CHAPTER 5 : MOLECULAR BASIS OF INHERITANCE

Page No. : **79-107**

Total Pages : **29**

Questions Asked : **70**

1-2 QUESTION PER PAGE AT AN AVERAGE

BUT, LETS SEE WHICH PAGE HAS MAXIMUM WEIGHTAGE

- **Which page has the maximum**

101 = 1 Page

% QUESTIONS

2010-2024		Page No.
	0	79,86,87,89,104
10,14,15,16(2),18 (2),19,22	1	85,80,94,97, 98, 99,102
11(2),17,20,22(2)	2	81,82,88,90,95, 103
10(2),11,12(2),14,15(3),16 17(2),18,19(2),20,22(3)	3	83,84,93,96,105, 106
10(3),11,13(2),14 15,16,17,19(2),20,22	4	91,92,100
10,13,15,18,20,22	5	101
24	6	84,90,92,95,100

MOLECULAR BASIS OF INHERITANCE

1. Nucleic acid: Polymer of Nucleotides eg: DNA & RNA
2. Nitrogen Base + Pentose sugar + Phosphate = Nucleotide
3. Nitrogen Base + Pentose sugar = Nucleoside

[RE-NEET-2024] [NEET-2019] [NCERT 80]

4. **Nitrogenous bases :** Purines (Adenine & Guanine)

   Pyrimidines (Cytosine, Uracil and Thymine) **[RE-NEET-2024]**

5. Thymine only present in DNA. Uracil present in RNA at the place of Thymine.

   DNA: Long polymer of deoxribonucleotides.

6. Acidic substance present in nucleus, 1st identified by **Friedrich Meischer** in 1869 & named as **Nuclein.**
7. In 1953, **James Watson & Francis Crick,** based on X-ray data diffraction (produced by **Maurice wilkins & Rosalind Franklin**) proposed a very simple & Famous Double Helix model for the structure of DNA.
8. **Chargaff Rule:** Ratio between Adenine & Thymine & Guanine & Cytosine are constant & equals one. For ds DNA

DNA.(NEET-2021, 2015) [NCERT 81]

9. **Complimentary:** If the sequence of base in one strand is known then the sequence in other strand can be predicted.
10. **Salient features of ds DNA**
    1. Made up of two polynucleotide chain, backbone constituted sugarphosphate & base projected inside.
    2. Two chains have anti-parallel polarity.
    3. Bases in two strands paired through hydrogen bond.

       $A = T$ & $G \equiv C$

(NEET-2020) [NCERT 81]

Always a purine comes opposite to pyrimidine (generate appx. uniform distance between the two strands of the helix)

4. The two chains are coiled in a right-handed fashion.

   Pitch of helix = 3.4 nm & roughly 10 bp in each turn.

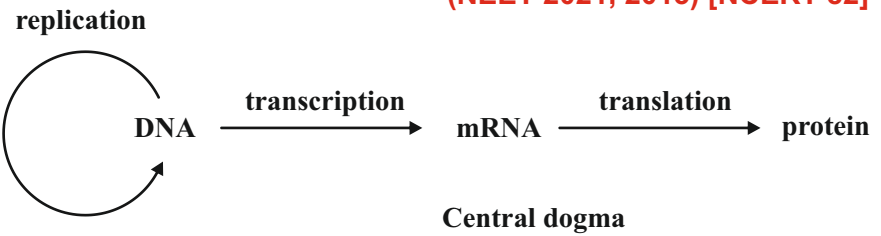
   Distance b/w a bp = 0.34 nm.

5. The plane of one base pair stacks over the other in double helix.

   (confers stability of the helical structure)

11. **Central Dogma** proposed by **Francis crick.** which states that genetic information flows from DNA ⇨ RNA ⇨ Protein.

