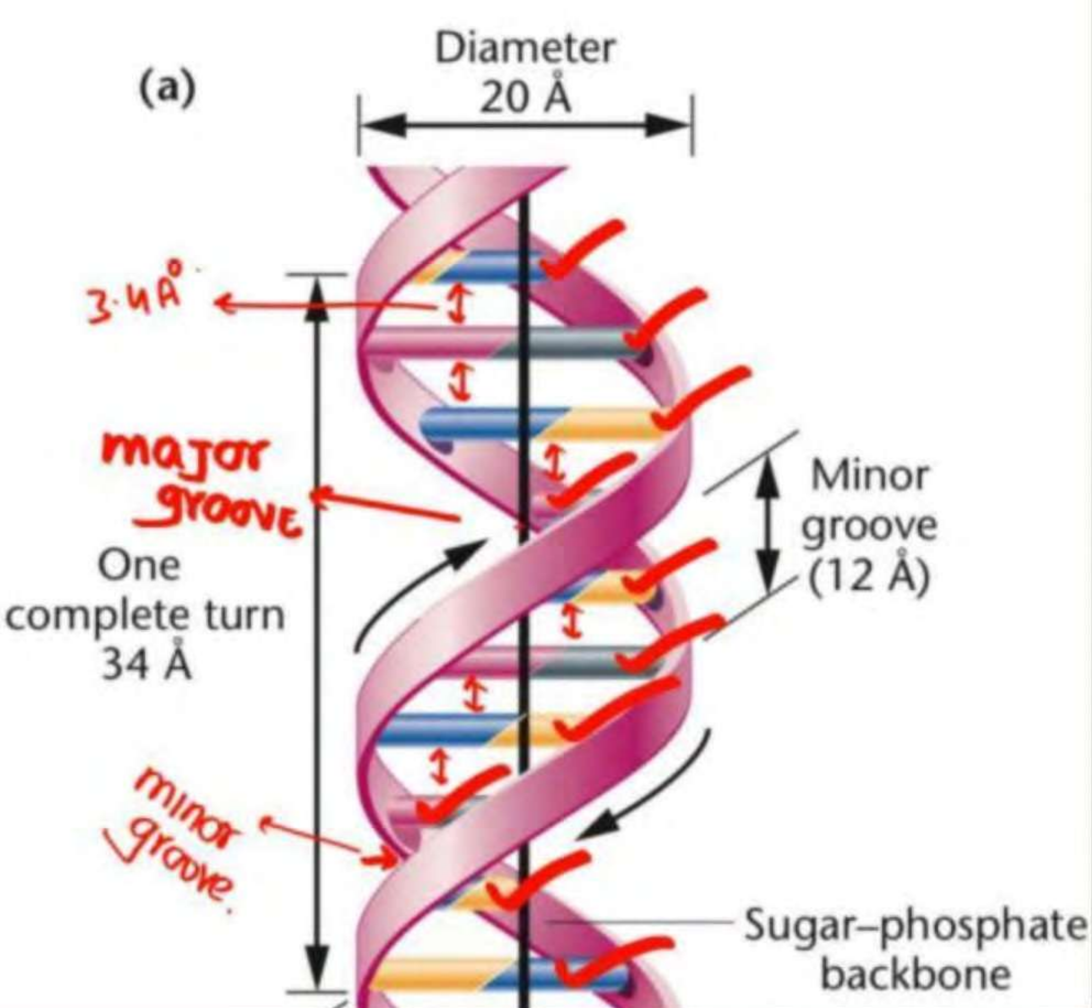
P.B = no. of BASE
$\boxed{6}$

STRUCTURE OF DNA

* FRANKLIN & WILIKIN ⟶ XRAY FALL ON DNA FIBRE
⟶ X RAY REFLECTED ⟶ PATTERN STUDY,
X-RAY DIFFACTION PATTERN OF DNA
(X-RAY CRYSTALLOGRAPHY)
DNA IS A HELICAL STRUCTURE
BUT THEY DIDN'T PROVIDE PROPER DNA STRUCTURE

