

DNA and Genomics

| Compare DNA and RNA. | | |
|----------------------------|---|---|
| Point of Comparison | DNA | RNA |
| Structure | Double stranded double helix. | Single stranded. Different parts of a single RNA molecule can base pair with each other via complementary base pairing to form a complex structure. |
| Size | Longer. | Shorter. |
| Pentose Sugar | Deoxyribose (–H atom attached to C2 instead of –OH group). | Ribose (–OH group attached to C2 instead of –H atom). |
| Nitrogenous Bases | Purines: Adenine and guanine . Pyrimidines: Cytosine and thymine . | Purines: Adenine and guanine . Pyrimidines: Cytosine and uracil . |
| Complementary Base Pairing | Two hydrogen bonds between adenine and thymine . Three hydrogen bonds between cytosine and guanine . | Two hydrogen bonds between adenine and uracil . Three hydrogen bonds between cytosine and guanine . |
| Ratio of Bases | A:T and C:G = 1:1 due to complementary base pairing . | No fixed ratio. |
| Forms | Only one form. | Several forms (mRNA, rRNA, tRNA). |
| Stability | Stable and resistant to enzymatic breakdown. | Unstable and reactive due to reactive 2' –OH group and single stranded nature that is more prone to nuclease activity. |
| Location | Nucleus. | Manufactured in nucleus but present in cytoplasm . |
| Amount | Constant for all somatic cells. | Varies in different cell types, stages of life cycle and levels metabolic activity. |

| | | |
|-----------------|--|---|
| DNA Replication | Describe the evidence for semi-conservative DNA replication. | |
| | <p>Parental <i>E. coli</i> are grown for many generations in ^{15}N medium as the only source of nitrogen such that only ^{15}N-^{15}N DNA molecules are present. These appear as the lowest band in cesium chloride solution.</p> <p>The <i>E. coli</i> is then transferred to a medium only containing ^{14}N and allowed to divide once. During semi-conservative DNA replication, the original ^{15}N-^{15}N DNA strands unzipped by the breaking of hydrogen bonds and each strand served as templates for the synthesis of the new strands. Since only ^{14}N DNA was present in the medium, the resulting DNA molecules were all hybrid DNA molecules where each is made up of one original ^{15}N strand and one new ^{14}N strand. This hybrid DNA molecule appears as the intermediate band in cesium chloride solution.</p> <p>Some of the cells were allowed to divide once more in the ^{14}N medium. Each hybrid ^{14}N-^{15}N DNA unzipped and were used as templates for semi-conservative DNA replication. Hence, half the DNA is hybrid ^{15}N-^{14}N DNA which appears as the intermediate band in cesium chloride solution and half is light ^{14}N-^{14}N DNA which appears as the uppermost band in cesium chloride solution.</p> | |
| | Describe the process of DNA replication. | |
| | Semi-Conservative Nature | Replication of DNA is semi-conservative where each parental strand of the DNA double helix unzips and separates through the breakage of hydrogen bonds and acts as templates for the synthesis of two new complementary strands via complementary base pairing , giving rise to two daughter DNA molecules , each consisting of one original and one newly synthesized strand. |
| | Before DNA Replication | Free deoxyribonucleoside triphosphates are manufactured in the cytoplasm and transported into the nucleus via nuclear pores . DNA replication occurs at S phase of interphase . |
| | Initiation | Replication of DNA begins at the origin of replication where helicase will bind. Helicase unzips the DNA molecule by breaking hydrogen bonds between complementary base pairs , separating the parental strands. Single stranded DNA binding proteins interact with the separated strands so that it will remain single stranded and can serve as a template for replication. Topoisomerase relieves overwinding strain ahead of replication forks by breaking, swiveling and rejoining DNA strands. Primase catalyzes the synthesis of a short RNA primer which provides a free 3' -OH end for DNA polymerase to recognize and start DNA synthesis. |