(NEET-2021, 2013) [NCERT 82]



Central dogma

12. In some viruses the flow of information is in reverse direction, that is from RNA to DNA

13. Another chemical name of **Thymine is 5-methyl uracil**

Packaging of DNA Helix

1. Length of DNA Helix = Total number of base pair X distance b/w two consecutive bp.

(NEET-2022) [NCERT 83]

2. Length of DNA is Typical mammalian cell = 2.2 meters.

(NEET-2020) [NCERT 83]

3. Length of DNA in E.coli = 1.36 mm.

14. In **Prokaryotes "Nucleoid"** term is used at the place of nucleus. DNA in nucleoid is a organised in large loops held by proteins.

15. **In Eukaryotes**

[RE-NEET-2024] [NEET-2021,23] [NCERT 83]

Histone : Positively charge & Basic

DNA : Negatively charge & Acidic

- Histone are rich in **Basic amino acid Lysine & Arginine**

(NEET-2022, 2021) [NCERT 83]

- Histones are organised to form a unit of eight molecules called **Histone Octamer** (H^2A, H^2B, H^3 & H^4)
- **Nucleosome:** Negatively charged DNA is wrapped around the positively charged histone octamer.

[RE-NEET-2024] [NEET 2022] [NCERT 84]

- A typical nucleosome contain **200 bp** of DNA helix.

[NEET 2022]

- Nucleosomes constitute the repeating unit of a structure in nucleus called **chromatin**. (thread like stained body seen in nucleus)
- Nucleosomes in chromatin are seen as **"Beads-on-string"** structure when viewed under microscope.
- Packaging of chromatin at higher level requires additional set of protein that referred to as Non-histone chromosomal **(NHC)** proteins.
- Loosely packed (Light strain) = Euchromatin (Active)

  Densely packed (Dark strains) = Heterochromatin (Inactive)

[RE-NEET-2024] [NEET 2022] [NCERT -84]

16. Bacterophage ø ×174 = 5386 nucleotides

Bacteriophage lambda = 48502 base pair

Escherichia coli = 4.6×10^{6} base pair

Human (Haploid) = 3.3×10^{9} base pair

(NEET-2014) [NCERT 80]

TRANSFORMING PRINCIPLE

17. **Frederick Griffith (1928).** experiments on **Streptococus pneumoniae bacteria** **[NEET 2024] [NCERT 84]**

18. Bacteria grown on a culture plate produce

1. Smooth shiny colonies (s) - Mucous (Polysaccharides) coat (Virulent)

2. Rough colonies → (Non-virulent)

19. S strain ⇨ injected into mice ⇨ Mice die

R strain ⇨ injected into mice ⇨ Mice live

S strain ⇨ injected into mice ⇨ Mice live

s strain (Heat killed)
R strain(live) ⟶ Injected into mice Mice die

[Recovered living S bacteria from dead mice]

20. **Conclusion:** Some transforming principle, transferred from the heat killed "S" strain, had enabled the "R" strain to synthesise a smooth polysaccharides coat & become virulent due to transfer of genetic material.

21. Biochemical nature of genetic material was **not** defined from his experiment.

BIOCHEMICAL CHARACTERISATION OF TRANSFORMING PRINCIPLE

22. Done by **Oswald Avery, colin Mac Leod & Mccarty.**

23. They purified biochemical nature of protein, DNA & RNA & find that DNA alone from S bacteria caused R Bacteria to become transformed.

24. Also, protein digesting enzyme (Protease), RNA digesting enzyme (RNAes) **did not** affect transformation, so transforming substance are not protein & RNA.

25. Digestion with DNase did **inhibit transformation** so, DNA caused the transformation. They concluded that DNA is the genetic material but **not all** biologists were convinced.

HERSHEY-CHASE EXPERIMENT (1952)

26. The **unequivacal proof that DNA is the genetic material** comes from this experiment.

(NEET-2023) [NCERT 85]

27. They worked with viruses that infect bacteria called **Bacteriophages.**

28. They used **E.coli bacteria**

29. Viruses grow on medium

    ⇨ contain radioactive phosphorous (DNA⇨ Radioactive)

    ⇨ contain radioactive sulphur (Protein⇨ Not radioactive)

30. Bacteria which was infected with viruses that had radioactive DNA were radioactive, indicating that DNA was the material that passed from virus to bacteria.

