COURSE: B Sc (Hons) ,Part -3

PAPER – 1- VIII

TOPIC- Genetics - 2

PREAPARED BY: Ajai Kishore Sharan

TOPICS COVERED

7. **Method of DNA sequencing**
8. **Gene interaction**
9. **Mutation**
10. **Cell cycle**
11. **Polyploidy**

TOPIC- 7

METHOD OF DNA SEQUENCING

DNA Sequencing:

The segments of specific DNA molecules obtained by recombinant DNA technology can be analyzed for determining their nucleotide sequence.

The methods commonly used for DNA sequencing are:

i. Enzymatic method or Sanger's Dideoxy method.

ii. Chemical method or Maxam-Gilbert Method.

iii. Automated method.

(i) Enzymatic method of DNA sequencing is also called as Sanger-Coulson method of sequencing of DNA molecules. This method involves the use of single stranded DNA as a template for DNA synthesis.

The dideoxynucleotide triphosphates (ddNTPs like ddCTP, ddGTP, ddATP, ddTTP) are incorporated in the growing chain and they terminate the chain synthesis because they are unable to form a phosphodiester bond with next deoxy-nucleotide triphosphate.

For sequencing, the reaction mixture is taken in four separate test tubes. In each test tube is added one particular ddNTP. As a result, different sizes of newly synthesized DNA strands are obtained in each test tube which are terminated by a particular ddNTP. These segments are then separated by electrophoresis and then the DNA sequences are obtained by reading the bands on autoradiogram from bottom to the top of gel.

(ii) Chemical method of DNA sequencing involves the degradation of DNA by using chemicals, rather than synthesis of new DNA. In this type of sequencing, the DNA sample is labeled radioactively at 3′ ends and separated into single strands. Sample is then divided into four test tubes, each treated with a specific chemical reagent which degrades only at specific nucleotide base like G or C or 'A and G' or 'C and T'.

As a result of this partial chemical cleavage, a number of differently sized fragments are obtained in each test tube. These fragments are separated by gel electrophoresis and then observed under

autoradiography to interpret the nucleotide sequence of sample DNA. Chemical method is not used very commonly because it is a slow and labour intensive process.

(iii) Automatic DNA sequencing methods have been developed by improvements in dideoxy-method. A number of automatic DNA sequencing machines have also been invented which are capable of sequencing thousands of nucleotides within few hours.

Such methods involve the tagging of fluorescent dyes to ddNTPs, slab gel sequencing systems, capillary gel sequencing systems and PCR-based DNA sequencing techniques. Such techniques are faster and more reliable.

Sanger method:

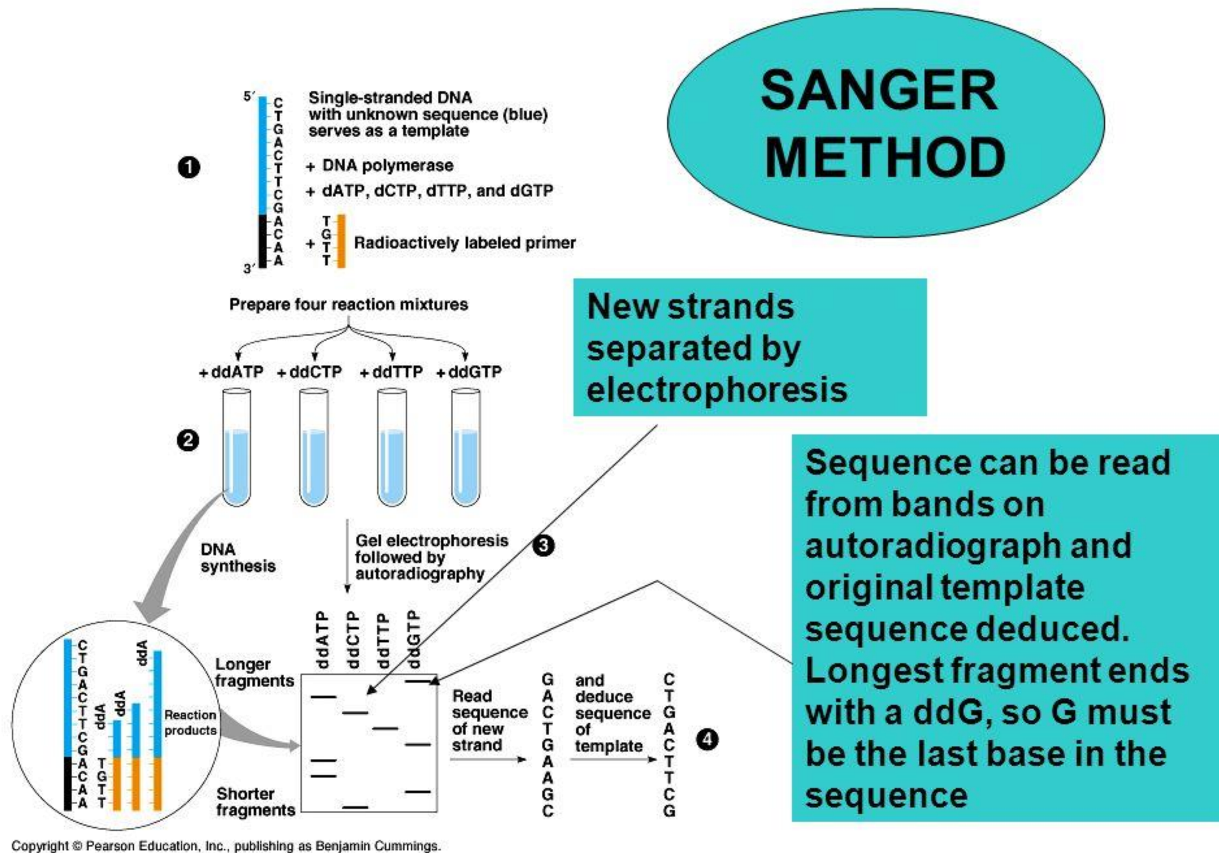
Sanger sequencing, also known as the chain termination method, is a technique for DNA sequencing based upon the selective incorporation of chain-terminating dideoxynucleotides (ddNTPs) by DNA polymerase during in vitro DNA replication. It was developed by Frederick Sanger and colleagues in 1977.