* TWO TYPE OF STUDY: HELP ⟶
WATSON & CRICK ⟶ TO GIVE
DETAIL STRUCTURE OF DNA, 1953
a) FRANKLIN & WILIKIN ✓
b) CHARGAFF RULE. ✓

① DNA made up of TWO POLYNUCLEOTIDE CHAIN
② BOTH CHAIN ARE ANTIPARALLEL.
(ONE CHAIN ⇒ PHOSPHATE AT ONE END
SECOND CHAIN ⇒ OH GROUP



WATSON & CRICK STRUCTURE

★ B-TYPE OF DNA, RIGHT HANDED DNA / CLOCKWISE

★ LENGTH OF DNA / HELIX LENGTH / PITCH OF DNA =

no. of Base pair x dist^n B/w Two Bp (vertical RISE PER BP)

⇒ 10 Base pair x 3.4 Å / 0.34nm

⇒ $\boxed{34 Å / 3.4 nm}$: 1 TURN OF DNA (HELIX LENGTH)

★ LENGTH OF HUMAN DNA:

no. of Base pair x dist^n B/w TWO BP

⇒ $6.6 \times 10^9 \times 0.34 \times 10^{-9}$ m

⇒ $\boxed{2.2 M}$

★ DIAMETER: 20 Å

★ DISTANCE B/W TWO CHAIN IS UNIFORM BECAUSE PURINE FORMS BOND WITH PYRIMIDINE AND VICE-VERSA.

⇒ COMPLEMENTARY BASE PAIRING : UNIQUE PROPERY OF DNA OR HALLMARK.

⇒ STABILITY OF DNA: HYDROGEN BONDING B/W BASE PAIR, BASE STACKING (ONE BASE PAIR ABOVE OTHER)

⇒ BACK BONE : SUGAR ↔ PHOSPHATE (PHOSPHODIESTER BOND)

⇒ BASE PROJECTED INSIDE

CHARGAFF RULE (VALID FOR DS DNA)

a) PURINE = PYRIMIDINE

$$A+G = C+T$$

$$\frac{A+G}{C+T} = 1$$

b) $\frac{A+T}{G+C}$ Ratio specific for species

c) Adenine equal to THYMINE

d) Guanine equal to cytosine

e) $A = T$ (2 Hydrogen BOND)

f) $G \equiv C$ (3 Hydrogen BOND)

g) SUGAR = PHOSPHATE.

CLIMAX

Q Adenine : 40

Cytosine : ?

⇒ A equal THYMINE

A : 40
T : 40
80

$A+T+G+C = 100$

$80 + G+C = 100$

$G+C = 100-80$

$G+C = 20$

GUANINE EQUAL TO CYTOSINE

$G = 10$

$C = 10$

Adenine : 10

Total H_2 BOND : ?

$A = 10$, $T = 10$

$A+T = 10+10 \Rightarrow \boxed{20 \text{ BASE}}$

⇒ 20 BASE = 10 BASE PAIR

A = T (one bp : 2 H_2 BOND)

$10bp \times 2 \Rightarrow \boxed{20\ H_2 \text{ BOND}}$

⇒ $G+C = 100-20$

= 80 BASE

80 BASE = 40 BASE PAIR

$G \equiv C$ (3 H_2 BOND)

$40 \times 3 \Rightarrow \boxed{120\ H_2 \text{ BOND}}$

140 H_2 BOND

Q : If adenine : 120

Total 20 coils/TURN IN DNA.

no of pyrimidine which form TRIPLE BOND.