31. **Steps:** Infection⇨ Blending ⇨ Centrifugation

32. Protein did not enter the bacteria from viruses.

33. DNA is therefore the genetic material that passed from virus to bacteria

PROPERTIES OF GENETIC MATERIAL

34. Above experiments proof that DNA is the genetic material but in **some viruses RNA is the genetic material eg: Tobacco mosaic viruses, QB bacteriophage.**

(NEET-2016) [NCERT 87]

35. **Criteria for genetic material**

    (I) Should be able to generate its replia **(Replication)**

    (ii) Should be **Chemically & structurally stable**

    (iii) Should provide the **scope for slow changes (Mutation)** that requires for evolution.

    (iv) Should be able to express itself in the form of **"Mendelian characters"**

36. Both the nucleic acid (DNA & RNA) have the ability to direct their duplications.

37. Genetic material should be stable enough **not to change** with different stages of life cycle, age **or** with change in the physiology of the organism.

38. Two strands being complementary, if seperated by heating come together when appropriate conditions are provided.

39. **2'-OH group** present at every nucleotide in RNA is **reactive** group & make RNA **liable & easily degradable.**

40. RNA are **catalytic & Reactive** as compared to DNA (less reactive & more stable).

41. Both DNA & RNA are **able to mutate.** RNA being unstable & mutate at a faster rate.

(NEET-2023) [NCERT 87]

42. Viruses having RNA genome & having shorter life span mutable & evolve faster.

(NEET-2023) [NCERT 87]

PROPERTIES OF GENETIC MATERIAL

43. Among two nucleic acid (DNA & RNA) DNA is the better genetic material.
44. RNA can directly code for protein synthesis & DNA depends on RNA for synthesis of protein.
45. For **storage of genetic information -** DNA & for **transmission of genetic information RNA is better.**
46. **RNA** was the **first genetic material** & essential for life process such as metabolism, Translation, splicing evolved around RNA.
47. **Semi conservative** model for DNA replication was given by **Watson & Crick.**

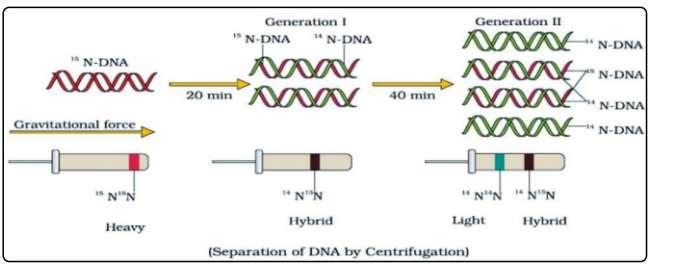
(NEET-2018) [NCERT 87]

48. **DNA replicate semiconservatively was proposed by-**
    1. Mathew Meselson & Franklin stahl **(E. Coli) (1958)**
    2. Taylor & colleagues **(Vicia faba) (1958)**

(NEET-2016) [NCERT 90]

MESELSON & STAHL EXPERIMENTS

49. Used heavy isotope of (N^{15}) **not** radioactive. **(NEET-2024)**
50. Grew **E.coli** in NH_4Cl medium.
51. DNA centrifugation by **CsCl** (Distinguish of heavy DNA from normal DNA)



Meselson and Stahl's Experiment

52. **E. coli** divide in **20 minutes.**

Taylor experiments

53. Use of **radioactive thymidine**

Machinery & Enzymes for Replication

54. Replication in E.coli requires a set of enzyme.

55. Main enzyme for replication is **DNA dependent DNA polymerase**

(NEET-2016) [NCERT 90]

56. DNA dependent DNA polymerase - Highly efficient enzyme & catalyses polymerisation in very **short time.**

57. Replication time in **E. coli is 18 minute.**

58. Average rate of polymerisation is **approx 2000 bp per second** (with high degree of acuracy)

59. Energetically replication is **very expensive process**

60. Deoxyribonucleoside triphosphate serve **dual purpose.**

    1. Acts as substrate
    2. Provide energy for polymerisation.

(NEET-2014) [NCERT 90]