i. Four reaction tubes are set up each con-taining single stranded DNA sample to be sequenced, ail four dNTPs (radioactively labelled) and an enzyme for DNA synthesis (DNA polymerase I).

ii. Each tube also contains a small amount of (much smaller amount relative to four dNTPs) one of the ddNTP, so that four tubes have each different ddNTP, bring-ing about termination at a specific base – Adenine (A), Cytosine (C), Thymine (T), and Guanine (G).

iii. The fragments generated by random incorporation of ddNTP leads to termi-nation of reaction and so the different fragments are produced which can be separated by high resolution polyacrylamide gel, four adjoining lanes are loaded by four different samples.

iv. The gel is then auto-radiographed, the position of different bands in each lane can be visualized, and based on the position of the bands, the DNA sequence can be read out very easily.



Maxam and Gilbert experiment on DNA sequencing

Maxam–Gilbert sequencing requires radioactive labeling at one 5′ end of the DNA fragment to be sequenced (typically by a kinase reaction using gamma-32P ATP) and purification of the DNA. ... The addition of salt (sodium chloride) to the hydrazine reaction inhibits the reaction of thymine for the C-only reaction.

i. The 3′ ends of DNA fragments are labelled.

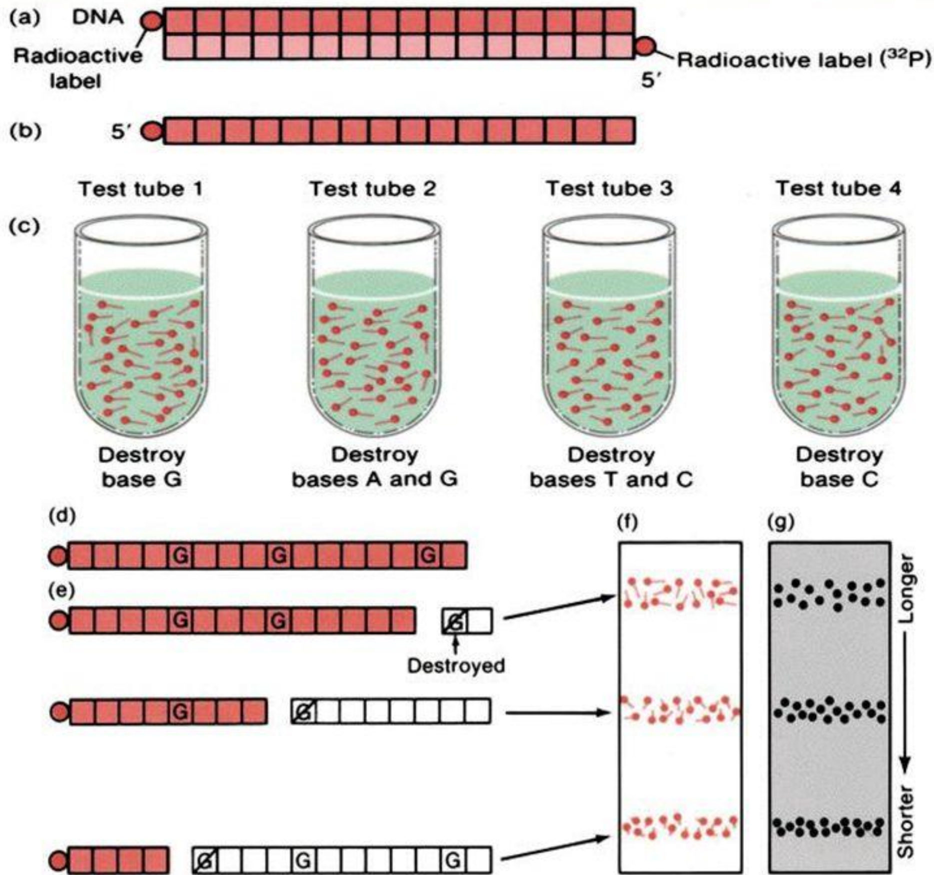
ii. The labelled strands are then separated, of which both strands are labelled at 3′ ends.

