2018 Gene Expression, Organisation and Control STQ MS

2018 / H2 / ACJC PRELIM / P2 Q3

1 tRNA molecules have an important role in gene expression. They can be found in the cytoplasm, mitochondria and chloroplasts of eukaryotic cells. Fig. 3.1 shows the structure of a tRNA molecule that is able to carry the amino acid threonine in the cytoplasm of a eukaryotic cell. It is 77 ribonucleotides long.

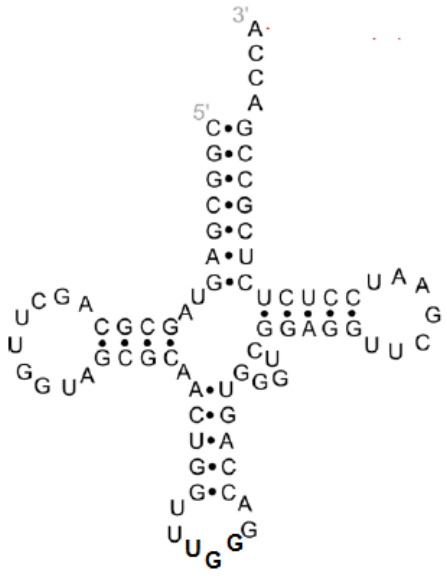


Fig. 3.1

(a) (i) With reference to Fig. 3.1, describe how the structure of a tRNA molecule differs from the structure of a mRNA molecule.

Category	tRNA	mRNA
1. Presence of double-stranded regions / Overall structure	Double-stranded regions / clover-leaf struct	Single-stranded / Linear structure
2. Presence of hydrogen bonds / complementary base pairing	Present	Absent
3. 3' end	3' CCA sequence	3' poly-A tail
4. 5' modified guanosine cap	Absent	Present
5. Anticodon	Has an anticodon	Made up of many codons
		@1m per valid comparison

[2]

(ii) Explain how these differences allow tRNA and mRNA molecules to perform their roles.

	tRNA	mRNA
Overall structure (Presence of hydrogen bonds to	1. Specific 3D conformation / clover-leaf structure is complementary to (active site of)	2. Linear structure allows it to be read by the ribosomes / binding to the small ribosomal subunit;

bring about double-stranded regions)	**aminoacyl-tRNA synthetase / (A, P-sites of) large ribosomal subunit;**		
3' end	**3. 3' CCA sequence allows binding to the amino acid;**	**4. The 3' poly-A tail determines the stability of the mRNA / duration of translation of the mRNA;**	
Anticodon	**5. Anticodon can complementary base-pair to codon for the correct amino acid to be added; (1 tRNA can only carry one amino acid)**	**6. Sequence of codons specify the sequence of amino acids in a polypeptide;**	
	@1m per structure-function relationship		

[2]

Fig. 3.2 shows a tRNA molecule that is able to carry the amino acid threonine in mitochondria. It is 62 ribonucleotides long.

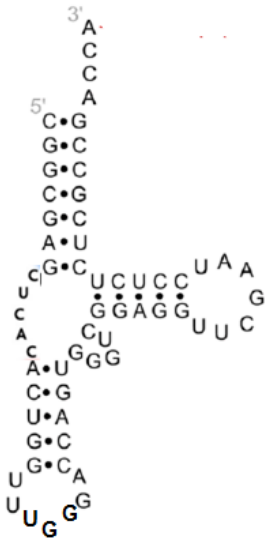


Fig. 3.2

(b) The structures of the tRNA molecules in the mitochondria and the cytoplasm of a eukaryotic cell are different although they are both able to carry the amino acid threonine. Suggest a reason for this difference.

1. **Mitochondria have 70S ribosomes, while 80S ribosomes are found in the cytoplasm;**
2. **Different tRNA molecules have specific 3D conformation that are complementary to the different A and P sites in mitochondrial and cytoplasmic ribosomes; OR**
3. **They are coded for by the different genes found in the mitochondrial DNA and nuclear DNA respectively;**
4. **Different sequences result in the formation of hydrogen bonds at different locations;** **[2]**
5. **AVP e.g. evolutionary reasons;**

There are 61 unique tRNA molecules in the cytoplasm of a eukaryotic cell.

(c) (i) Explain why there are 61 unique tRNA molecules in the eukaryotic cell.

1. **The codon / anticodon is made up of 3 nucleotides and there are 4 different bases, hence 64 possible unique permutations of triplet codes;**
2. **Stop codons do not code for amino acids/ bind to a release factor;**
3. ***There are 3 stop codons, hence this gives 61 unique codons. 61 tRNA molecules will have anticodons that can complementary base pair to these 61 unique codon sequences;**

Pt 3 is compulsory to score full marks

[2]

(ii) Scientists found that there are more than 120 gene loci coding for tRNA molecules in the nuclear DNA, many of which are duplicate copies of the same tRNA gene.

Suggest an advantage of having more than 120 gene loci coding for the 61 tRNA molecules in the eukaryotic cell.

1. **Rapid synthesis of tRNA molecules;**
2. **If one copy of the tRNA gene is mutated, there are other / duplicate copies to ensure functional tRNA is synthesised;** [1]

(d) Explain how the structure of RNA polymerase allows for the synthesis of tRNA molecules.

1. **The active site has a specific/complementary 3D conformation, and it binds to the promoter/template strand of the tRNA genes;**
2. **The specific 3D conformation of the active site is also specific/complementary to ribonucleotides and the DNA template;**
3. **Catalytic residues in the active site help to catalyse the formation of the phosphodiester bonds between the 3' OH group of the one nucleotide and 5' phosphate group of the other nucleotide;**
4. **Active site contains catalytic residues that break hydrogen bonds between the strands in DNA molecules to expose the template strand;**
5. **Ref to action of enzymes, e.g. lower activation energy, binding sites for general transcription factors;** [3]

[Total: 12]

2018 / H2 / AJC PRELIM / P2 Q2

2 RNA molecules play important roles within cells. One of the major types of RNA found in all cells is the ribosomal RNA (rRNA).

Fig. 2.1 shows rRNA molecules forming the large ribosomal subunit in eukaryotes.

