2.7 DNA replication, transcription and translation

Essential Idea: Genetic information in DNA can be accurately copied and can be translated to make the proteins needed by the cell.

The image shows an electron micrograph of a Polysome, i.e. multiple ribosomes simultaneous translating a molecule of mRNA. The central strand is the mRNA, The darker circular structures are the ribosomes and the side chains are the newly formed polypeptides.

By Chris Paine
https://bioknowledgy.weebly.com/

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## Applications and Skills

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2.7.U2 Helicase unwinds the double helix and separates the two strands by breaking hydrogen bonds.

Helicase
- The ‘ase’ ending indicates it is an enzyme
- This family of proteins varies, but are often formed from multiple polypeptides and doughnut in shape

2.7. U2 Helicase unwinds the double helix and separates the two strands by breaking hydrogen bonds.

1. DNA Helicase unwinds and unzips DNA

- Unwinds the DNA Helix
- Separates the two polynucleotide strands by breaking the hydrogen bonds between complementary base pairs
- ATP is needed by helicase to both move along the DNA molecule and to break the hydrogen bonds
- The two separated strands become parent/template strands for the replication process
2.7. U3 DNA polymerase links nucleotides together to form a new strand, using the pre-existing strand as a template.

DNA Polymerase

- The ‘ase’ ending indicates it is an enzyme
- This protein family consists of multiple polypeptides sub-units
- This is DNA polymerase from a human.
- The polymerisation reaction is a condensation reaction
2.7. U3 DNA polymerase links nucleotides together to form a new strand, using the pre-existing strand as a template.

**2. DNA Polymerase creates complementary strands**

- DNA polymerase always moves in a 5’ to 3’ direction
- DNA polymerase catalyses the covalent phosphodiester bonds between sugars and phosphate groups
- DNA Polymerase proof reads the complementary base pairing. Consequently mistakes are very infrequent occurring approx. once in every billion bases pairs

Free nucleotides are collected by DNA polymerase and attached to the new strand by complementary base pairing.

- Free nucleotides are deoxynucleoside triphosphates
- The extra phosphate groups carry energy which is used for formation of covalent bonds
2.7. U3 DNA polymerase links nucleotides together to form a new strand, using the pre-existing strand as a template.

**DNA replication moves in a 5' to 3' direction**

- This means the **5' end of the new strand**

Free nucleotides in the nucleus
(deoxynucleoside triphosphates)

- DNA polymerase always moves in a 5’ to 3’ direction
- DNA polymerase catalyses the covalent phosphodiester bonds between sugars and phosphate groups
2.7.U1 The replication of DNA is semi-conservative and depends on complementary base pairing.

A purine must base-pair with a pyrimidine:

1. Each of the nitrogenous bases can only pair with its partner (A=T and G=C) this is called **complementary base pairing**.

2. The two new strands formed will be identical to the original strand.
2.7.U1 The replication of DNA is semi-conservative and depends on complementary base pairing.

3. Each new strand contains one original and one new strand, therefore DNA Replication is said to be a **Semi-Conservative** Process.
Polymerase Chain Reaction (PCR)

- Typically used to copy a segment of DNA – not a whole genome
- Used to amplify small samples of DNA
- In order to use them for DNA profiling, recombination, species identification or other research.
- The process needs a thermal cycler, primers, free DNA nucleotides and DNA polymerase.

Review: 3.5. U2 PCR can be used to amplify small amounts of DNA.

Learn the detail using the virtual lab and/or the animation:

http://www.sumanasinc.com/webcontent/animations/content/pcr.html

http://www.slideshare.net/gurustip/genetic-engineering-and-biotechnology-presentation
**Review:** 2.7.A1 Use of Taq DNA polymerase to produce multiple copies of DNA rapidly by the polymerase chain reaction (PCR).

After clicking on the myDNA link choose techniques and then amplifying to access the tutorials on the polymerase chain reaction (PCR).

Alternatively watch the McGraw-Hill tutorial
2.7.A1 Use of Taq DNA polymerase to produce multiple copies of DNA rapidly by the polymerase chain reaction (PCR).

To summarise:

PCR is a way of producing large quantities of a specific target sequence of DNA. It is useful when only a small amount of DNA is available for testing e.g. crime scene samples of blood, semen, tissue, hair, etc.

PCR occurs in a thermal cycler and involves a repeat procedure of 3 steps:
1. **Denaturation**: DNA sample is heated to separate it into two strands
2. **Annealing**: DNA primers attach to opposite ends of the target sequence
3. **Elongation**: A heat-tolerant DNA polymerase (Taq) copies the strands

- One cycle of PCR yields two identical copies of the DNA sequence
- A standard reaction of 30 cycles would yield 1,073,741,826 copies of DNA (2^{30})
2.7.S2 Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

Before Meselson and Stahl’s work there were different proposed models for DNA replication. After their work only semi-conservative replication was found to be biologically significant.
2.7.S2 Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

**Question** Which model of DNA replication - conservative, dispersive, or semi-conservative - applies to *E. coli*?

**Experiment**

1. **15N medium**
   - DNA from bacteria that had been grown in medium containing 15N appeared as a single band.