$G \equiv C \rightarrow$ PYRIMIDINE

PURINE

⇒ 1 TURN = 10bp

⇒ 20 TURN = $20 \times 10 = 200bp = \boxed{400 \text{ Base}}$

A : 120
T : 120
A+T : 240

⇒ $G+C = 400-240$

$G+C = 160$ Base

Guanine equal to cytosine

80 80

NOTE

ϕ x 174 ⇒ 5386 base/NUCLEOTIDE, SS CIRCULAR DNA. (Length equal to number of Base)

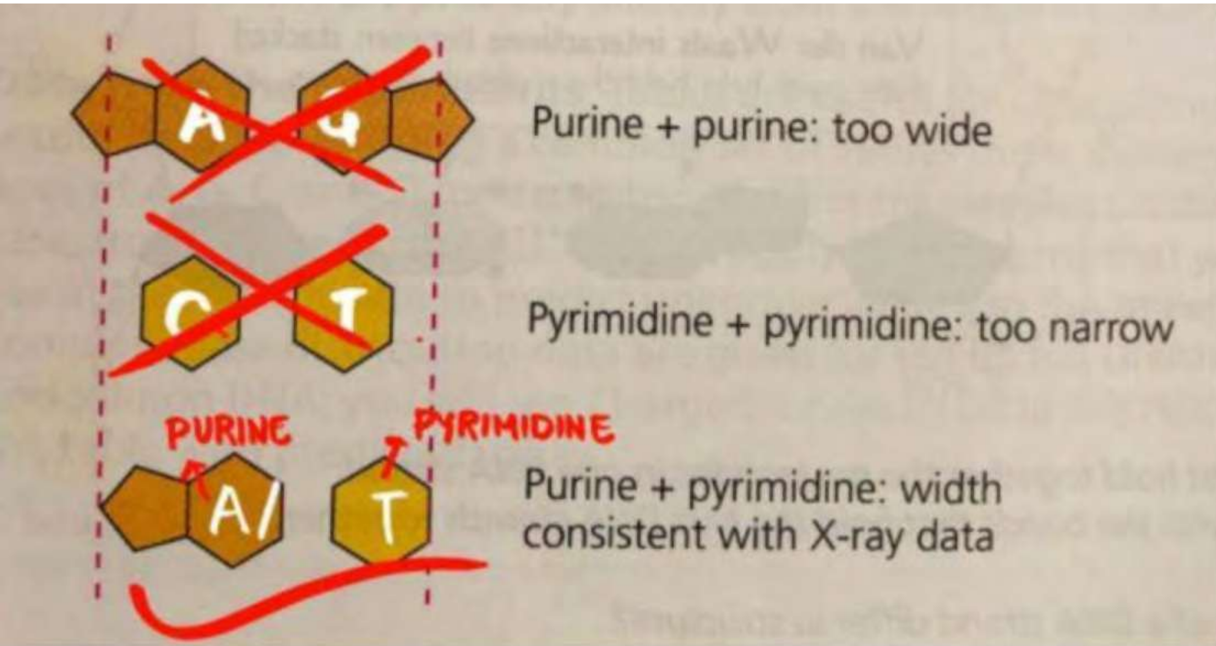
λ PHAGE ⇒ 48502 basepair, ds Linear DNA

E. coli ⇒ 4.6×10^6 bp, Haploid

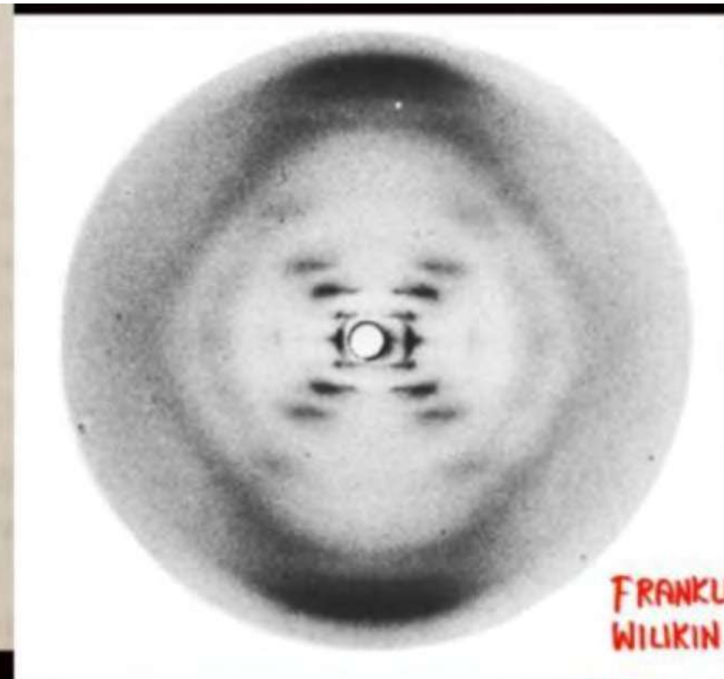
HUMAN (DIPLOID) ⇒ 6.6×10^9 bp ⇒ 46 chromosome