iii. The mixture is divided into four sam-ples, each treated with a different reagent having the property of destroy-ing either only G or only C or A and G, T and C; the concentration is adjusted in such a way that 50% of target base is destroyed.

iv. Fragments of different sizes having 32P are produced.

v. Electrophoresis is done using each of the four samples in four different lanes of the gel.

vi. Autoradiograph of the gel helps to deter-mine the sequence from the position of bands in four lanes.



TOPIC- 8

INTERACTION OF GENE

By crossing purple and white pea plants, Mendel found the offspring were purple rather than mixed, indicating one color was dominant over the other.Mendel's Law of Segregation states individuals possess two alleles and a parent passes only one allele to his/her offspring.Mendel's Law of Independent Assortment states the inheritance of one pair of factors (genes) is independent of the inheritance of the other pair.If the two alleles are identical, the individual is called homozygous for the trait; if the two alleles are different, the individual is called heterozygous. Mendel cross-bred dihybrids and found that traits were inherited independently of each other.Hence Mendel believed in Purity of gamete and no mixing up of dominant and recessive character to form an intermediate type.

In 1900, working independently of one another, biologists Erich Tschermak, Hugo de Vries, and Karl Erich Correns each published data that reasserted Mendel's historic principles of heredity. Each scientist came to this rediscovery from a slightly different perspective.

Tschermak, an Austrian botanist, coincidentally started pea plant breeding experiments in 1898. He performed these experiments for two years before he accidentally discovered a reference to Mendel's work from thirty years earlier.When he read Mendel's papers, Tschermak found that he had duplicated many of Mendel's breeding experiments, and, embarrassingly, his own work was not as thorough.

The Austrian published his own findings and gave credit to Mendel for performing the original breeding work. Tschermak is known for applying the genetic principles he helped rediscover to developing wheat-rye hybrids and a disease-resistant oat hybrid.

Hugo de Vries, whose primary concern was understanding how evolution worked, was a professor at the University of Amsterdam. De Vries wanted to find a genetic basis for Charles Darwin's theory of natural selection to understand how species could change over time.

De Vries studied the evening primrose and found that, after cultivating the plant for years, several varieties arose through abrupt, unexplained genetic changes. Based on these changes, he came up with a theory of mutation in which he hypothesized that rapid alterations in organisms could explain how evolution could quickly produce new species.

For eight years, starting in 1892, De Vries conducted breeding experiments that led him to the same laws of heredity that Mendel had discovered. When he reported his own work, de Vries was very careful to attribute his concepts to Mendel.

Karl Correns was a German botanist at the University of Tübingen in the 1890's. By coincidence, Correns conducted breeding experiments with peas that reproduced Mendel's experiments. In a survey of the literature, Correns found Mendel's papers, published many years earlier. Much of Correns's life work was spent in developing additional evidence to support Mendel's hypotheses.

Correns was the first researcher to suggest that if certain genes were physically close to each other, they might be "coupled" in some way and be consistently inherited in offspring. His concept explained why some traits did not seem to follow Mendel's law of independent assortment,which stated that all traits separated independently of one another when inherited by offspring.

Gene interaction

Gene interactions occur when two or more different loci (gene locations) affect the outcome of a single trait. The most common type of gene interaction is known as epistasis.

Epistasis is the interaction between genes that influences a phenotype. Genes can either mask each other so that one is considered "dominant" or they can combine to produce a new trait. It is the conditional relationship between two genes that can determine a single phenotype of some traits

Recessive Epistasis [9:3:4 Ratio

When recessive alleles at one locus mask the expression of both (dominant and recessive) alleles at another locus, it is known as recessive epistasis. This type of gene interaction is also known as supplementary epistasis. A good example of such gene interaction is found for grain colour in maize.