61. DNA dependent DNA polymerase catalyses the polymerisation in **only one direction** that is 5' ⇨3'

62. One strand (the template with polarity 3'⇨5') replication is **continuous** & other (template with polarity 5'⇨3') it is **Discontinuous.**

(NEET-2017) [NCERT 90]

63. Discontinuous synthesised fragments are jointed by the enzyme **DNA ligase.**

64. Replication does not initiate randomly at any place in DNA, a definite region in E. coli where replication originate called **origin of replication.**

65. Replication of DNA takes place at S-phase of the cell cycle.

TRANSCRIPTION

66. Process of copying genetic information from one strand of the DNA into RNA.

67. Principle of complimentarily governs the process of transcription **except** Adenine now forms base pair with uracil instead of thymine.

(NEET-2018) [NCERT 91]

68. In transcription only a segment of DNA & only one of the strands of DNA is copied into RNA.

69. **If both strands copied during transcription then**

    1. They would code for RNA molecule with different sequences & one segment of DNA would be coding for two different protein (complicates genetic information transfer mechinery)
    2. Two RNA molecules forms Ds RNA & prevent splicing (Protein synthesis).

TRANSCRIPTION UNIT

1. A promoter (5' end) **(NEET-2024)**
2. The structural gene
3. A terminator (3' end)

70. Enzyme for transcription **DNA dependent RNA polymerase.**

71. This enzyme catalyses the polymerisation in only **one direction** 5'⇨3'

72. Polarity 3'⇨5' referred to **template strand.**

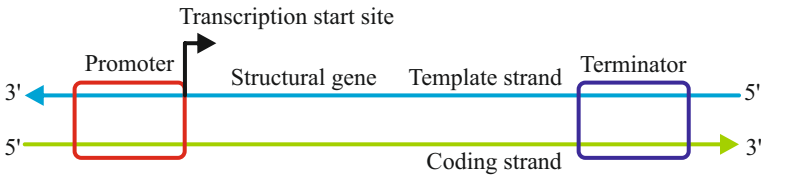
(NEET-2014,2024) [NCERT 92]

73. Polarity (5'⇨3'), sequence same as RNA **(except thymine at the place of uracil).** is displace during transcription.

(NEET-2023)

74. Strand which **do not code** for anything is refered to as **coding strand.**

75. Schematic structure of a transcription unit



76. **All the reference point** while defining a transcription unit is made with **coding strand.**

77. **Promoter:** is a DNA sequence that provides binding site for RNA polymerase

78. **Terminator:** usually defines the end of the process of transcription.

79. **Cistron:** As a segment of DNA coding for a polypeptides

(NEET-2016) [NCERT 93]

80. **Structural gene:** Monocistronic (mostly Eukaryotes)

Polycistronic (mostly prokaryotes OR Bacteria)

81. The gene is Eukaryotes are split.

82. Intron: Also called Intervening sequence, do not appear in mature or processed RNA

83. The split-gene arrangement further complicates the definition of a gene in terms of a DNA segment.

(NEET-2021) [NCERT 93]

84. Inheritance of a character is also affected by promoter & regulatory sequences of a structural gene.

TYPE OF RNA & PROCESS OF TRANSCRIPTION:

85. **In Bacteria:**

- **Three major type of RNAs:** mRNA, tRNA & rRNA.
- All three RNAs are needed to synthesise a protein in a cell

- **mRNA:** Provides template, **tRNA**- brings amino acid & reads genetic code & **rRNA** play structural & catalytic role during translation.
- Single DNA dependent RNA polymerase catalyses transcription of all types of RNA in bacteria.
- RNA polymerase binds to promoter & initiate transcription.
- **Three steps in transcription**
    1. Initiation
    2. Elongation
    3. Termination
- **It uses nucleoside triphosphates** as substrate & polymerise in template dependend fashion.
- At terminator region, the nascent RNA falls off, so also RNA polymerase (terminator)

86. RNA polymerase catalyses **all three steps.** It associated transiently with initiation-factor & terminator factor to initiate & terminate the transcription.