2. **Transfer to 14N medium and replicate**
   - After one round of replication, the DNA appeared as a single band intermediate between that expected for DNA with 15N and that expected for DNA with 14N.

3. **Replication in 14N medium**
   - After a second round of replication, DNA appeared as two bands, one in the position of hybrid DNA (half 15N and half 14N) and the other in the position of DNA that contained only 14N.

4. **Replication in 14N medium**
   - Samples taken after additional rounds of replication appeared as two bands, as in step 3.

**Results**

- **Light (14N)**
- **Heavy (15N)**

**Conclusion** DNA replication in *E. coli* is semi-conservative.

Learn about Meselson and Stahl’s work with DNA to discover the mechanism of semi-conservative replication.


Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

At the start of a Meselson and Stahl experiment (generation 0) a single band of DNA with a density of 1.730 g cm$^{-3}$ was found. After 4 generations two bands were found, but the main band had a density of 1.700 g cm$^{-3}$.

a. Explain why the density of the main band changed over four generations. (2)

b. After one generation one still only one DNA band appears, but the density has changed.
   i. Estimate the density of the band. (1)
   ii. Which (if any) mechanisms of DNA replication are falsified by this result? (1)
   iii. Explain why the identified mechanism(s) are falsified. (1)

c. Describe the results after two generations and which mechanisms and explain the identified mechanism(s) (if any) are falsified as a consequence. (3)

d. Describe and explain the result found by centrifuging a mixture of DNA from generation 0 and 2. (2)
2.7.2 Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

At the start of a Meselson and Stahl experiment (generation 0) a single band of DNA with a density of 1.730 g cm$^{-3}$ was found. After 4 generations two bands were found, but the main band had a density of 1.700 g cm$^{-3}$.

a. Explain why the density of the main band changed over four generations. (2)
- $N_{15}$ isotope has a greater mass than $N_{14}$ isotope due to the extra neutron
- Generation 0 contained DNA with exclusively $N_{15}$ isotopes (giving it a greater density)
- With each generation the proportion $N_{14}$ isotope (from free nucleotides) increases as the mass of DNA doubles
- After four generations most strands contain only $N_{14}$ isotope – the dominant band at a density of 1.700 g cm$^{-3}$.
- $N_{15}$ isotope remains, but is combined in strands with $N_{14}$ isotope – a second band at a density between 1.730 and 1.700 g cm$^{-3}$. 
2.7.S2 Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

At the start of a Meselson and Stahl experiment (generation 0) a single band of DNA with a density of 1.730 g cm\(^{-3}\) was found. After 4 generations two bands were found, but the main band had a density of 1.700 g cm\(^{-3}\).

b. After one generation only one DNA band appeared, but the density had changed.
   i. Estimate the density of the band. (1)
      • The band would contain equally amounts of N\(_{14}\) isotope and N\(_{15}\) isotope
      • Density of an all N\(_{15}\) isotope band is 1.730 g cm\(^{-3}\).
      • Density of an all N\(_{14}\) isotope band is 1.700 g cm\(^{-3}\).
      • Density of an the mixed isotope band is the average of the two:
        \[ \frac{1.730 \text{ g cm}^{-3} + 1.700 \text{ g cm}^{-3}}{2} = 1.715 \text{ g cm}^{-3} \]

   ii. Which (if any) mechanisms of DNA replication are falsified by this result? (1)
       • conservative replication

   iii. Explain why the identified mechanism(s) are falsified. (1)
       • For conservative replication to be the case two bands should appear in all generations after generation 0
2.7.S2 Analysis of Meselson and Stahl’s results to obtain support for the theory of semi-conservative replication of DNA.