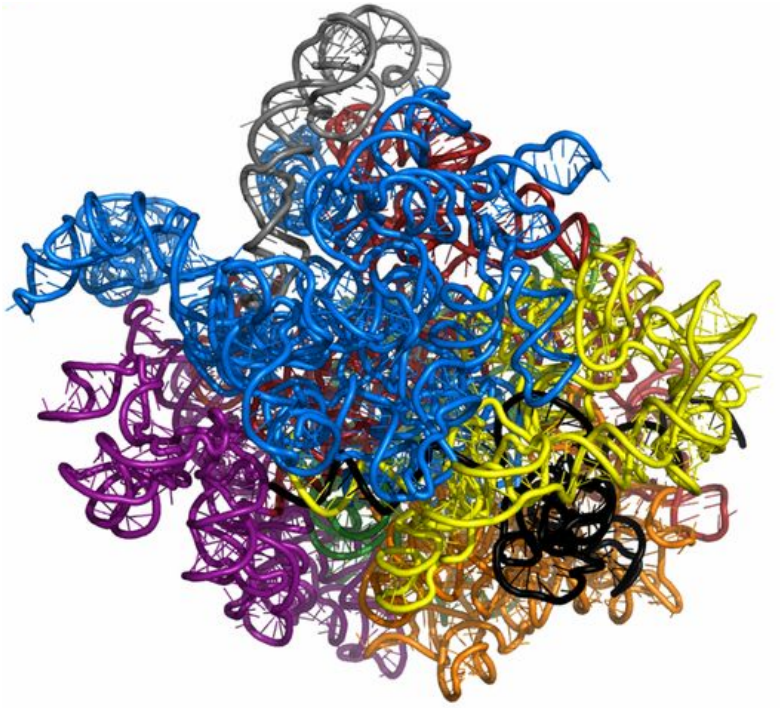


Fig. 2.1

(a) Explain why the rRNA molecules must adopt the shapes shown in Fig. 2.1.

How each shape is formed (max 2)

- **Single stranded RNA folds back** upon itself due to
- **Complementary base-pairing** via **hydrogen bonds** / presence of **complementary** stretches of **base**s that can form **hydrogen bonds** (
- Forming a **double helical** structure

Purpose

- to **stabilize the molecule**
- *Max 2 marks for binding*: to form a **binding site** whose **shape is complementary** to **ribosomal proteins / small ribosomal subunit / tRNA molecules**

[3]

(b) Another important RNA molecule found in eukaryotic cells is the telomerase RNA. Telomerase RNA is found within the telomerase enzyme, an enzyme essential for elongating telomeres.

(i) Outline how RNA molecules such as telomerase RNA and rRNA are synthesised.

- **Transcription** of
- the **gene** for **telomerase RNA/ rRNA**
- **by RNA polymerase**
- catalyzing formation of **phosphodiester bonds**
- between **RNA nucleotides**
- which were added via **complementary base pairing**
- using (one of the two strand of) **DNA** as **template**
- elongation occurs in the **5' to 3'** direction of the RNA strand

(½ m each) [3]

Fig. 2.2 shows the mode of action of telomerase.

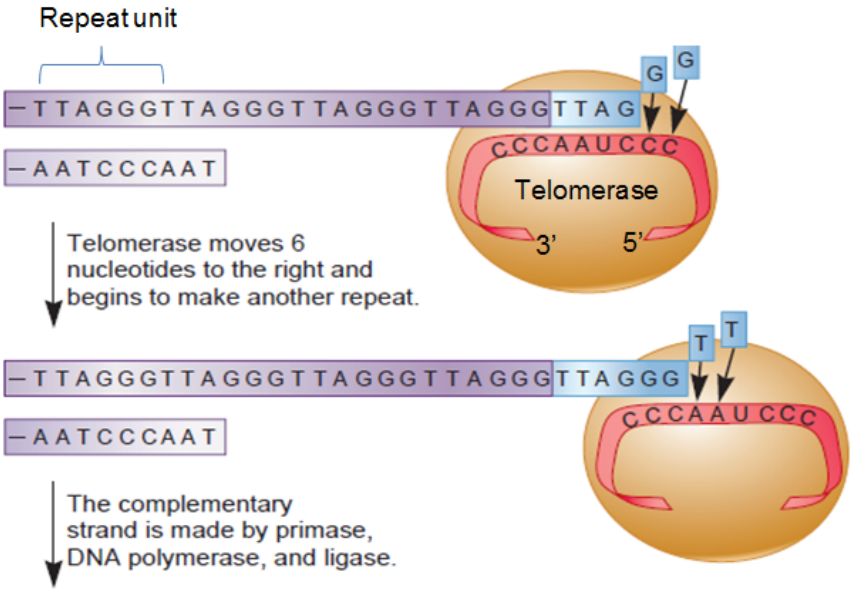


Fig. 2.2

(ii) Describe **three** visible differences between telomere elongation shown in Fig. 2.2 and translation.

	Telomere elongation	Translation
Monomers	**DNA nucleotides**	**Amino acid**
Bonds formed between monomers	**Phosphodiester bonds**	**Peptide bonds**
Enzyme involved in synthesis the bond between monomers	**Telomerase/ reverse transcriptase**	**Peptidyl transferase**
Movement of enzyme	Moves a distance of **6 nucleotides** each time	Moves a distance of **3 nucleotides / 1 codon** each time

[3]

[Total:9]

2018 / H2 / AJC PRELIM / P2 Q3

3 Eukaryotes regulate the expression of their genes at various levels of protein synthesis.

(a) Describe the effect of histone acetylation on gene expression.

Any 2

- when **lysine** on histones tails are acetylated their **positive charges** are **neutralized**

- there is **decreased interactions of histone tails** with **neighbouring nucleosomes / decreased interaction of histone tails with the (negatively charged) DNA / DNA less tightly wound around histones**

- **Chromatin** structure become **less compact/ condensed /** forms **euchromatin**

Compulsory pt– to answer " effect on effect on gene expression)

- Transcriptional machinery like **RNA polymerase** *(reject DNA polymerase)* and **transcription factors** *(must give these two egs)* will can **bind** to the **promoter of genes** in the acetylated region to / form the **transcription inititation complex**/ Allow transcription to occur / gene to be transcriptional active

[3]

(b) Eukaryotic gene expression can also be regulated at translation initiation after the mRNA is synthesised.

Fig. 3.1 shows translation occurring on an eukaryotic mRNA.

