VP AIR TEST NEET (2025-26)

Remedial Test

Botany | **CLASS - 12**

DURATION: 25 Minutes | **Date: 13-06-2025** | **M. MARKS: 180**

ANSWER KEY

1.	(4)	24.	(2)
2.	(2)	25.	(2)
3.	(4)	26.	(1)
4.	(2)	27.	(4)
5.	(4)	28.	(2)
6.	(2)	29.	(3)
7.	(3)	30.	(2)
8.	(1)	31.	(2)
9.	(3)	32.	(4)
10.	(2)	33.	(3)
11.	(4)	34.	(3)
12.	(2)	35.	(1)
13.	(3)	36.	(3)
14.	(2)	37.	(3)
15.	(3)	38.	(3)
16.	(3)	39.	(4)
17.	(4)	40.	(2)
18.	(4)	41.	(2)
19.	(1)	42.	(4)
20.	(1)	43.	(1)
21.	(2)	44.	(3)
22.	(4)	45.	(1)
23.	(2)		

1. **(4)**

* The repressor of the *lac* operon is synthesised (all-the-time – constitutively) from the *i* gene. The repressor protein binds to the operator region of the operon and prevents RNA polymerase from transcribing the operon. In the presence of an inducer, such as lactose or allolactose, the repressor is inactivated by interaction with the inducer. This allows RNA polymerase access to the promoter and transcription proceeds.
* If lactose is provided in the growth medium of the bacteria, the lactose is transported into the cells through the action of permease.

2. **(2)**

The cellular factory responsible for synthesising proteins is the ribosome. The ribosome consists of structural RNAs and about 80 different proteins.

3. **(4)**

z gene-codes for the product that is responsible for the hydrolysis of the disaccharide *y* gene-codes for the product that increases permeability of the cell to β-galactosides *a* gene-encodes a transacetylase.
The *lac* operon consists of one regulatory gene i.e the *i* gene.

4. **(2)**

When the small subunit encounters an mRNA, the process of translation of the mRNA to protein begins.

- In its inactive state, ribosomes exists as two subunits; a large subunit and a small subunit.
- Formation of a peptide bond requires energy. While energetically favoured once charged tRNAs are close, the overall process, including amino acid activation, consumes energy.
- Amino acids are added one by one, translated into Polypeptide sequences dictated by DNA and represented by mRNA.

5. **(4)**

* In splicing, the introns are removed and exons are joined in a defined order.
* The RNA polymerase I transcribes rRNAs (28S, 18S, and 5.8S).
* The technique of DNA Fingerprinting was initially developed by Alec Jeffreys.
* The fragments were sequenced using automated DNA sequencers that worked on the principle of a method developed by Frederick Sanger.
* Sanger is also credited for developing method for determination of amino acid sequences in proteins.

6. **(2)**

- Monocistronic genes are characteristic of eukaryotes, and polycistronic genes are characteristic of prokaryotes.
- Splicing is a eukaryotic process. Prokaryotic genes (polycistronic) do not undergo splicing.
- Eukaryotic genes (monocistronic) typically contain introns; prokaryotic genes (polycistronic) generally lack introns.

7. **(3)**

* In the given figure, the step shown is termination of transcription in bacteria. The label A, B and C are respectively RNA, RNA polymerase and rho factor.
* RNA polymerase is an enzyme that synthesizes the formation of RNA from a DNA template during transcription. Rho factor is a termination factor which releases RNA from the DNA template releases RNA from the DNA template

8. **(1)**

The DNA polymerases on their own cannot initiate the process of replication. Also the replication does not initiate randomly at any place in DNA. There is a definite region in *E. coli* DNA where the replication originates. Such regions are termed as origin of replication.

9. **(3)**

The correct order of enzyme action during DNA replication:
Helicase: Unwinds the DNA double helix.
Primase: Synthesizes short RNA primers.
DNA dependent DNA Polymerase : Main enzyme for synthesizing new DNA strands (elongation).
DNA Ligase**:** Joins the Okazaki fragments on the lagging strand.

10. **(2)**

The technique of DNA Fingerprinting was initially developed by Alec Jeffreys. He used a satellite DNA as probe that shows very high degree of polymorphism. It was called as Variable Number of Tandem Repeats (VNTR). The technique, as used earlier, involved Southern blot hybridisation using radiolabelled VNTR as a probe. It included
(i) isolation of DNA,
(ii) digestion of DNA by restriction endonucleases,

(iii) separation of DNA fragments by electrophoresis,
(iv) transferring (blotting) of separated DNA fragments to synthetic membranes, such as nitrocellulose or nylon,
(v) hybridisation using labelled VNTR probe, and
(vi) detection of hybridised DNA fragments by autoradiography.

11. (4)

The correct sequence of the Hershey-Chase experiment is:

- Viruses were grown on a medium containing radioactive phosphorus or radioactive sulfur.
- Radioactive phages were allowed to attach to *E. coli* bacteria.
- The virus particles were separated from the bacteria by spinning them in a centrifuge.
- The viral coats were removed from the bacteria by agitating them in a blender.
- Bacteria that were infected with viruses that had radioactive DNA were radioactive.