At the start of a Meselson and Stahl experiment (generation 0) a single band of DNA with a density of 1.730 g cm\(^{-3}\) was found. After 4 generations two bands were found, but the main band had a density of 1.700 g cm\(^{-3}\).

c. Describe the results after two generations and which mechanisms and explain the identified mechanism(s) (if any) are falsified as a consequence. (3)

- **2 bands:**
  - **One band containing a mixture of N\(_{15}\) and N\(_{14}\) isotopes** – semi-conservative replication preserves the DNA strands containing N\(_{15}\) isotopes, but combines them with N\(_{14}\) nucleotides during replication.
  - **One band containing all N\(_{14}\) isotopes** - during replication from generation 1 to generation 2. The new strands consisting of of N\(_{14}\) isotopes are replicated using N\(_{14}\) nucleotides creating strands containing just N\(_{14}\) isotopes.
  - **Dispersive replication is falsified** as this model would continue to produce a single band, containing proportionally less N\(_{15}\) isotope.
At the start of a Meselson and Stahl experiment (generation 0) a single band of DNA with a density of 1.730 g cm⁻³ was found. After 4 generations two bands were found, but the main band had a density of 1.700 g cm⁻³.

d. Describe and explain the result found by centrifuging a mixture of DNA from generation 0 and 2. (2)

- **3 bands:**
  - **One band from generation 0 containing all N₁⁵ isotopes** – no replication has occurred
  - **One band from generation 2 containing a mixture of N₁⁵ and N₁⁴ isotopes** – semi-conservative replication preserves the DNA strands containing N₁⁵ isotopes, but combines them with N₁⁴ nucleotides during replication.
  - **One band from generation 2 (all replicated DNA) containing all N₁⁴ isotopes** – during replication from generation 1 to generation 2. The new strands consisting of N₁⁴ isotopes are replicated using N₁⁴ nucleotides creating strands containing just N₁⁴ isotopes.
2.7.U4 Transcription is the synthesis of mRNA copied from the DNA base sequences by RNA polymerase.
2.7.U5 Translation is the synthesis of polypeptides on ribosomes.

Q - What is the purpose of **transcription** and **translation**?

A - These processes work together to create a polypeptide which in turns folds to become a protein. Proteins carry many essential functions in cells. For more detail review 2.4.U7 Living organisms synthesize many different proteins with a wide range of functions.

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<th>Transport of nutrients and gases</th>
<th>Cell adhesion</th>
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<td>Cytoskeletons</td>
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<td>Blood clotting</td>
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<td>Membrane transport</td>
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Use the learn.genetics tutorial to discover one example:

[Use the learn.genetics tutorial to discover one example](http://learn.genetics.utah.edu/content/molecules/firefly/)

**How a Firefly’s Tail Makes Light**

**Step 1:** Cells in the firefly’s tail produce luciferase enzyme

**Step 2:** Luciferase drives a chemical reaction that generates light

- [Catalysis](#)
- [Tensile strengthening](#)
- [Transport of nutrients and gases](#)
- [Cell adhesion](#)
- [Muscle contraction](#)
- [Cytoskeletons](#)
- [Blood clotting](#)
- [Membrane transport](#)
- [Hormones](#)
- [Receptors](#)
- [Packing of DNA](#)
- [Immunity](#)
2.7.U4 Transcription is the synthesis of mRNA copied from the DNA base sequences by RNA polymerase.

2.7.U5 Translation is the synthesis of polypeptides on ribosomes.

**TRANSCRIPTION**: In the nucleus, the cell's machinery copies the gene sequence into messenger RNA (mRNA), a molecule that is similar to DNA. Like DNA, mRNA has four nucleotide bases - but in mRNA, the base uracil (U) replaces thymine (T).

**TRANSLATION**: The protein-making machinery, called the ribosome, reads the mRNA sequence and translates it into the amino acid sequence of the protein. The ribosome starts at the sequence AUG, then reads three nucleotides at a time. Each three-nucleotide codon specifies a particular amino acid. The "stop" codons (UAA, UAG and UGA) tell the ribosome that the protein is complete.

[Image](http://learn.genetics.utah.edu/content/molecules/transcribe/)
Transcription is the process by which an RNA sequence is produced from a DNA template:

Three main types of RNA are predominantly synthesised:

- **Messenger RNA (mRNA):** A transcript copy of a gene used to encode a polypeptide
- Transfer RNA (tRNA): A clover leaf shaped sequence that carries an amino acid
- Ribosomal RNA (rRNA): A primary component of ribosomes

We are focusing on mRNA

http://www.nature.com/scitable/topicpage/Translation-DNA-to-mRNA-to-Protein-393
2.7.U4 Transcription is the synthesis of mRNA copied from the DNA base sequences by RNA polymerase.

- The enzyme RNA polymerase binds to a site on the DNA at the start of a gene (The sequence of DNA that is transcribed into RNA is called a gene).
- RNA polymerase separates the DNA strands and synthesises a complementary RNA copy from the antisense DNA strand.
- It does this by covalently bonding ribonucleoside triphosphates that align opposite their exposed complementary partner (using the energy from the cleavage of the additional phosphate groups to join them together).
- Once the RNA sequence has been synthesised:
  - RNA polymerase will detach from the DNA molecule
  - RNA detaches from the DNA
  - The double helix reforms
- Transcription occurs in the nucleus (where the DNA is) and, once made, the mRNA moves to the cytoplasm (where translation can occur).
Translation is the process of protein synthesis in which the genetic information encoded in mRNA is translated into a sequence of amino acids in a polypeptide chain. A ribosome is composed of two halves, a large and a small subunit. During translation, ribosomal subunits assemble together like a sandwich on the strand of mRNA:

- Each subunit is composed of RNA molecules and proteins
- The small subunit binds to the mRNA
- The large subunit has binding sites for tRNAs and also catalyzes peptide bonds between amino acids
The amino acid sequence of polypeptides is determined by mRNA according to the genetic code.