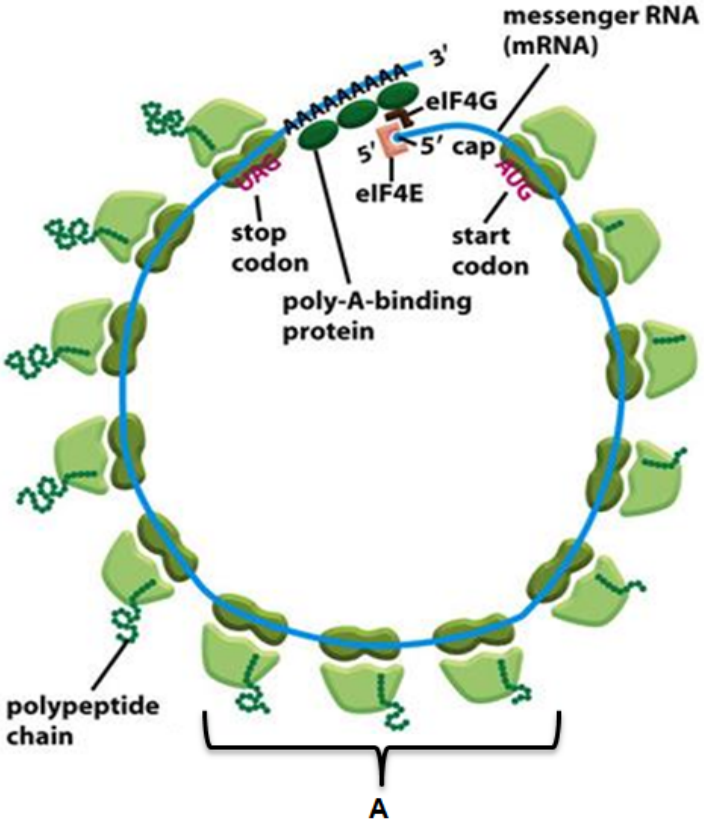


Fig. 3.1

(i) Explain the significance of the pattern of translation, labelled **A** in Fig. 3.1**.**

- Identify A: **Polyribosomes / polysomes/ multiple ribosomes** work on translating **one** messenger RNA

- Significance of A**: single** mature mRNA is used to make **many copies of the same / identical polypeptide simultaneously /** enables a cell to synthesise **many copies of the same type of polypeptide very quickly**

- **single** mature mRNA is used to make **many copies** of the **same (type)** of **polypeptide simultaneously /** enables a cell to synthesise **many copies** of the **same type of polypeptide very quickly**

[2]

(ii) During translation initiation, translation initiation factors like eIF4E and eIF4G form part of a complex which aid in recruiting ribosomal subunits to mRNA.

With reference to Fig. 3.1, describe the role of the poly-A tail and 5' cap in the assembly of ribosomes.

- **poly-A binding protein** binds to the **poly-A tail**
- which in turn recruit/ attract **eIF4G** to bind to **poly-A binding proteins**
- **eIF4E** binds to **5'cap**
- **eIF4E binds** to **eIF4G**
- to assemble into(part of) **translation initiation complex** (which aid in recruiting ribosomal subunits to mRNA)

(1/2 m each)

[2]

(iii) State **one** other function of the poly-A tail.

- The longer the poly-A tail the longer the time need for the tail to be shorten to a critical length for mRNA degradation to set in completely (allowing more time for translation)

- (Proteins will bind to the 3' poly-A tail and) facilitate mRNA transport through the nuclear pore, out of the nucleus.

- Poly-A tail may be recognized by proteins which binds and prevent degradation [1]

(c) In mammals, sex is determined by the X and Y chromosomes, females being XX and males XY. In females, the expression of all the genes on one of the two X chromosomes in each cell is inactivated throughout the life of the female. This ensures that the effective dosages of products of X-linked genes are equal in males and females since a double dose of X-linked genes may potentially be toxic.

Suggest if the inactivation of gene expression on the X chromosome occurs via chromatin modification or at translation initiation. Explain your answer.

- Chromatin level [3]
- *Link chromatin structure to gene expression*: Chromatin **condensation** → **long term repression/inhibition** of the genes
- repressing at chromatin level saves resources because cells do not need to use resources to produce the mRNA only to not use the mRNA for translation at all / idea of many mRNA would be formed from 1 gene , it is inefficient/ use of much more resources to inactivate so many mRNA compared to just inactivating 1 gene

[Total: 11]

2018 / H2 / DHS PRELIM / P2 Q4

Question 4

(a)

- A codon is three nucleotides/bases on mRNA that specify an amino acid
- It is where the corresponding tRNA anticodon will complementary base-pairs
- signals the start of translation if it is a start codons/AUG
- signals the termination of translation if it is a stop codons/UAA, UAG, UGA

(b)

- Single base pair substitution mutation from guanine to adenine on DNA template strand.
- Results in the substitution/replacement of an amino acid from alanine to valine.

(c)

- Ref. alanine and valine have different R groups
- could result in more extensive hydrophobic interaction between β peptides and thus forming amyloid plaques.

2018 / H2 / JJC PRELIM / P2 Q4

5 Fig. 4.1 shows the elongation phase of translation.

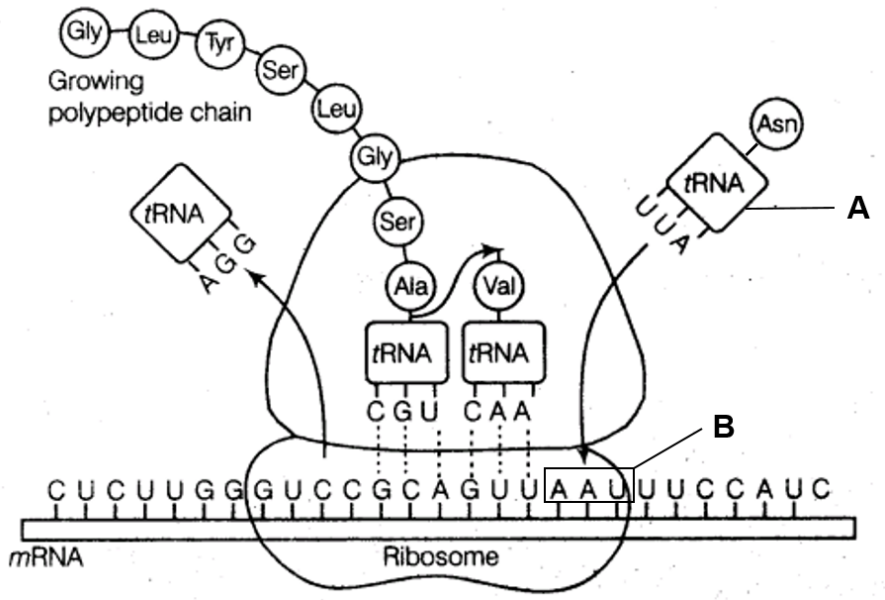


Fig. 4.1

(a) On Fig. 4.1, draw an arrow to show the direction of translocation of the ribosome. [1]

(b) Name the structures **A** and **B** in Fig. 4.1. [2]

A: aminoacyl-tRNA ;
B: codon ;

(c) Explain how the molecular structure of **A** is related to its functions. [2]

Structure
1. **Has anticodon (loop) that complementary base pairs with a particular codon on the mRNA**
2. **Attached covalently to its specific amino acid coded for by the anticodon of the tRNA at the CCA stem**

Function (OWTTE)
3. **To transfer amino acids present in the cytoplasm to the ribosome ;**
4. **To act as an intermediate molecule between the codon of mRNA and the amino acid sequence of the polypeptide strand ;**