There are three colours of grain in maize, viz., purple, red and white. The purple colour develops in the presence of two dominant genes (R and P), red colour in the presence of a dominant gene R, and white in homozygous recessive condition (rrpp).

A cross between purple (RRPP) and white (rrpp) grain colour strains of maize produced plants with purple colour in F1. Inter-mating of these F1 plants produced progeny with purple, red and white grains in F2 in the ratio of 9 : 3 : 4 .

Parents — Purple Grains PPRR × White Grains pprr

↓

F_1 — PpRr Purple Grains

F_2

	PR	Pr	pR	pr
PR	PPRR [P]	PPRr [P]	PpRr [P]	PpRr [P]
Pr	PPRr [P]	PPrr [W]	PpRr [P]	Pprr [W]
pR	PpRR [P]	PpRr [P]	ppRR [R]	ppRr [R]
pr	PpRr [P]	Pprr [W]	ppRr [R]	pprr [W]

P = Purple, R = Red, and W = White grains

Fig. 8.2. Recessive epistasis for grain colour in maize. The normal dihybrid segregation ratio of 9 : 3 : 3 : 1 is modified to 9 : 3 : 4 in F_2.

Dominant Epistasis [12 : 3 : 1 Ratio]:

When a dominant allele at one locus can mask the expression of both alleles (dominant and recessive) at another locus, it is known as dominant epistasis. In other words, the expression of one dominant or recessive allele is masked by another dominant gene. This is also referred to as simple epistasis.

An example of dominant epistasis is found for fruit colour in summer squash. There are three types of fruit colours in this cucumber, viz., white, yellow and green. White colour is controlled by dominant gene W and yellow colour by dominant gene G. White is dominant over both yellow and green.

The green fruits are produced in recessive condition (wwgg). A cross between plants having white and yellow fruits produced F1 with white fruits. Inter-mating of F1 plants produced plants with white, yellow and green coloured fruits in F2 in 12 : 3 : 1 ratio F. This can be explained as follows.

AaBb × AaBb
white | white

	AB	Ab	aB	ab
AB	AA BB White	AA Bb White	Aa BB White	Aa Bb White
Ab	AA Bb White	AA bb White	AA Bb White	Aa bb White
aB	Aa BB White	Aa Bb White	aa BB Yellow	aa Bb Yellow
ab	Aa Bb White	Aa bb White	aa Bb Yellow	aa bb Green

AB – 9 White
Ab – 3 White
aB – 3 Yellow
ab – 1 Green

Dominant [Inhibitory] Epistasis [13 : 3 Ratio]:

In this type of epistasis, a dominant allele at one locus can mask the expression of both (dominant and recessive) alleles at second locus. This is also known as inhibitory gene interaction. An example of this type of gene interaction is found for anthocyanin pigmentation in rice.

The green colour of plants is governed by the gene I which is dominant over purple colour. The purple colour is controlled by a dominant gene P. When a cross was made between green (IIpp) and purple (iiPP) colour plants, the F1 was green. Inter-mating of F1 plants produced green and purple plants in 13 : 3 ratio in F2 . This can be explained as follows.

13/16 = White
3/16 = coloured

White leg horn × White plymouth Rock
AABB ↓ aabb
AaBb × AaBb
White White

	AB	Ab	aB	ab
AB	AABB White	AABb White	AaBB White	AaBb White
Ab	AABb White	AAbb* Coloured	AaBb White	Aabb* Coloured
aB	AaBB White	AaBb White	aaBB White	aaBb White
ab	AaBb White	Aabb* Coloured	aaBb White	aabb White

AB = 9 white
Ab = 3 coloured
aB = 3 white
ab = 1 white

13 : 3
White : Coloured

Duplicate Recessive Epistasis [9 : 7 Ratio]:

When recessive alleles at either of the two loci can mask the expression of dominant alleles at the two loci, it is called duplicate recessive epistasis. This is also known as complementary epistasis. The best example of duplicate recessive epistasis if found for flower colour in sweet pea.

The purple colour of flower in sweet pea is governed by two dominant genes say A and B. When these genes are in separate individuals (AAbb or aaBB) or recessive (aabb) they produce white flower.

A cross between purple flower (AABB) and white flower (aabb) strains produced purple colour in F1. Inter-mating of F1 plants produced purple and white flower plants in 9 : 7 ratio in F2 generation (Fig. 8.5). This can be explained as follows.Here recessive allele a isepistatic to B/b alleles and mask the expression of these alleles. Another recessive allele b is epistatic to A/a alleles and mask their expression.