[RE-NEET-2024] [NEET-2021] [NCERT 94]

87. In **Bacteria,** mRNA does not require any processing. Since transcription & translation take place in same compartment.

88. Transcription & translation can be **coupled** in Bacteria.

TRANSCRIPTION IN EUKARYOTES

89. Two additional complexities
    1. Three RNA polymerase present in nucleus.
    - **RNA polymerase I :** rRNAs (28s, 18s, 5.8s)

[RE-NEET-2024] [NEET-2021][NCERT 95]

- **RNA polymerase II :** mRNA (hnRNA)

- **RNA polymerase III:** tRNA (5 sr RNA, sn RNA)

(NEET-2021,23,24)[NCERT-95]

2. Primary transcripts contain both the exon & Intron & are non functional.

90. **Splicing:** Removal of intron & joining of Exon.

(NEET-2012,2024) [NCERT 95]

91. hn RNA undergoes two additional processing - capping & Tailing

Capping : Unusual nucleotide (methyl guanosine triphosphate) are added at 5'end of m RNA

(NEET-2021) [NCERT 95]

Tailing : Adenylate residues (200-300) are added at **3'-end** in template independent manner.

92. Fully processed hnRNA now called mRNA, transported out of nucleus for translation. **(NEET-2021) [NCERT 95]**

GENETIC CODE

Translation led to the proposition of a genetic code that could direct the sequence of amino acid during the synthesis of proteins.

93. The proposition & deciphering of genetic code were most challenging.

Genetic code given by a **Physicist George Gamow,** who argued that only **4 bases** & code for **20 amino acid.**

94. He suggested that in order to code for all 20 amino acids, the code should be made up of three nucleotides.

95. More daunting task ⇨ codon was triplet.

96. **Chemical method developed by Har Gobind khorana was** instrumental in synthesising RNA molecules with defined combinations of bases **(Homopolymers & copolymers).**

(NEET-2024)

97. **Marshall Nirenberg's** cell free system for protein synthesis finally helped the code to be deciphered.

98. **Severo ochoa enzyme (Polynucleotide phosphorylase)** help in polymerising RNA with defined sequences in **template independent manner.**

99. **Salient features of genetic code**

(NEET-2019, 2013) [NCERT 95]

1. Codon is **triplet.** 61 codons code for amino acid. 3 codons do not code for any amino acids, functions as **stop codon** (UAA, UAG, UGA)
2. One codon codes for only one amino acid ⇨ **unambiguous & specific**
3. Codon is read in mRNA in a **continous fashion, no punctuations.**
4. The codon is **nearly universal**
5. AUG has dual functions (Also acts as initiator codon)

(NEET-2016)[NCERT 96]

100. From bacteria to human UUU code for phenylalanine.

101. Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion.

102. Insertion or deletion of three or its multiple bases or delete one or multiple codon, reading frame remains unaltered from that point onwards.

Referred to as **Frame-shift insertion or deletion mutation**.

(NEET-2019, 2017) [NCERT 97]

tRNA (Adapter molecule): Given by **Francis Crick**

103. He postulated the presence of an adapter molecule that would on one hand read the code & on other hand would bind to specific amino acids.

104. The tRNA, called **sRNA** (soluble RNA)

105. tRNA has an **anticodon loop,** an **amino acid acceptor end.**

106. For initiation, there is another specific tRNA referred to an initiator tRNA.

107. There is no **tRNA for stop codons.**

108. **Secondary structure of** tRNA look like a **clover-leaf**

109. **Actual structure,** the tRNA is compact molecule looks like **inverted L.**

TRANSLATION

110. Process of polymerisation of amino acids to form a polypeptide.

111. The order & sequence of amino acids are defined by the sequence of bases in the mRNA.

112. Formation of a peptide bond requires energy

(NEET-2022, 2020) [NCERT 98]

113. **Charging of tRNA or aminoacylation of tRNA-** Aminoacids itself activated in the presence of ATP & linked to their cognate tRNA.