12. (2)

The 2'-OH group present in every nucleotide of RNA makes it more reactive (labile) and susceptible to degradation, unlike DNA which lacks this hydroxyl group at the 2' position of the ribose sugar.

13. (3)

The sigma (σ) factor is an initiation factor that associates with the core RNA polymerase to enable it to specifically recognize and bind to the promoter sequence on the DNA, thereby initiating transcription.

14. (2)

The correct sequential order during protein synthesis(translation);

- Amino acid linked to tRNA, sequentially binds to the appropriate codon: This is the first step where the charged tRNA docks at the ribosome, recognizing the codon.
- Formation of peptide bond between successive amino acids: Once the new amino acid-tRNA is in place, a peptide bond forms between the incoming amino acid and the growing polypeptide chain.
- Ribosome moves from codon to codon along the mRNA: After peptide bond formation, the ribosome translocates to the next codon, making room for the next charged tRNA.
- Release factor binds to the stop codon**:** This event occurs during the termination phase, not the elongation phase

15. (3)

RNA polymerase moves along the DNA template strand in the 3'→5' direction, and the RNA molecule is synthesized in the 5'→3' direction, antiparallel to the template strand.

16. (3)

Meselson-Stahl proved that DNA replicates semi conservatively. It was shown first in *Escherichia coli* and subsequently in higher organisms, such as plants and human cells.

17. (4)

- Eukaryotes have three different RNA polymerases. RNA polymerase II transcribes the precursor of messenger RNA (hnRNA), which subsequently undergoes processing to form mRNA.
- RNA polymerase III is responsible for transcription of tRNA, 5srRNA, and snRNAs

18. (4)

DNA as an acidic substance present in nucleus was first identified by Friedrich Meischer in 1869.

19. (1)

RNA polymerase binds to promoter and initiates transcription (Initiation). It uses nucleoside triphosphates as substrate and polymerises in a template depended fashion following the rule of complementarity.

20. (1)

In HGP the fragments were sequenced using automated DNA sequencers that worked on the principle of a method developed by Frederick Sanger. These sequences were then arranged based on some overlapping regions present in them. This required generation of overlapping fragments for sequencing. Alignment of these sequences was humanly not possible. The genetic and physical maps on the genome was generated using information on polymorphism of restriction endonuclease recognition sites, and some repetitive DNA sequences known as microsatellites.

21. (2)

The coding strand (or sense strand) of DNA has a sequence identical to the mRNA, with the only difference being that DNA contains Thymine (T) where RNA contains Uracil (U). The mRNA is complementary to the template strand (antisense strand). The presence of thymine at the place of uracil confers additional stability to DNA.

22. **(4)**

DNA polymorphism is observed in non coding DNA sequences. The probability of such variation to be observed in non-coding DNA sequence would be higher as mutations in these sequences may not have any immediate effect/impact in an individual's reproductive ability. These mutations keep on accumulating generation after generation, and form one of the basis of variability/polymorphism.

23. **(2)**

AUG has dual functions. It codes for Methionine (met), and it also act as initiator codon.
UAA, UAG, UGA are stop terminator codons.
UGG code for tryptophan(Trp).

24. **(2)**

The average gene consists of 3000 bases, but sizes vary greatly, with the largest known human gene being dystrophin at 2.4 million bases.

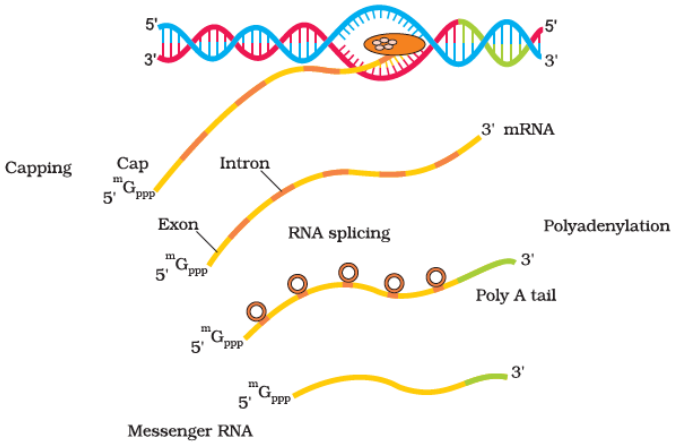
25. **(2)**

- RNA polymerase binds to the promoter to initiate transcription and unwinds the DNA.
- RNA polymerase synthesizes RNA in a 5'→3' direction.
- RNA polymerase uses the template strand (3'→5') as a template, not the coding strand. The coding strand has the same sequence as the mRNA (with T replaced by U).
- Termination occurs at the terminator sequence, and in prokaryotes, it can be Rho-dependent or Rho-independent.

26. **(1)**

- The promoter is said to be located towards 5′-end (upstream) of the structural gene (the reference is made with respect to the polarity of coding strand). By switching position of promotor with terminator, the definition of coding and template strands could be reversed.
- The strand which has the polarity (5′→3′) and the sequence same as RNA (except thymine at the place of uracil), is displaced during transcription. Strangely, this strand (which does not code for anything) is referred to as coding strand.
- The strand that has the polarity 3′→5′ acts as a template, and is also referred to as template strand.
- The terminator is located towards 3′-end (downstream) of the coding strand.