Hence in F2, plants with A-B-(9/16) genotypes will have purple flowers, and plants with aaB-(3/16), A-bb-(3/16) and aabb (1/16) genotypes produce white flowers. Thus only two phenotypic classes, viz., purple and white are produced and the normal dihybrid segregation ratio 9 : 3 : 3 : 1 is changed to 9 : 7 ratio in F2 generation

Interaction: Homozygous recessive of either gene A or B produce white

9/16 Purple
7/16 White

White flowers × White flower
CCpp × PPcc
CcPp × CcPp
Purple Purple

CP = 9 Purple
Cp = 3 White
cP = 3 White
cp = 1 White
9 : 7
Purple White

	CP	Cp	cP	cp
CP	CCPP Purple	CCPp Purple	CcPP Purple	CcPp Purple
Cp	CCPp Purple	CCpp White	CcPp Purple	Ccpp White
cP	CcPP Purple	CcPp Purple	ccPP White	ccPp White
cp	CcPp Purple	Ccpp White	ccPp White	ccpp White

Supplementary genes are two independent dominant genes interacting to produce a phenotypic expression different from that produced by either gene alone. of the first gene. For example, the development of grain colour in maize is governed by 2 dominant genes 'R' and 'P'

Topic- 9

MUTATION

A mutation, which may arise during replication and/or recombination, is a permanent change in the nucleotide sequence of DNA. Damaged DNA can be mutated either by substitution, deletion or insertion of base pairs. Mutations, for the most part, are harmless except when they lead to cell death or tumor formation. Because of the lethal potential of DNA mutations cells have evolved mechanisms for repairing damaged DNA.

Types of Mutations

There are three types of DNA Mutations: base substitutions, deletions and insertions.

1. Base Substitutions

Single base substitutions are called point mutations, recall the point mutation Glu -----> Val which causes sickle-cell disease. Point mutations are the most common type of mutation and there are two types.

Transition: this occurs when a purine is substituted with another purine or when a pyrimidine is substituted with another pyrimidine.

Transversion: when a purine is substituted for a pyrimidine or a pyrimidine replaces a purine.

Point mutations that occur in DNA sequences encoding proteins are either silent, missense or nonsense.

Silent: If abase substitution occurs in the third position of the codon there is a good chance that a synonymous codon will be generated. Thus the amino acid sequence encoded by the gene is not changed and the mutation is said to be silent.

Missence: When base substitution results in the generation of a codon that specifies a different amino acid and hence leads to a different polypeptide sequence. Depending on the type of amino acid substitution the missense mutation is either conservative or nonconservative. For example if the structure and properties of the substituted amino acid are very similar to the original amino acid the mutation is said to be conservative and will most likely have little effect on the resultant proteins structure / function. If the substitution leads to an amino acid with very different structure and properties the mutation is non conservative and will probably be deleterious (bad) for the resultant proteins structure / function (i.e. the sickle cell point mutation).

Nonsense: When a base substitution results in a stop codon ultimately truncating translation and most likely leading to a nonfunctional protein.

2. Deletions

A deletion, resulting in a frameshift, results when one or more base pairs are lost from the DNA . If one or two bases are deleted the translational frame is altered resulting in a garbled message and nonfunctional product. A deletion of three or more bases leave the reading frame intact. A deletion of one or more codons results in a protein missing one or more amino acids. This may be deleterious or not.

3. Insertions

The insertion of additional base pairs may lead to frameshifts depending on whether or not multiples of three base pairs are inserted. Combinations of insertions and deletions leading to a variety of outcomes are also possible.

Causes of Mutations

Errors in DNA Replication

On very, very rare occasions DNA polymerase will incorporate a noncomplementary base into the daughter strand. During the next round of replication the missincorporated base would lead to a mutation. This, however, is very rare as the exonuclease functions as a proofreading mechanism recognizing mismatched base pairs and excising them.

Errors in DNA Recombination

DNA often rearranges itself by a process called recombination which proceeds via a variety of mechanisms. Occasionally DNA is lost during replication leading to a mutation.

Chemical Damage to DNA

Many chemical mutagens, some exogenous, some man-made, some environmental, are capable of damaging DNA. Many chemotherapeutic drugs and intercalating agent drugs function by damaging DNA.

Radiation

Gamma rays, X-rays, even UV light can interact with compounds in the cell generating free radicals which cause chemical damage to DNA.

DNA Repair

Damaged DNA can be repaired by several different mechanisms.