1+4 / 2+3 / 2+4

(d) Describe the phase of translation that occurs before elongation. [3]

1. **A <u>small ribosomal subunit</u> recognises and <u>binds to the 5' end of the mRNA</u> and travels along the mRNA until it <u>reaches the first AUG</u> / <u>start codon</u> ;**
2. **A special <u>initiator tRNA</u> carrying the <u>amino acid methionine (Met)</u> / <u>anticodon UAC</u>, binds to the start codon AUG on the mRNA ;**
3. **The union of mRNA, initiator tRNA, and a small ribosomal subunit is followed by the attachment of a <u>large ribosomal subunit</u>, completing a <u>translation initiation complex</u> ;**
4. **Proteins called <u>initiation factors</u> and <u>GTP</u> are required to bring all these components together ;**

(e) State two differences between translation in prokaryotes and translation in eukaryotes. [2]

	Features	prokaryotes	eukaryotes	
1.	**Ribosomes involved**	**Involves 70S ribosomes**	**Involves 80S ribosomes**	**;**
2.	**Continuous/ simultaneous transcription and translation**	**Translation is continuous/ simultaneous with transcription**	**Translation is separated/ not simultaneous with transcription**	**;**
3.	**mRNA involved in translation**	**mRNA used is usually polycistronic/code for many proteins/ act as template for the synthesis of many polypeptides**	**mRNA used is monocistronic/code for one protein/ act as template for the synthesis of one polypeptide;**	**;**
4.	**Location**	**Translation occurs on free ribosomes only**	**Translation occurs on free ribosomes or ribosomes attached to endoplasmic reticulum**	**;**

[Total: 10]

2018 / H2 / NYJC PRELIM / P2 Q5

2

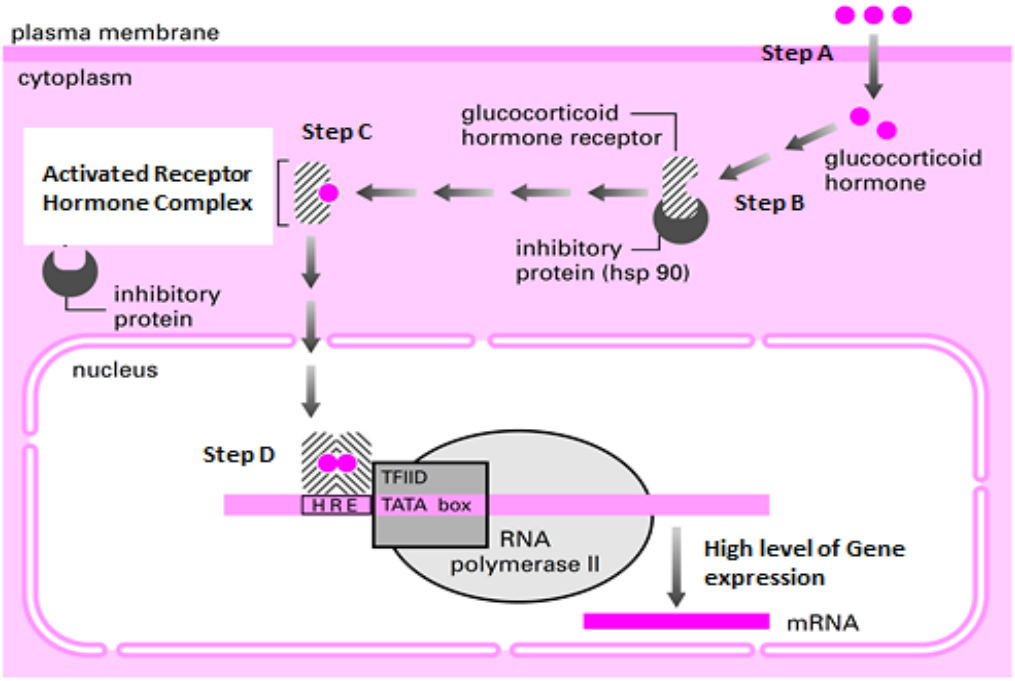
3

4

5

6 Glucocorticoids are steroid hormones produced by the adrenal cortex that increase the transcription of several genes important in carbohydrate and protein metabolism.

Fig. 5.1 below shows how glucocorticoids can pass through the plasma membrane to enter the cytosol and bind to glucocorticoid hormone receptors. In the absence of glucocorticoid hormone, its receptor remains in the cytosol and is inactive.



Hormone response element (HRE)

Fig. 5.1

(a) (i) Glucocorticoid hormone receptor is a class of transcription factors. With reference to **Fig. 5.1**, explain how receptor hormone complex (Step C) can be activated.

Being a steroid hormone, glucocorticoids are hydrophobic and can pass through the hydrophobic core of the phospholipid bilayers ;

It binds to hormone receptor and remove inhibitory protein (hsp90) thereby activating the receptor hormone complex ;

@ Ref to binding of glucocorticoid hormone to inactivated glucocorticoid receptor

@ which leads to removal of Hsp90 protein forming the glucocorticoid receptor–hormone complex

[2]

(ii) Suggest how glucocorticoid hormone receptor is able to bind to the specific region of the DNA known as HRE site shown in step D of **Fig. 5.1**.

Activated receptor hormone complex enter nucleus via nuclear pores ;

Dimerise ;

The dimer has a dna binding domain that can recognise the base sequence of HRE site ;

Complementary in terms of shape size charge and orientation ;

- **This occurs via Specific DNA - protein interactions which depend upon the sequence of bases in the DNA. [1]**
- **These DNA - protein interactions are mediated by the following bonds [1]:**
  - **Hydrogen bonding**
  - **Ionic interactions: Salt bridges; R groups of protein - DNA backbone interactions**

Other forces: van der Waals, hydrophobic

[2]

(iii) With reference to **Fig. 5.1**, explain how high level of gene expression may be regulated by activated receptor hormone complex within the nucleus.

With the binding of dimerised activated receptor hormone complex to HRE site, it recruits TFIID to bind to tata box of promoter ;

Which recruits RNA polymerase II ;

Stabilises the transcription initiation complex ;

Increasing rate of transcription ;

Forming more mRNA → translation of proteins → high levels of gene expression

- **The glucocorticoid receptor–hormone complex acts as an activator which binds to the HRE which is an enhancer sequence / distal control element.**
- **The activators bind to certain general transcription factors such as TFIID and mediator proteins / Recruits basal Transcription factors**
- **Stabilises / increases the binding affinity of RNA polymerase II to TATA Box / Promoter sequence, and increase the rate of formation of stable / stability of transcription initiation complex for RNA synthesis to begin.**

[3]

Fig. 5.2 below shows the various steps involved in the processing of primary RNA transcript.