| | | | |
|-----------------|---|---|---|
| DNA Replication | Describe the process of DNA replication. | | |
| | Synthesis | <p>DNA polymerase adds free nucleotides to the free 3' –OH group of the DNA via complementary base pairing between the template strand and free deoxyribonucleoside triphosphates where adenine forms two hydrogen bonds with thymine and guanine forms three hydrogen bonds with cytosine. DNA polymerase catalyzes the formation of phosphodiester bonds between adjacent nucleotides.</p> <p>The new DNA strand is synthesized in the 5' to 3' direction as the active site of DNA polymerase is complementary in shape and charge to the free 3' –OH group of the growing DNA strand.</p> <p>One of the daughter strands known as the leading strand is synthesized continuously towards replication fork in the 5' to 3' direction. The other strand known as the lagging strand is synthesized discontinuously away from the replication fork, giving rise to Okazaki fragments.</p> <p>RNA primers are then removed and replaced by deoxyribonucleotides by another DNA polymerase. DNA ligase catalyzes the formation of phosphodiester bonds between the Okazaki fragments and adjacent nucleotides on each of the DNA fragments, sealing the nicks.</p> | |
| | End of Replication | The complementary parental and daughter strands rewind into a double helix. | |
| Transcription | Describe the process of transcription. | | |
| | Stage | Eukaryotes | Prokaryotes |
| | Initiation | <p>General transcription factors first assemble along the promoter and then recruit RNA polymerase and attach it on the promoter, forming the transcription initiation complex.</p> | <p>Sigma factors associate with the core RNA polymerase, forming the RNA polymerase holoenzyme, which scans along the DNA until the sigma factor recognizes and binds to the promoter.</p> |
| | <p>RNA polymerase will then unzip DNA double helix by breaking hydrogen bonds between complementary base pairs. Only the 3' to 5' strand is used as the template strand (non-coding strand, anti-sense strand) for the synthesis of a complementary mRNA strand.</p> | | |

| Transcription | Describe the process of transcription. | | |
|---------------|--|--|---|
| | Stage | Eukaryotes | Prokaryotes |
| | Elongation | <p>Free ribonucleotides bind to the DNA template strand by complementary base pairing where adenine forms two hydrogen bonds with uracil and cytosine forms three hydrogen bonds with guanine.</p> <p>RNA polymerase catalyzes the formation of phosphodiester bonds between adjacent ribonucleotides to form the sugar phosphate backbone. The mRNA strand is synthesized in the 5' to 3' direction. The region of DNA that has just been transcribed will reanneal.</p> | |
| | Termination | <p>RNA polymerase transcribes a sequence on the template DNA which codes for the polyadenylation sequence (AAUAAA) in the pre-mRNA. Endonucleases bind at a point downstream of the polyadenylation sequence to cut and free the pre-mRNA from the RNA polymerase, causing RNA polymerase to dissociate from the template DNA strand.</p> | <p>RNA polymerase transcribes a termination sequence on the template DNA. This causes the transcribed terminator mRNA sequence to fold back to form a hairpin loop, which acts as a termination signal that causes the mRNA and RNA polymerase to be released and dissociate from the template DNA strand.</p> |
| | Post-Transcriptional Modification | <p>Addition of a 5' methylguanosine cap.</p> <p>RNA splicing by spliceosomes which excises introns and joins exons at precise intron-exon boundaries with the use of ATP.</p> <p>Synthesis of the poly A tail by poly A polymerase which adds adenine nucleotides downstream of the polyadenylation sequence.</p> | - |
| | Simultaneous Transcription | <p>Several molecules of RNA polymerase can simultaneously transcribe the same gene, increasing the amount of mRNA transcribed from it, helping the cell synthesize the encoded protein in large amounts.</p> | |

| Translation | Describe the process of translation | | |
|-------------|-------------------------------------|--|---|
| | Stage | Eukaryotes | Prokaryotes |
| | Amino Acid Activation | <p>Each specific amino acid is covalently attached to the 3' CCA stem of a tRNA molecule with a specific anticodon to form an aminoacyl-tRNA molecule.</p> <p>This attachment is catalyzed by aminoacyl-tRNA synthetase, which has a specific active site that is complementary in shape and charge to a tRNA molecule with a specific anticodon and a specific amino acid to be attached with the corresponding tRNA molecule.</p> | |
| | Initiation | <p>Translation initiation factors and initiator tRNA carrying methionine bind to the small ribosomal subunit which then recognizes and binds to the 5' methylguanosine cap of the mRNA and moves in the 5' to 3' direction in search of the start codon AUG.</p> | <p>Translation initiation factors bind to the small ribosomal subunit and facilitate its binding to the Shine-Dalgarno sequence so that the start codon is correctly positioned before the initiator tRNA binds.</p> |
| | | <p>The anticodon of the initiator tRNA will complementary base pair with the start codon AUG on the mRNA. The binding of the large ribosomal subunit will complete the ribosome forming the translation initiation complex.</p> | |
| | | <p>The initiator tRNA is at the peptidyl-tRNA binding site (P site) leaving the aminoacyl-tRNA binding site (A site) vacant for incoming aminoacyl-tRNA molecules.</p> <p>Translation requires the usage of GTP.</p> | |
| | Elongation | <p>A second aminoacyl-tRNA carrying the next amino acid in the chain binds to the A site by complementary base pairing between its anticodon and the second codon on mRNA. Peptidyl transferase of the large ribosomal subunit catalyzes the formation of a peptide bond between the adjacent amino acids.</p> <p>Methionine dissociates from the initiator tRNA as a result and remains bound to the second amino acid at the A site. The ribosome translocates in the 5' to 3' direction, shifting the first tRNA to the exit site (E site) allowing it to be released into the cytosol. The tRNA with the growing polypeptide chain is now at the P site and the A site will hold a new incoming aminoacyl-tRNA with an anticodon complementary to the next codon on the mRNA. The polypeptide is synthesized from the N terminal to the C terminal.</p> | |