114. It two charged tRNA are brought close enough the formation of peptidebond between them would be favoured energetically.

115. The presence of a catalyst would enhance the rate of peptide bond formation.

116. Ribosomes in its inactive state consists of **two sub unit**

- Larger subunits
- Smaller subunits

117. Also some additional sequences that are not translated that is UTR. (untranslated regions)

118. **UTRs present** at both **5''-end** (before start codon) & **3'-end** (after stop codon required for efficient translation process.

- Ribosomes = RNAs + 80 different proteins

(NEET-2023)[NCERT-99]

119. Three steps : Initiation, Elongation, Termination

120. Ribosomes moves from codon to codon along the mRNA - Translocation

121. Translation dictated by DNA & represented by mRNA.

122. Termination: Release factor bind to the stop codon & releasing the complete polypeptide from the ribosomes.

REGULATION OF GENE EXPRESSION

123. **Very broad term that** may occur at various levels

124. In Eukaryotes it regulated at **several levels.**

    1. Transcriptional level (Formation of primary transcript)
    2. Processing level (Regulation of splicing)
    3. Transport of mRNA from nucleus to cytoplasm
    4. Translational level

125. The development & differentiation of embryo into adult organism are results of the coordinated regulation of expression of several sets of genes.

126. In prokaryotes, control of the rate of **transcriptional initiation** is the site for control of gene expression.

127. **Lac operon**

    1. Given by **Geneticist, Francois Jacob & a biochemist, Jacque Monod.**

    (NEET-2018,2024) [NCERT 100]

    2. Lac refers to **Lactose (Inducer)**

    (NEET-2016) [NCERT 100]

    3. Consists of three structural gene & one regulatory gene

Regulatory gene: "I" gene (inhibitor)

Structural gene : Z - gene code for beta-galactosidase (B-gal)

[RE-NEET-2024] [NEET-2019,23]

Y-gene code for permease

(NEET-2022,23,2014)

a - gene code for transacetylase

[NCERT 100]

128. B-galactosidase responsible for the hydrolysis of the disaccharides, Lactose into monomeric units Glucose & Galactose.

129. Permease, increase permeability of cell to B-galactosides.

(NEET-2024)

130. All three genes products in lac open are required for metabolism of lactose.

131. In the **absence of Inducer** (Lactose) repressor binds to operator region & prevents RNA polymerase from transcribing the operon.

132. In the presence of Inducer repressor protein inactive, operator gene Free for transcription & translation process.

133. A very low level of expression of lac operon has to be present in the cell all time otherwise lactose cannot enter the cells.

134. Glucose **or** Galactose **cannot** act as inducer for lac operon.

[RE-NEET-2024]

135. Regulation of lac operon by repressor is referred to as **Negative regulation** **(NEET-2015) [NCERT 101]**

Lac operon is under control of positive regulation as well.

HGP. (Human Genome Project) : Mega Project

136. H.G.P. a very ambitious project of sequencing human genome, **launched** in 1990 & **completed in 2003,** it is a **13 year project.**

137. Human genome have appx. **3×10^9 bp** & cost of sequencing required is **US $ 3 per bp.**

138. Total estimated cost of project would be appx. **9 billion us dollers**

139. HGP was closely associated with the rapid development of new area in biology called **Bioinformatics.**

GOALS OF HGP

140. Approx 20,000 - 25,000 genes in human DNA.

141. Determine the sequences of the three billion chemical base pair that make up human DNA.

142. Store this information in databases.

143. Improve toos for data analysis.

144. Transfer related technique to other sectors (like industries).

145. Address the **ethical, Legal and social issues (ELSI)** that may arises from the project.

- HGP was co-ordinated by **US department of energy and National Institute of Health.**
- During early years of HGP, the wellcome trust (U.K.) become a major partner additional contributions come from **Japan, France, Germany, China and others.**
- **Many non-human model organisms, such as -**

  Bacteria, yeast, Caenorhabditis elegans (a free living non-pathogenic nematode), Drosophila (fruit fly), plants (rice and Arabidopsis), etc., have also been sequenced.