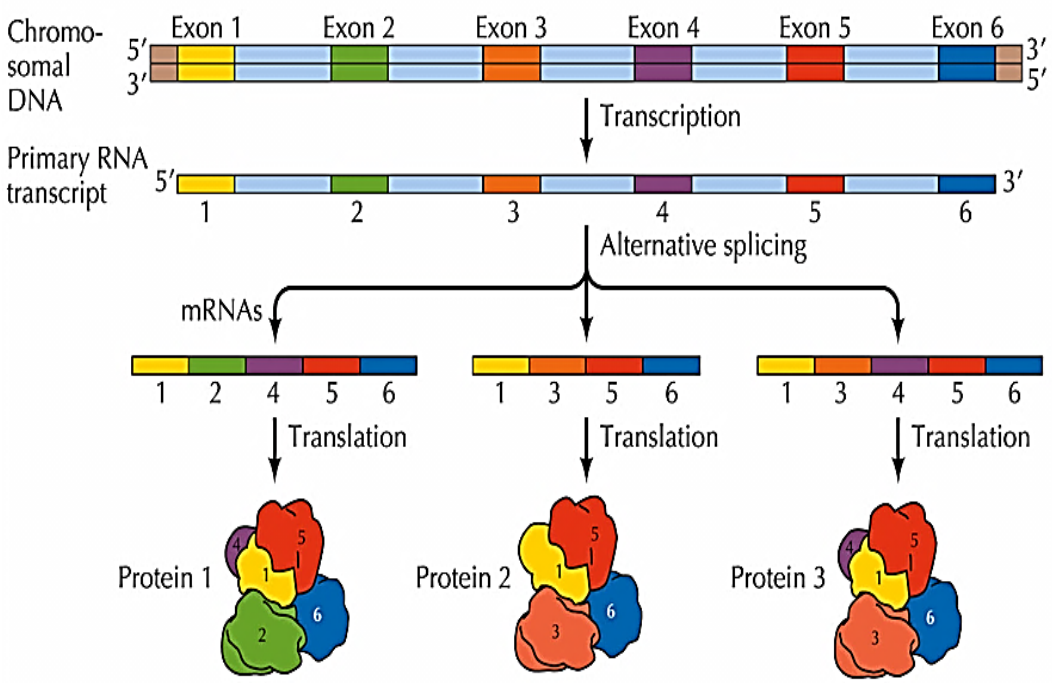


Fig. 5.2

(b) (i) Explain why alternative splicing is essential in eukaryotic cells from an evolutionary view point.

Allow more proteins to be translated from a smaller number of genes

Proteins can result in change in phenotypes which provide more variation to cope with the ever changing environments

Allow for smaller genomes to be stored in cells

1. **This process allows a single gene to code for different types of proteins / This allows eukaryotic genome to direct the synthesis of many more proteins than would be expected from its fixed protein-coding genes**
2. **Particular exons of a gene may be included within, or excluded from, the final, processed messenger RNA (mRNA) produced from that gene.**
3. **Ref to proteins translated from alternatively spliced mRNAs will contain differences in their amino acid sequence and, often, in their biological functions leading to variations to occur in a population. e.g. phenotypes etc.**

(Accept either point 2 or 3, but not both together.)

[3]

(ii) Prior to completion of alternative splicing, the primary RNA is modified in several important ways. Explain how **one** of these ways helps to regulate gene expression.

5' capping – facilitate export to cytoplasm and ribosomal binding and stability

3' poly A tail – regulate half life of mature mRNA and hence amount of proteins formed

Any one of the following:

- **Primary mRNA is capped by the addition of 7-methylguanosine cap to 5' end of the transcript to protect the growing RNA transcript from degradation by RNases.**

A poly-A tail is added to the 3' end by the enzyme poly-A polymerase. The poly-A tail has several functions: (1) It protects against RNases/ exonuclease and therefore increases the stability of mRNA molecules in the cytoplasm, (2) both it and the 5' cap are required for transit through the nuclear pore from the nucleus to cytoplasm, and (3) it increases the efficiency of translation on the ribosomes.

[1]

2018 / H2 / PJC PRELIM / P2 Q3

7 The central dogma of molecular biology describes the flow of genetic information from DNA to messenger RNA (mRNA) to protein.

(a) A molecule involved in the flow of genetic information from mRNA to protein is transfer RNA (tRNA). Outline the role of tRNA in the production of a polypeptide. [2]

a. **tRNA attaches to a specific acid and carries it to the ribosome during the elongation phase of translation;;**
b. **where the anti-codon on the incoming tRNA forms hydrogen bonds / ref. to complementary base pairing, with the codon on the mRNA;**
c. **peptide bond formation then takes place between the amino acid attached to this tRNA molecule and the adjacent amino acid in the polypeptide chain;**

Each step in the flow of information from DNA to mRNA to protein provides the eukaryotic cell with a potential control point for regulating its functions by adjusting the amount and type of proteins synthesised.

Fig. 3.1 shows the regulation of gene expression of the albumin gene during transcription in eukaryotes. The albumin gene is associated with two control elements and a promoter.

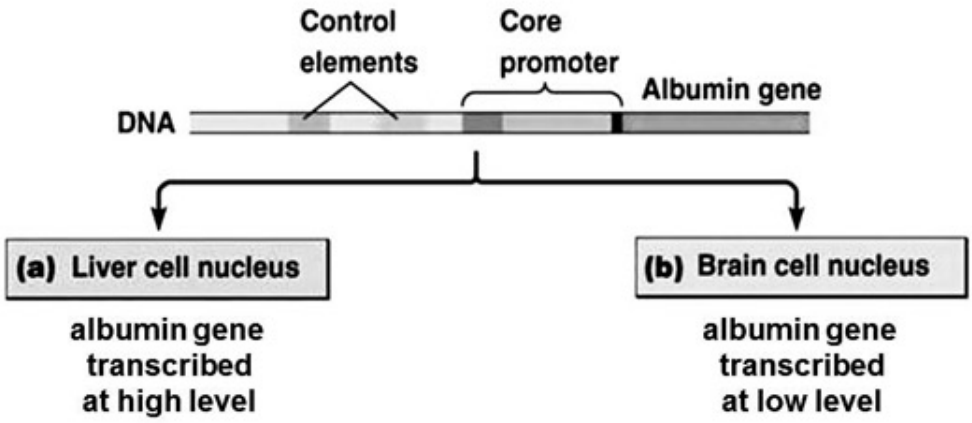


Fig. 3.1

(b) Explain how differential albumin gene expression in liver cells and brain cells is possible. [3]

a. **Control elements associated with the albumin gene are recognised by specific transcription factors (STFs) which bind to the control elements;;**
b. **and increase the rate of transcription of the albumin gene by stabilizing the transcription initiation complex (TIC) / higher rate of assembly of the TIC;;**
c. **These STFs are found in liver cells, therefore albumin gene is transcribed at high levels in liver cells;;**
d. **Brain cells do not contain these STFs that specifically bind to these two control elements associated with the albumin gene, so there is only a basal / low level of transcription of the albumin gene in brain cells;**

max. 3

[Turn Over

In a normal person, the fragile X mental retardation protein (FMRP), regulates the synthesis of neuron proteins by stopping ribosomal translocation on target mRNAs. Fig. 3.2 shows how patients with fragile X syndrome (FXS) have non-functional FMRP, resulting in accelerated synaptic protein synthesis that leads to abnormal synaptic function and intellectual disability.