27. **(4)**



A. In capping an unusual nucleotide (methyl guanosine triphosphate) is added to the 5′-end of hnRNA.
B. Intron (non coding sequence)
C. Exon (coding sequence)
D. It is the fully processed hnRNA, now called mRNA, that is transported out of the nucleus for translation.
E. RNA splicing- primary transcripts contain both the exons and the introns and are non-functional. Hence, it is subjected to a process called splicing where the introns are removed and exons are joined in a defined order.

28. **(2)**

Satellite DNA forms the bulk of the human genome and do not code for protein. DNA from every tissue (such as blood, hair-follicle, skin, bone, saliva, sperm etc.), from an individual show the same degree of polymorphism. The satellite DNA is classified into many categories, such as micro-satellites, mini-satellites etc. These sequences normally do not code for any proteins, but they form a large portion of human.

29. **(3)**

Scientists have identified about 1.4 million locations where singlebase DNA differences (SNPs – single nucleotide polymorphism, pronounced as 'snips') occur in humans.
The information of SNPs in human genome promises to revolutionise the processes of finding chromosomal locations for disease-associated sequences and tracing human history.

30. **(2)**

In simple terms, if an inheritable mutation is observed in a population at high frequency, it is referred to as DNA polymorphism.

31. **(2)**

The tRNA, then called sRNA (soluble RNA), was known before the genetic code was postulated. The amino acid attaches to the soluble RNA at 3' – end.

32. **(4)**

The secondary structure of tRNA has been depicted that looks like a clover-leaf. In actual structure, the tRNA is a compact molecule which looks like inverted L.

33. **(3)**

It is because of the requirement of the origin of replication that a piece of DNA if needed to be propagated during recombinant DNA procedures, requires a vector. The vectors provide the origin of replication.

34. **(3)**

RNA is reactive and less stable than DNA.

35. **(1)**

In tailing, adenylate residues (200-300) are added at 3′-end in a template independent manner. The DNA-dependent RNA polymerase also catalyse the polymerisation in only one direction, that is, 5'→3', the strand that has the polarity 3'→5' acts as a template, and is also referred to as template strand. The other strand which has the polarity (5'→3') and the sequence same as RNA (except thymine at the place of uracil), is displaced during transcription. An mRNA also has some additional sequences that are not translated and are referred as untranslated regions (UTR). The UTRs are present at both 5' -end (before start codon) and at 3' -end (after stop codon).

36. **(3)**

Fully processed hnRNA, called mRNA, is transported out of the nucleus for translation.

37. **(3)**

Erwin Chargaff's rules, derived from his experimental observations, state that in any double-stranded DNA molecule:

- The amount of Adenine (A) is approximately equal to the amount of Thymine (T).
- The amount of Guanine (G) is approximately equal to the amount of Cytosine (C).

This means that the ratio of A:T is approximately 1:1, and the ratio of G:C is also approximately 1:1. These findings were crucial for Watson and Crick in determining the double helix structure of DNA, as they indicated specific base pairing (A with T, and G with C).

38. **(3)**

AUG has dual functions. It codes for Methionine (met), and it also act as initiator codon.

39. **(4)**

- Expressed Sequence Tags All the genes that are expressed as RNA.
- VNTR - A satellite DNA that shows very high degree of polymorphism.
- RNA polymerase III -Synthesizes tRNA in eukaryotic cells.
- In prokaryotes, such as, *E. coli*, though they do not have a defined nucleus, the DNA is not scattered throughout the cell. DNA (being negatively charged) is held with some proteins (that have positive charges) in a region termed as 'nucleoid

40. **(2)**

There are two types of nitrogenous bases – Purines (Adenine and Guanine), and Pyrimidines (Cytosine, Uracil and Thymine). Cytosine is common for both DNA and RNA and Thymine is present in DNA. Uracil is present in RNA at the place of Thymine

41. **(2)**

It is now proven that DNA replicates semiconservatively. It was shown first in *Escherichia coli* by Matthew Meselson and Franklin Stahl. Experiments involving use of radioactive thymidine to detect distribution of newly synthesised DNA in the chromosomes was performed on *Vicia faba* (faba beans) by Taylor and colleagues in 1958. The experiments proved that the DNA in chromosomes also replicate semiconservatively.

42. **(4)**

Essential life processes (such as metabolism, translation, splicing, etc.), evolved around RNA, implying RNA was involved in basic metabolic pathways.

43. **(1)**

Beta-galactosidase (β-gal), which is primarily responsible for the hydrolysis of the disaccharide. In lac operon The *y* gene codes for permease, which increases permeability of the cell to b-galactosides. The *a* gene encodes a transacetylase.

Bacteriophage lambda has 48502 base pairs (bp).

44. **(3)**

The negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called nucleosome.

45. **(1)**

The split-gene arrangements represent probably an ancient feature of the genome.

■■■