HUMAN (genome) . Haploid set of chromosome ⇒ 23 chromosome

3.3×10^9 bp

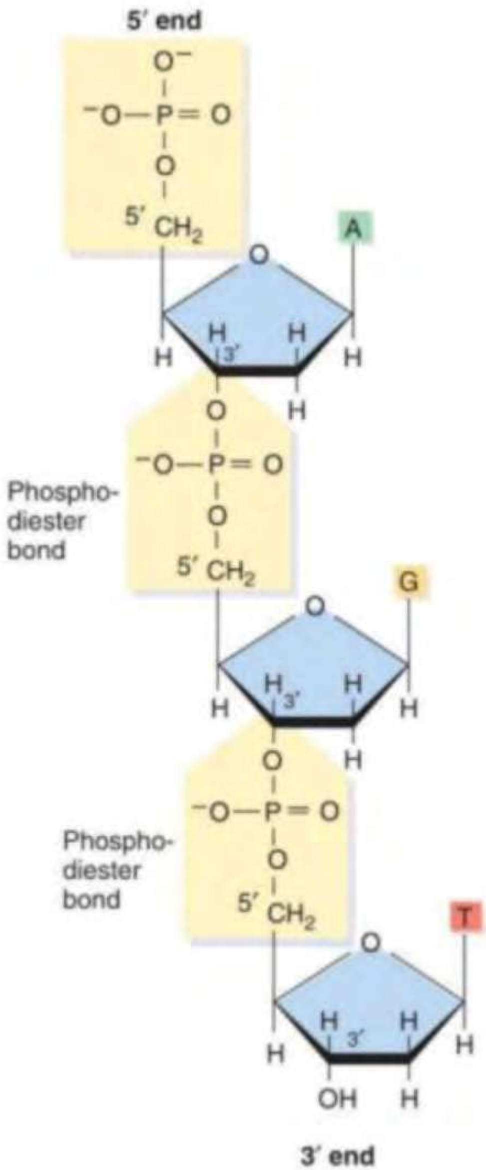


Why the distance B/W TWO CHAIN IS UNIFORM ?