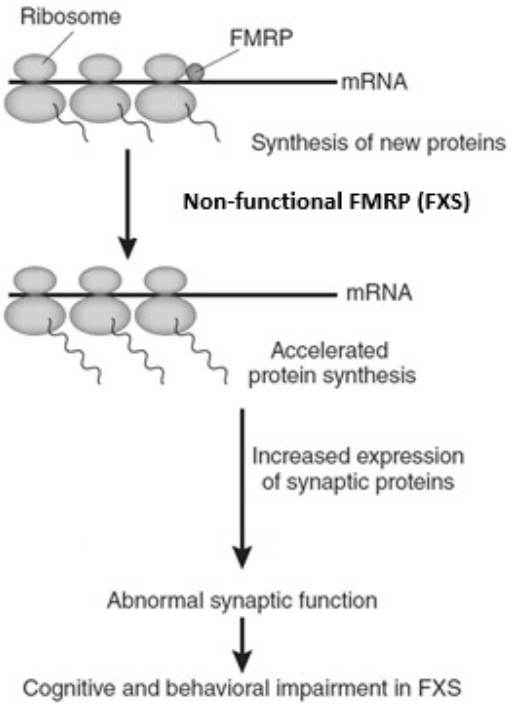


Fig. 3.2

(c) **(i)** State the level of control by FMRP on synaptic protein expression. [1]

Translational control;;

(ii) Describe one other control mechanism of a similar level as **(c)(i)**. [2]

a. **initiation factors;;**

b. **Activation of initiation factors facilitate the initiation of translation;;**

OR

c. **binding of regulatory proteins to 5' untranslated regions (5'UTR) of mRNA;;**
d. **hence preventing initiation of translation / binding of ribosome to mRNA;**

OR

e. **mRNA degradation / half-life of mRNA;**
f. **more translation for mRNA with longer poly(A) tails as such mRNA can serve as a template for translation for a longer time;**

Research pertaining to gene regulation can contribute significantly to the treatment of genetic diseases. Spinal muscular atrophy (SMA) is a heritable motor neuron disease where patients have insufficient levels of functional survival motor neuron (SMN) protein in their motor neurons and muscle. Genetic studies have shown that all SMA patients have at least one copy of the functional SMN gene at another chromosomal locus (a result of chromosomal duplication), which is not expressed.

Scientists have shown in a study that trichostatin A (TSA), a histone deacetylase inhibitor, caused increased SMN protein levels, improved motor function and survival in mice.

Fig. 3.3 shows some results from the study. Different doses of TSA were injected in the mice and after two hours, muscle tissues were isolated. The levels of acetylated histone H3, histone H4 and SMN mRNA were measured.

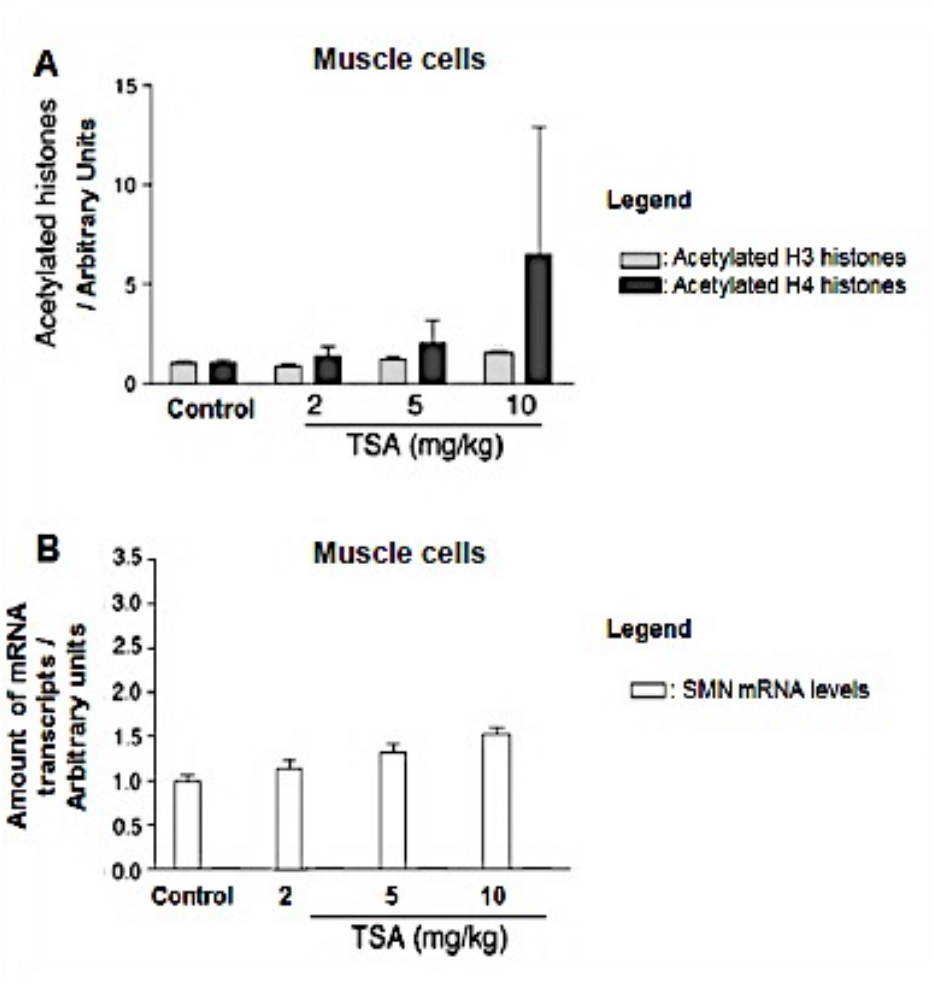


Fig. 3.3

(d) With reference to Fig. 3.3,

(i) describe the effect of TSA on the amount of SMN mRNA transcripts in muscle cells. [1]

as amount of TSA increases from 0mg/kg to 10mg/kg, the amount of mRNA transcripts in muscle cells increases from 1.0 a.u. (in the control cells) to 1.5 a.u.;;

[Turn Over

(ii) explain the effect of an increase in H4 histone acetylation on the regulation of transcription of the SMN gene in muscle cells. [3]