Methodologies : Two major approaches -

I. Expressed sequence Tags (EST)

[NEET 2019,23] [NCERT 102]

ii. Sequence Annotation (SA)

146. Identifying all genes that expressed as RNA - **EST.**

147. Sequencing the whole set of genome that contains all the coding and non-coding sequence, and different regions in the sequence with functions.-**SA.**

[NEET-2022] [NCERT 103]

148. Commonly used **host** - **Bacteria** and **Yeast.**

149. **Vectors** are - **BAC** (Bacterial artificial chromosomes)
- **YAC** (Yeast artificial chromosomes)

[NEET-2023] [NCERT 103]

150. **Frederick Sanger,** credited for developing method for determination of amino acid sequence in proteins and Also the fragments were sequenced using automated DNA sequences.

151. The sequence of chromosomes 1 was completed only in **May 2006.**

SALIENT FEATURES OF HUMAN GENOME

152. Human genome contains **3164.7 million nucleotide bases.**

153. Average gene consists of **3000 bases.** Largest known human gene **Dystrophin (2.4 million bases)**

154. Total number of genes is estimated at 30,000 - much lower than previous estimates of 80,000 to 1,40,000 genes.

155. All most all **(99.9%)** nucleotide bases are exactly the same in all peoples.

156. Functions are unknown for over **50 per cent** discovered genes.

157. **Less than 2 percent** of the genome codes for proteins.

158. Repeated sequences make up very large portionof human genome.

159. Chromosome 1 has most gene **(2968)** and **Y has** the fewest **(231)**

160. Scientist have identified about **1.4 million** locations where single base DNA differences **(SNPs-Single Nucleotides Polymorphism)** occurs in human.

- **DNA Fingerprinting :** Technique developed by **Alec Jeffreys.**

161. Involves identifying differences in some specific region of DNA sequence called as **Repetitive DNA.** (a small streteched of DNA repeated many times).

162 Repetitive DNA seperated from bulk genomic DNA as different peaks during density gradient centrifugation.

163. The bulk DNA forms a major peak and other small peaks are reffered to as **satellite DNA.**

164. Satellite DNA classified into many categories **based on**

- Base composition (A : T rich or G : C rich)
- Length of segment.
- Number of repetitive units.

165. Satellite DNA

- Micro-satellite
- Mini-satellite

166. These sequences normaly do not code for any proteins but they form a large protein of human genome and show high degree of polymorphism and forms basis of DNA fingerprinting.

[NEET 2015] [NCERT 105]

167. DNA from every tissue (like blood, hair follicles, skin, Bone, saliva, Sperm etc) from an individual show the same degree of polymorphism.

(Useful in identification in forensic applications).

168. Polymorphisms are inheritable from parents to children.

[NEET-2022] [NCERT 105]

169. **DNA fingerprinting** is the basis of **paternity testing,** in case of disputes.

170. **Allelic frequency greater than 0.01.**

171. **Alec Jeffreys** used a **satellite DNA** as probe that shows very high degree of polymorphism, called **VNTR (Variable number of Tandem repeats)**

[NEET 2018] [NCERT 106]

172. Involved **southern blot** hybridisation using **radiolabelled VNTR** as a probe. **It include -**

    1. Isolation of DNA
    2. Digestion of DNA by restricted endonucleases.
    3. Seperation of DNA fragments by electrophorosis.
    4. Transferring (Blotting) of seperated DNA fragments to **syntheticmembrane** such as **nitrocellulose** or **nylon.**
    5. Hybridisation using labelled VNTR probe.
    6. Detection of hybrid DNA fragments by **autoradiography.**

173. The VNTR belongs to a class of satellite DNA **(mini-satellite)**

174. The numbers of repeat show very high degree of polymorphism.

175. Size of VNTR varies from 0.1 to 20 kb.

176. After hybridisation with VNTR probe, the autoradiogram gives many band of different sizes. (gives characteristic pattern of individual DNA)

177. This bands **differs** from individual to individual in a population **except :** in case of monozygotic twins.