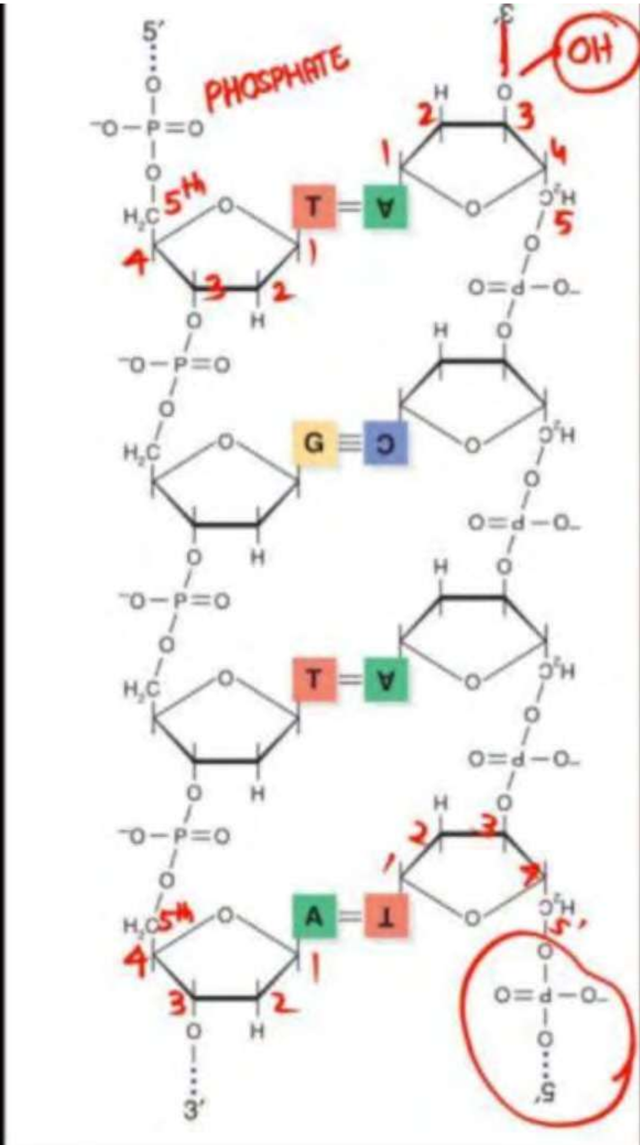


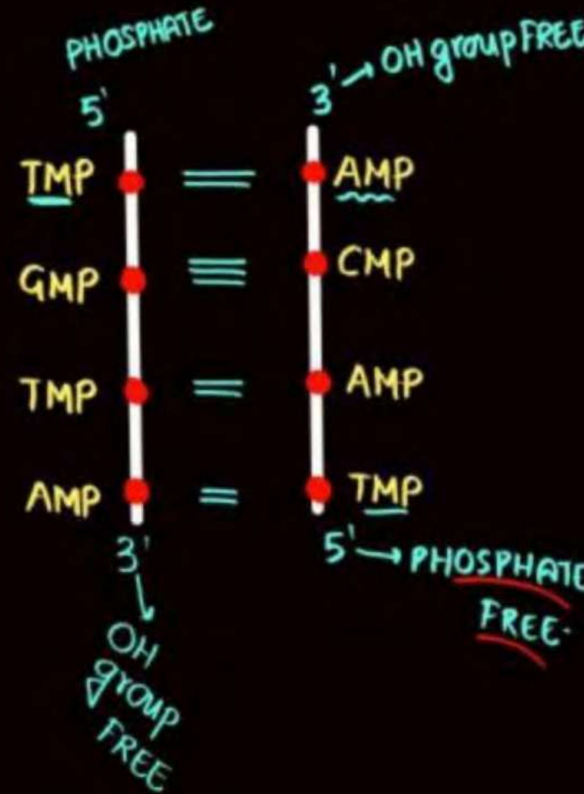
FRANKLIN & WILKIN:

X-RAY DIFFRACTION PATTERN OF DNA.



5′ end
Phospho-
diester
bond
Phospho-
diester
bond
A
G
T
3′ end


5'
PHOSPHATE
OH
T
A
G
C
T
A
A
T
3'
5'


PHOSPHATE
5'
3' → OH group FREE
TMP
AMP
GMP
CMP
TMP
AMP
AMP
TMP
3'
OH group FREE
5' → PHOSPHATE FREE.

CENTRAL DOGMA.

CRICK.

$$DNA \xrightarrow{\text{TRANSCRIPTION}} mRNA \xrightarrow{\text{TRANSLATION}} PROTEIN$$

REPLICATION

UNIDIRECTIONAL FLOW.

Exception: IN SOME VIRUS (RETROVIRUS)

$$DNA \xleftarrow[\text{TRANSCRIPTION}]{\text{REVERSE}} RNA \xrightarrow{\text{TRANSLATION}} PROTEIN$$

(REVERSE TRANSCRIPTASE

BIDIRECTIONAL