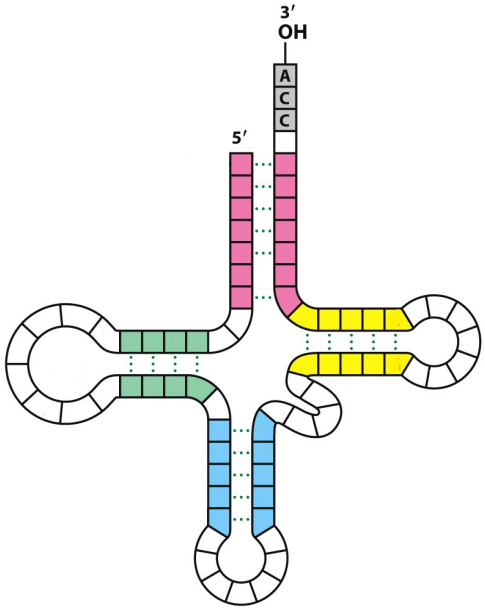
a. H4 histone tails rich in positively charged amino acid residues (e.g. lysine) interact strongly / form ionic bonds with negatively charged phosphate groups of the DNA backbone;;
b. When there is an increase in H4 histone acetylation, addition of the acetyl group neutralises the positive charge on the histone tails;;
c. reducing its affinity to DNA, chromatin now has a looser structure;
d. and transcription factors now have easier access to the genes in the acetylated region, thus promoting initiation of transcription;

max. 3

[Total: 12]

2018 / H2 / RVHS PRELIM / P2 Q3

3 Fig. 3.1 shows the structure of a tRNA.



Source: Biochem, Seventh edition, 2012

Fig. 3.1

(a) Describe how the structure of tRNA allows for its role in translation. [4]

1. **3' CCA end of tRNA**
2. **Serve as attachment site of a specific amino acid**
3. **Contains anticodon at one end**
4. **Specifies the identity of amino acid attached to (the 3' CCA end of the) tRNA**
5. **(Sequence of bases of) anticodon able to complementary base pair**
6. **With the corresponding mRNA codon**
7. **(T) loop**
8. **binds to rRNA of ribosome (via base-pairing)**
9. **(D) loop**
10. **for binding to amino-acyl tRNA synthetase (that attaches tRNA with its specific amino acid)**
11. **tRNA folds into a clover-leaf shape (2-D structure)/L-shape (3-D structure)**
12. **to reduce steric hindrance**

Synthetic RNA, which binds to bacterial mRNA, could interfere with translation. Fig. 3.2 shows the sequences of a bacterial mRNA and two different synthetic RNA.

Bacterial mRNA

5'- GUCAACCAUGCCAAUUAUCACGGACAUUCAUGGUAGGCCUUAGUAGACAACUG-3

Synthetic RNA 1

5'- CAGUUGUCUA-3'

Synthetic RNA 2

5'- CUAGGUUGAC-3'

Fig. 3.2

(b) With reference to Fig. 3.2, suggest how synthetic RNA binds to mRNA. [1]

Synthetic RNA and mRNA

1. **forms hydrogen bonds**
2. **between complementary base-pair**

The effectiveness of synthetic RNA 1 and 2 are investigated by introducing them to separate bacterial cultures and incubating for 24 hours. The results of the investigation is shown in Fig. 3.3.

Fig. 3.3

(c) With reference to Fig. 3.2 and Fig. 3.3, explain the results of the investigation. [6]

1. **Synthetic RNA 1 will bind to 3' end of bacterial mRNA**
2. **Ribosome can still bind to 5' end of mRNA**
3. **Stabilises mRNA**
4. **Polypeptide for growth synthesised**
5. **for cell to divide / undergo binary fission**
6. **Synthetic RNA 2 will bind to 5' end of bacterial mRNA**
7. **to form double stranded RNA**
8. **Block binding of ribosome to (5' end) mRNA (for translation)/block AUG**
9. **Proteins for normal cellular functions not produced**
10. **killing bacteria**

(d) Suggest a limitation of using synthetic RNA as an oral antibiotic for bacterial infections in humans. [1]

1. **Synthetic RNA broken down during digestion**
2. **Kills good bacteria in gut**
3. **Enters human cells and inhibit translation**

[Total: 12]

2018 / H2 / SAJC PRELIM / P2 Q2

QUESTION 8

Fig. 2.1 shows Process X in an eukaryotic cell which produces ribosomal RNA (rRNA).

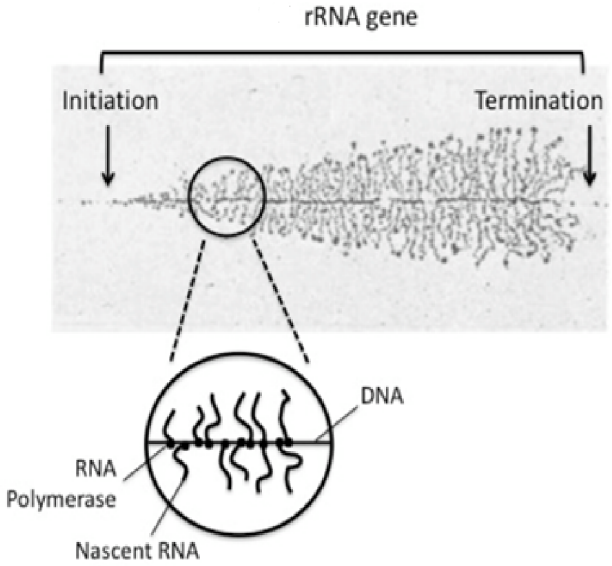


Fig. 2.1

(a)(i) Name the Process X occurring in **Fig. 2.1**.

……[1]

1. Transcription

(ii) List one molecule **not mentioned in Fig. 2.1** that is required for Process X.

……[1]

1. General Transcription factor (Reject: Specific transcription factor due to it not a real requirement for transcription)
   / ribonucleotides
   / transcription initiation factors;

(iii) Describe how RNA polymerase is able to recognise and bind to the promoter on DNA and not to other DNA regions.

……[2]

1. Ref. RNA polymerase has a domain complementary in shape to general transcription factors which bind to TATA box of promoter
2. General Transcription factors contain a **DNA-binding domain** [Reject: active site] which recognize and bind to specific DNA sequence in the **promoter** ;

3. Ref. **Nucleotide sequence** / length / major and minor grooves of promoter offers a **complementary shape** to DNA-binding domain of RNA polymerase ;

[Reject: complementary base pairing]

(iv) Explain for the observed pattern of Process X in **Fig. 2.1**.