Mismatch Repair

Sometimes DNA polymerase incorporates an incorrect nucleotide during strand synthesis and the 3' to 5' editing system, exonuclease, fails to correct it. These mismatches as well as single base insertions and deletions are repaired by the mismatch repair mechanism. Mismatch repair relies on a secondary signal within the DNA to distinguish between the parental strand and daughter strand, which contains the replication error. Methylation of the sequence GATC occurs on both strands sometime after DNA replication. Because DNA replication is semi-conservative, the new daughter strand remains un methylated for a very short period of time following replication. This difference allows the mismatch repair system to determine which strand contains the error. A protein, MutS recognizes and binds the mismatched base pair.

Nucleotide Excision Repair (NER)

NER in human cells begins with the formation of a complex of proteins XPA, XPF, ERCC1, HSSB at the lesion on the DNA. The transcription factor TFIIH, which contains several proteins, then binds to the complex in an ATP dependent reaction and makes an incision. The resulting 29 nucleotide segment of damaged DNA is then unwound, the gap is filled (DNA polymerase) and the nick sealed (ligase).

Direct Repair of Damaged DNA

Sometimes damage to a base can be directly repaired by specialized enzymes without having to excise the nucleotide.

Recombination Repair

This mechanism enables a cell to replicate past the damage and fix it later.

Regulation of Damage Control

DNA repair is regulated in mammalian cells by a sensing mechanism that detects DNA damage and activates a protein called p53. p53 is a transcriptional regulatory factor that controls the expression of some gene products that affect cell cycling,

Role of Mutation in Crop improvement

Conventional mutation techniques have often been used to improve yield, quality, disease and pest resistance in crops, or to increase the attractiveness of flowers and ornamental plants. More than 1700 mutant varieties involving 154 plant species have been officially released. In some economically important crops, e.g. barley, durum wheat and cotton, mutant varieties occupy the majority of cultivated areas in many countries. Mutation techniques have become one of the major tools in the breeding of ornamentals such as Alstroemeria, Begonia, Chrysanthemum, Carnation, Dahlia and Streptocarpus. The use of in vitro techniques such as anther culture, shoot

organogenesis, somatic embryogenesis and protoplast fusion can overcome some of the limitations in the application of mutation techniques in both seed and vegetative propagated crops. In vitro culture in combination with induced mutations can speed up breeding programmes, from the generation of variability, through selection, to multiplication of the desired genotypes. The expression of induced mutations in the pure homozygote obtained through microspore, anther or ovary culture, can enhance the rapid recovery of the desired traits. In some vegetative propagated species, mutations in combination with in vitro culture technique, may be the only method of improving an existing cultivar. Currently, many molecular studies rely on the induction and identification of mutants in ’model species’ for construction and subsequent saturation of genetic maps, understanding of developmental genetics and elucidation of biochemical pathways. Once identified and isolated, the genes that encode agronomically-important features can be either introduced directly into crop plants or used as probes to search for similar genes in crop species. It seems most likely that the recent developments based on these technologies will soon provide improved methods for selection of desired mutants.

Plant mutation can be artificially affected by Mutagenic agentsand its utilization for production of superior variety which is called as plant mutation breeding.Some of the crops in which this knowledge has been authentically utilized are:

1. Rice 2. Wheat 3. Cotton 4.Sugarcane

Mutation breeding and its role in evolution.

Mutation breeding and its role in evolution was explained by Hugo de Vries in 1901.According to this theory:

1) Mutation carries the chance of selection.

2) Mutant arises through new species.

3) Mutation can be due to change in the chromosome number.

Mutation breeding-selection of Plants

a) Mutation breeding in self-pollinating plants

b) Mutation breeding in cross pollinating plants

c) This can take place in vegetative propagating plants.

d) In seed propagating plants

Topic- 10

Cell cycle

The cell cycle is an ordered series of events involving cell growth and cell division. The cell cycle has two major phases

1 The interphase and

2. the Mitotic phase.

During interphase the cell prepares itself by accumulating nutrient and raw material for mitotic phase, During this stage which is divided into G1, s and G2