| Translation | Describe the process of translation | | |
|-------------|-------------------------------------|--|-------------|
| | Stage | Eukaryotes | Prokaryotes |
| | Termination | This process continues until a stop codon UAA, UAG or UGA is reached at the A site . Release factors enters the A site causing hydrolysis of the bond between the polypeptide chain and the tRNA in the P site . The polypeptide is released from the ribosome where it will complete its folding into its necessary secondary and tertiary structures. The ribosome disassembles into its subunits. | |
| | Polyribosomes | Several ribosomes translating a single mRNA strand is known as a polyribosome . It allows for a faster rate of protein synthesis especially when there is a greater demand for the protein. | |

| Compare DNA replication, transcription and translation. | | | |
|---|--|---|---|
| Point of Comparison | DNA Replication | Transcription | Translation |
| Process | Synthesis of two daughter DNA molecules from both strands of a DNA template. | Synthesis of RNA using a 3' to 5' DNA template. | Synthesis of polypeptide from the sequence of codons on mRNA . |
| Product | Double stranded DNA made up of deoxyribonucleotides linked by phosphodiester bonds | Single stranded mRNA made up of ribonucleotides linked by phosphodiester bonds . | Polypeptide made up of amino acids linked by peptide bonds . |
| Template Read In | 3' to 5' direction. | 3' to 5' direction. | 5' to 3' direction. |
| Product Made In | 5' to 3' direction. | 5' to 3' direction. | N to C terminus. |
| Begins At | Origin of replication. | Promoter. | Start codon AUG. |
| Ends At | Telomere/When replication bubbles meet. | Termination sequence. | Stop codon UAG, UAA, UGA. |
| Location | Nucleus. | Nucleus. | Ribosomes in cytoplasm or rough endoplasmic reticulum. |

| | | |
|-----------|------|--|
| Structure | DNA | <p>DNA is made up of deoxyribonucleotides with deoxyribose sugar, nitrogenous bases and phosphate groups. A molecule of DNA is a double helix made up of two polynucleotide strands with a sugar phosphate backbone, with nucleotides linked by covalent phosphodiester bonds.</p> <p>The two strands run from the 5' phosphate end to the 3' hydroxyl end in opposite directions. Hence, they are antiparallel. The two strands of the double helix are at a constant width of 2 nm apart. Each complete turn of the double helix has 10 base pairs and a distance of 3.4 nm.</p> <p>They are held together by hydrogen bonds between complementary base pairs of the two complementary DNA strands, with adenine base pairing with thymine, forming two hydrogen bonds and guanine base pairing with cytosine, forming three hydrogen bonds. Hence, the ratio of purines to pyrimidines is 1:1.</p> |
| | | <p>RNA is made up of ribonucleotides with ribose sugar, nitrogenous bases and phosphate groups. A molecule of RNA is a single stranded polynucleotide chain with a sugar phosphate backbone, with ribonucleotides linked by covalent phosphodiester bonds. It contains the purines of adenine and guanine, and the pyrimidines of uracil and cytosine.</p> |
| | mRNA | <p>Messenger RNA is single stranded. In eukaryotes, mRNA contains a coding region starting with the start codon AUG and ending with a stop codon UAG, UAA or UGA. It also has 3' and 5' untranslated regions upstream of the start codon and downstream of the stop codon respectively.</p> |
| | tRNA | <p>Transfer RNA is single stranded but segments fold back upon itself and form complementary base pairs with adenine forming two hydrogen bonds with uracil and cytosine forming three hydrogen bonds with cytosine at certain regions to form a 3D L-shaped structure or a 2D cloverleaf structure.</p> <p>It has 3 loops. On one loop, there is an anticodon that binds to a specific mRNA codon via complementary base pairing. On another loop, there is a 3' end with the CCA stem that serves as the attachment site for a specific amino acid that corresponds to the anticodon.</p> |
| | rRNA | <p>Ribosomal RNA is single stranded and wound into a complex structure comprising single and double helices. It associates with a set of ribosomal proteins to form the large and small subunits of ribosomes.</p> |