……[2]

1. **Shorter** RNA transcripts seen at the **beginning** of the DNA template strand, which get **longer** till the **end** of the transcription unit, (where the transcripts detach from the DNA template after transcription termination)
2. Due to simultaneous transcription of rRNA gene **by multiple RNA polymerases**, (causing RNA transcripts to extend perpendicularly from DNA template strand) ;

(v) State the roles of rRNA in protein synthesis.

……[2]

1. The rRNA in ribosomes holds the tRNA and mRNA together in **close proximity**, via **complementary base pairing / hydrogen bonds**
2. positions the new amino acid for addition to the carboxyl end of the growing polypeptide
3. rRNA peptidyl transferase activity catalyzes formation of a peptide bond between the new amino acid and the polypeptide chain
4. Ref. rRNA associate with proteins to form ribosomal subunits / ribosomes (which synthesizes proteins)

(b) During protein synthesis in cells of an embryo, all tRNA molecules with UAC anticodon sequence, are observed to be bound to arginine amino acid instead of methionine.

(i) Suggest how these tRNA molecules attached with the wrong amino acid might arise.
……[2]

1. Ref. possible mutation in the **gene** sequence for the aminoacyl tRNA synthetases,
2. resulting in **altered 3D conformation** of active site
   which is **complementary** (in shape) to the amino acid arginine and the corresponding tRNA with anticodon UAC

(ii) Suggest and explain the effect of this wrong pairing of amino acid to tRNA on the embryo.
……[3]

1. ref. altered **primary sequence** of polypeptides (all methionine replaced by arginine) and folding of polypeptides to **tertiary structure** / 3D conformation is affected;
2. ref. **non-functional proteins** made in cells
3. ref. possible disruption of metabolic processes in the **cell** / cells might die easily, **embryo cannot further develop** into a fetus

[Total: 13m]

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9 Table 9.1 provides statements regarding the bonds found in four biological molecules.

Table 9.1

statement	protein	DNA	messenger RNA	cellulose
hydrogen bonds stabilise the molecule	✓	✓	×	✓
subunits are joined by peptide bonds	✓	×	×	×

(a) Complete Table 9.1 by indicating with a tick (✓) or a cross (×) whether the statements apply to proteins, DNA, messenger RNA and cellulose.

You should put a tick or a cross in each box of the table. [2]

(b) Telomeres are parts of chromosomes. Describe the function of telomeres. [4]

1a. **Protects the organism's genes from being lost with each cycle of DNA replication** / genetic material / DNA
1b. **due to gap at the 5' end of each replicated DNA strand / DNA shortened**

2a. **Protect chromosomal ends from degradation**
2b. **by binding proteins to form telomere caps.**

3a. **Prevents ends of chromosomes attaching** to **each other**
3a. **prevents apoptosis** / prevent chromosomal ends from activating cell's system for monitoring DNA damage.

4a. **Enables lengthening of telomeres** by
4b. providing a **recognition site** for the **enzyme telomerase.**

(c) A piece of mRNA is 660 nucleotides long but the DNA coding strand from which it was transcribed is 870 nucleotides long.

(i) Explain this difference in number of nucleotides. [1]
- **Introns present in DNA**
- **Introns absent in mRNA**

OR
- **introns removed by RNA splicing**

(ii) What is the maximum number of amino acids in the protein translated from this piece of mRNA? Explain your answer. [2]

Number of amino acids **220 OR 219**
Explanation

1. **3 bases code** for **1 amino acids**

(d) Identify **one** other process that leads to the formation of mature mRNA and state its function. [2]

1. Addition of 5' cap

[Significance]

2. **facilitate the binding of** Translation Initiation Factors and **small ribosomal subunit** for translation to occur.
   OR
2. **facilitate the export of mature mRNA** from nucleus to cytoplasm for translation
   OR
2. **protect the mature mRNA from degradation** by RNase in the cytoplasm

OR

1. Addition of 3' poly-A tail or 3' polyadenylation

[Significance]

2. **facilitate the export of mature mRNA** from nucleus to cytoplasm for translation
   OR
3. **protect the mature mRNA from degradation** by RNase in the cytoplasm

(e) Describe **one** difference between the structure of mRNA and tRNA. [1]

Any one:

1. **mRNA** has **no base-pairing within** its **structure** while **tRNA** has **base-pairing between** regions to **fold back on itself**.
2. **mRNA** has **3' poly-A tail** while **tRNA** has **3' CCA end**.
3. **mRNA** does **not** have **hydrogen bonds** different regions of the single strand while **tRNA** has **hydrogen bonds** at different regions which cause it to **fold back on itself**.
4. **mRNA** is **linear** while **tRNA** **cloverleaf** shape;
5. **mRNA** has **no binding site for amino acids** while tRNA has.
6. **mRNA** **longer**/larger/more nucleotides than tRNA
7. **Mrna** **different** for **each gene**/many kinds, **only few/**20/64 **kinds of tRNA**;

[Total: 12]

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10 Telomeres have a nucleotide sequence that is repeated as many as 2000 times. This repetition is shown in Fig. 3.1. Attached to the DNA of the telomere are protein units.

(a) (i) What sequence of bases is repeated in the complementary polynucleotide shown in Fig. 3.1? [1]

- AATCCC / adenine adenine thymine cytosine cytosine cytosine;; (first 6)

(ii) Suggest one reason for the presence of protein units in the telomere. [1]

- Protect the DNA from degradation;;
- Prevent binding of transcription factors and RNA polymerase to the DNA;;
- Enables homologous chromosomes to pair during meiosis;;
- AVP;;

(b) In the past, repeating sequences were referred to as "junk DNA". Explain why the term "junk DNA" is misleading in the context of telomere. [2]

- "Junk" implies no, function / purpose;; ora
- Repeating sequences of telomeres serve to protect genes from being eroded via successive rounds of replication, maintain the integrity of chromosomal end, and limit the lifespan of cells;;

(c) The repetitive base sequence of telomere DNA is an example of a non-coding base sequence.

Explain what is meant by non-coding. [1]

- Not transcribed to form a product (protein / polypeptide / amino acid sequence);;

(d) A study of individual telomere lengths and its correlation with age is shown in Fig. 3.2.

Account for the trend line shown in Fig. 3.2. [4]

1. Increase in age from 20 to 70, decrease in telomere length from 7.8 kb to 6.5 kb;
2. More, cell division / generations of cells / mitosis / replication;
3. Loss of, telomere / DNA / nucleotides / part of chromosome, at each replication;
4. Due to end replication problem;
5. During DNA replication, when the last RNA primer is removed / excised;
6. At the 3' end of parental template strand / 5'end of daughter strand, it is not replaced by corresponding DNA sequence;
7. As DNA polymerase cannot add new nucleotides; without an existing 3'OH end;
8. Idea of resulting daughter DNA strand being shorter than the parental DNA strand;

[Total: 9]