G1 Phase

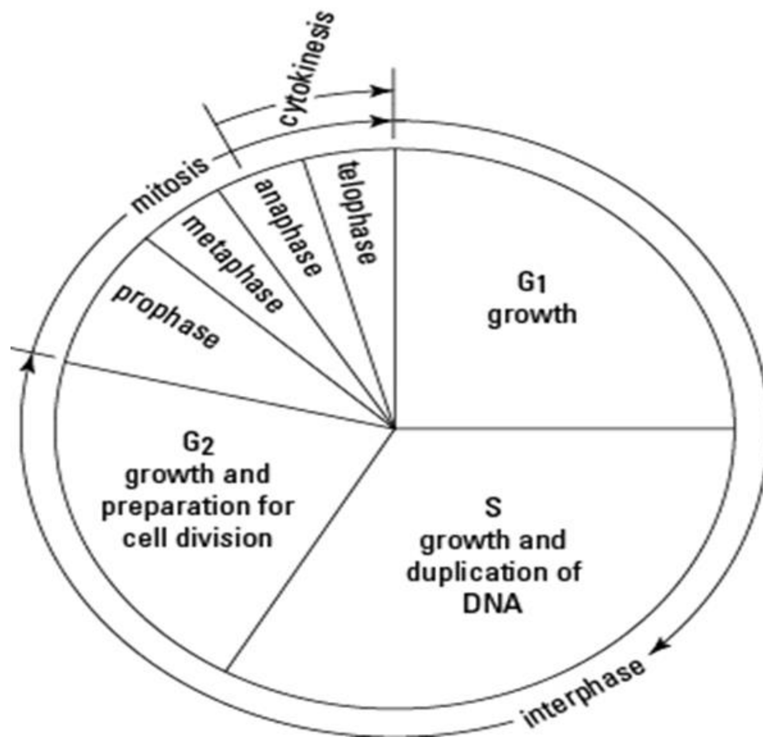
During this phase little change is visible although the cell is biochemically very active. The cell during this stage remains busy accumulating building blocks for new DNA molecule besides conserving the existence of native parental DNA. Associated proteins for such action are also synthesized. Enough energy sources is required for DNA replication for the cell conserves during this phase.

S phase

S phase is the period of wholesale DNA synthesis during which the cell replicates its genetic content; a normal diploid somatic cell with a 2N complement of DNA at the beginning of S phase acquires a 4N complement of DNA at its end. (Recall that N = 1 copy of each chromosome per cell [haploid]; 2N = 2 copies [diploid].) The duration of S phase may vary from only a few minutes in rapidly dividing, early embryo cells to a few hours in most somatic cells. Early embryo cells generally "live off" the accumulated stores of maternal RNA and proteins present in the egg and are transcriptionally silent, whereas cells in later development and mature organisms must actively transcribe subsets of their genes to survive and maintain specialized functions. The longer time required for the latter to complete S phase probably allows these cells to coordinate DNA replication with transcription and to preserve higher-order gene and chromatin structural information that influences gene expression for transmission to progeny cells.

G2 phase

During this stage the cell stores energy and synthesizes proteins required for manipulation of Chromosomes. G2 phase and the beginning of mitosis are denoted by a 4-N DNA content. Following DNA replication and prior to cell division (cytokinesis), cells must maintain the integrity and proximity of the recently duplicated chromosomes (sister chromatids).



Different stages of Cell Cycle

Topic-11

Polyploidy

Polyploidy is the condition whereby a biological cell or organism has more than two homologous sets of chromosomes, with each set essentially coding for all the biological traits of the organism. A haploid (n) only has one set of chromosomes. A diploid cell (2n) has two sets of chromosomes. Polyploidy involves three or more times the haploid number of chromosomes. Polyploid types are termed according to the number of chromosome sets in the nucleus: triploid (three sets; 3n), tetraploid (four sets; 4n), pentaploid (five sets; 5n), hexaploid (six sets; 6n), and so on.

To define this further, homologous chromosomes are those non-identical chromosomes that contain information for the same biological features and contain the same genes at the same loci, but possibly different genetic information, called alleles, at those genes. For example, two chromosomes may have genes encoding eye color, but one may code for brown eyes, the other for blue. Non-homologous chromosomes, representing all the biological features of an organism, form one set, and the number of sets in a cell is called ploidy. In diploid organisms (most plants and animals), each homologous chromosome is inherited from a different parent. But polyploid organisms have more than two homologous chromosomes.

Organisms with more than 2 sets of chromosomes are polyploidy When there are 3 sets, this is called triploid, or 3n, and organisms with 4 sets are called tetraploid, or 4n.

There are three types of polyploidy,

Autopolyploidy: Autopolyploidy appears when an individual has more than two sets of chromosomes, both of which from the same parental species..

Allopolyploidy: Allopolyploidy, on the other hand, occurs when the individual has more than two copies but these copies, come from different species

Auto-allopolyploidy: This term was used by Kostoff in 1939 to denote a condition where an allopolyploid individual also shows the characteristics of auto-polyploidy for one or more genomes. If there are two genomes, e.g. A and B, the auto-allopolyploid may be AAAABB, AABBBB or AAAABBBB. Thus auto-allopolyploidy is possible from the level of hexaploidy (6x) and above.