| | | | |
|-------|---|--|---|
| Roles | DNA | The main role of DNA is to store information and pass it from one generation to the next. | |
| | | Explain why DNA is a suitable store of information. | |
| | | Structure | Function |
| | | There is weak hydrogen bonding between the two DNA strands. | DNA is able to separate and act as a template during semi-conservative DNA replication during S phase of interphase where a new strand is synthesized via complementary base pairing where adenine forms two hydrogen bonds with thymine and cytosine forms three hydrogen bonds with guanine. Hence, it can be replicated accurately and daughter cells have identical copies of DNA as the parent cell and the coded information can be readily accessed . |
| | mRNA | There are numerous hydrogen bonds holding the two strands of DNA together. Adjacent nucleotides in each strand are joined by strong covalent phosphodiester bonds . | DNA is a stable molecule and can be passed on to the next generation without the loss of genetic information . |
| | | DNA is double stranded . | There is a backup of code as one strand can serve as a template for the repair of the other if a mutation occurred. |
| | <p>mRNA is a single stranded polynucleotide formed by transcription of DNA. It acts as a carrier of genetic code. Since mRNA is freely mobile, it is able to carry genetic information from the gene on the DNA in nucleus out to ribosomes in the cytoplasm or rough endoplasmic reticulum where translation takes place, through nuclear pores.</p> <p>mRNA contains triplet base codes known as codons that each specify a specific amino acid. The specific sequence of codons code for the amino acid sequence of a single polypeptide. During translation, mRNA acts a template with codons interacting with anticodons of a specific tRNA molecule carrying a specific amino acid through complementary base pairing.</p> <p>mRNA has recognition sites that allow it to bind to the small ribosomal subunit at the start of translation. It has start and stop codons to determine the first and last amino acids to be added to a polypeptide chain during translation.</p> <p>Gene expression can be regulated either by varying the rate of mRNA synthesis during transcription or its rate of breakdown.</p> | | |

| | | |
|-------|------|--|
| Roles | tRNA | Each tRNA has a specific anticodon that is matched to a specific amino acid . It carries amino acids to the ribosome, where the specific base pairing of the anticodon on tRNA to codon on mRNA via complementary base pairing ensures that the sequence of bases on mRNA is translated into a specific sequence of amino acids in the forming polypeptide chain . |
| | rRNA | <p>rRNA associates with a set of ribosomal proteins to form the large and small subunits of ribosomes.</p> <p>It allows the small ribosomal subunit to bind to mRNA via complementary base pairing where adenine forms two hydrogen bonds with uracil and guanine forms three hydrogen bonds with cytosine.</p> <p>The rRNA in the large ribosomal subunit enables binding of aminoacyl-tRNAs to the peptidyl-tRNA binding site and amino-acyl tRNA binding site. Peptidyl transferase on the large ribosomal subunit is a rRNA molecule which catalyzes the formation of peptide bonds in the polypeptide.</p> |
| | | <p style="text-align: center;"><u>Outline the main features of the genetic code.</u></p> <p>The genetic code refers to the relationship between nucleotide bases and amino acids. It describes the manner in which a particular nucleotide sequence is translated into its corresponding amino acid sequence.</p> <p>The genetic code is</p> <ol style="list-style-type: none"> A triplet code in which each codon codes for one amino acid. Universal where the same codon codes for the same amino acid in all organisms. Degenerate so a given amino acid may be coded for by more than one codon. In most cases, the difference in the triplet code lies in the third base. Non-overlapping and can be read as successive codons. In other words, each in a triplet code is only used once. Continuous and there are no nucleotides skipped between the codons Includes stop and start codons. The start codon, AUG signals the initiation site of translation of the mRNA into a sequence of amino acids. It codes for amino acids methionine. The stop codons, UAG, UAA and UGA do not code for any amino acid, as there is no tRNA with an anticodon complementary to these codons. They act as stop signals for the termination of polypeptide chain synthesis during translation. |