Polyploid crops

In plant breeding, the induction of polyploids is a common technique to overcome the sterility of a hybrid species. Triticale is the hybrid of wheat (Triticum turgidum) and rye (Secale cereale). It combines sought-after characteristics of the parents, but the initial hybrids are sterile. After

polyploidization, the hybrid becomes fertile and can thus be further propagated to become triticale. Polyploid plants in general are more robust and sturdy than diploids. In the breeding of crops, those plants that are stronger and tougher are selected. Thus, many crops have unintentionally been bred to a higher level of ploidy:

Triploid crops: banana, apple, ginger

Tetraploid crops: durum or macaroni wheat, maize, cotton, potato, cabbage, leek, tobacco, peanut, kinnow, Pelargonium

Hexaploid crops: chrysanthemum, bread wheat, triticale, oat

Octaploid crops: strawberry, dahlia, pansies, sugar cane

Some crops are found in a variety of ploidy. Apples, tulips and lilies are commonly found as both diploid and as triploid. Daylilies (*Hemerocallis*) cultivars are available as either diploid or tetraploid. Kinnows can be tetraploid, diploid, or triploid.

In the case of bananas, while the original bananas contained rather large seeds, triploid (and thus seedless) cultivars have been selected for human consumption. Cultivated bananas are sterile (parthenocarpic), meaning that they do not produce viable seeds. Lacking seeds, another form of propagation is required. These are propagated asexually from offshoots of the plant.

<u>Polyploids can be stable or sterile</u>

Like diploids (2n=2x), stable polyploids generally have an even number of copies of each chromosome: tetraploid (2n=4x), hexaploid (2n=6x), and so on. The reason for this is clear from a consideration of meiosis. Remembering that the purpose of meiosis is to reduce the sum of the genetic material by half, meiosis can equally divide an even number of chromosome sets, but not an odd number. Thus, polyploids with an odd number of chromosomes (e.g. triploids, 2n=3x) tend to be sterile, even if they are otherwise healthy.

Cytological behaviour of autopolyploid is briefly discussed as below:

I) Due to abnormalities in meiotic cell division, functional gametes are rarely formed in triploids. They are mostly sterile and rarely set seed on selfing or out-crossing.

(II) Autotetraploids:

These usually show greater vigour, increased cell size, mainly in stomata and guard cells. Plants show gigantic growth but rate of fertility is lowered. Example of stable Autotetraploids are Black gram, Wheat, Rice, Chilli etc

(c) Auto-pentaploids:

These behave like tetraploids. The phenotype may differ.

(d) Auto-hexaploids:

These are more stable. Meiosis may be more regular and fertility high. Multivalents already occur.

(ii) Allopolyploids:

Polyploidy may also result from doubling of chromosome number of F1 hybrid which is derived from two distinctly different species. This is a product of two different set of genome designated as A and B. The hybrid produced will have a set of genome from A and a set of genome from B. Such polyploids are also called as Allotetraploids or amphidiploids.

Russian Geneticist G.D. Karpechenko (1927) by crossed Raphanus sativus (2n = 18) and Brassica oleracea (2n = 18). The hybrid formed by crossing these two species is itself a diploid (2n = 18). It contains only one set of chromosome of radish (n = 9) and one set of chromosome of cabbage (n = 9) . The hybrid differs from both the parents and showed many characters of both. The product is sterile because pairing of chromosome could not occur. During this hybridization sometimes gametes are formed gamete which contains one complete set of radish chromosomes and one complete set of cabbage chromosomes. When such gametes combine a plant is produced which contains two sets of radish chromosome and two sets of cabbage chromosomes (18+18 = 36). A regular and fertile plant was produced which exhibited leaves like radish and root like cabbage. This was named as Raphanobrassica. During the recent years a new genus Triticale has been synthesised by combining the chromosome of Triticum duram and Secale cereale (rye). This new genus Triticale is a very useful allopolyploid (2n = 56).

. **Aneuploidy or secondary polyploidy = (heteroploidy**):

Another type of difference in the chromosome number is known as aneuploidy (not true ploidy in which.

Blakeslee (1910) discovered in Datura stromonium, the first case of aneuploidy. When a diploid individual having one chromosome represented three or four times instead of twice is called as polysomic.

When the chromosome complement is increased by one chromosome, it is called trisomic (2n + 1). These are found in Drosophila and more common in plants. Organisms containing 2n—1 chromosomes are called monosomic but they are neither fertile and nor vigorous.

If the increase is in two or more different chromosomes, each having one extra homologue, then it is called double trisomic (2n + 1 + 1). When both the chromosome of a given pair are missing, the individual is called a nullisomic (2n—2). These are inviable in some species but viable in

others.If there are two homologues added to a chromosome pair, then it is called tetrasomic (2n + 2) and when it is 2n + 2+ 2 and so on, it is called double tetrasomic. Polysomics form trivalents, quadrivalents according to the duplications. Trisomy has led to pollen sterility.