The length of mRNA molecules varies - the average length for mammals is approximately 2,200 nucleotides (this translates to approximately 730 amino acids in the average polypeptide).

Only certain genes in a genome need to be expressed depending on:
- Cell specialism
- Environment

Therefore not all genes (are transcribed) and translated.

If a cell needs to produce a lot of a certain protein (e.g. β cells in the pancreas specialize in secreting insulin to control blood sugar) then many copies of the required mRNA are created.

Messenger RNA (mRNA): A transcript copy of a gene used to encode a polypeptide.
2.7.U7 Codons of three bases on mRNA correspond to one amino acid in a polypeptide.

The genetic code is the set of rules by which information encoded in mRNA sequences is converted into proteins (amino acid sequences) by living cells.

- **Codons are a triplet of bases** which encodes a particular amino acid.
- As there are four bases, there are **64 different codon combinations** \((4 \times 4 \times 4 = 64\)
- The codons can translate for **20 amino acids**

- Different codons can translate for the same amino acid (e.g. GAU and GAC both translate for Aspartate) therefore the genetic code is said to be **degenerate**
- The order of the codons determines the amino acid sequence for a protein
- The **coding region always starts with a START codon** (AUG) therefore the first amino acid in all polypeptides is Methionine
- The **coding region of mRNA terminates with a STOP codon** - the STOP codon does not add an amino acid – instead it causes the release of the polypeptide

Amino acids are carried by **transfer RNA (tRNA)**
The anti-codons on tRNA are complementary to the codons on mRNA.
2.7.U8 Translation depends on complementary base pairing between codons on mRNA and anticodons on tRNA.

**Key components** of translation that enable genetic code to synthesize polypeptides

- **tRNA molecules** have an anticodon of three bases that binds to a complementary codon on mRNA.
- **tRNA molecules** carry the amino acid corresponding to their codon.
- **mRNA** has a sequence of codons that specifies the amino acid sequence of the polypeptide.
- **Ribosomes**: act as the binding site for mRNA and tRNA, catalyse the peptide bonds of the polypeptide.

![Diagram of protein synthesis](https://upload.wikimedia.org/wikipedia/commons/0/0f/Peptide_syn.png)
2.7. U8 Translation depends on complementary base pairing between codons on mRNA and anticodons on tRNA.

An **outline of translation** and polypeptide synthesis

- **The mRNA contains a series of codons (3 bases) each of which codes for an amino acid.**
- **mRNA binds to the small subunit of the ribosome.**
- **The large subunit binds to the small subunit of the ribosome. There are three binding sites on the large subunit of the ribosome, but only two can contain tRNA molecules at a time.**
- **tRNA molecules contain anticodons which are complementary to the codons on the mRNA. tRNA molecules bind to a specific amino acid that corresponds to the anticodon.**

https://upload.wikimedia.org/wikipedia/commons/0/0f/Peptide_syn.png
2.7.U8 Translation depends on complementary base pairing between codons on mRNA and anticodons on tRNA.

An **outline of translation** and polypeptide synthesis

A peptide bond is formed between the two amino acids (carried by the tRNAs)

The ribosome moves along the mRNA and presents codons in the first two binding sites

**tRNAs with anticodons complementary to the codons bind (the bases are linked by the formation of hydrogen bonds)**
Translation depends on complementary base pairing between codons on mRNA and anticodons on tRNA.

An **outline of translation** and polypeptide synthesis

The process (i.e. the last two steps) repeats forming a polypeptide.

Another tRNA carrying an amino acid binds to the first site and a second peptide bond is formed.

As the ribosome moves along mRNA a tRNA moves to the third binding site and detaches.
2.7.S1 Use a table of the genetic code to deduce which codon(s) corresponds to which amino acid.
2.7.S3 Use a table of mRNA codons and their corresponding amino acids to deduce the sequence of amino acids coded by a short mRNA strand of known base sequence.
2.7.S4 Deducing the DNA base sequence for the mRNA strand.

The diagram summarizes the process of protein synthesis. You should be able to use a section of genetic code, transcribe and translate it to deduce the polypeptide synthesized.
Practice transcribing and translating using the learn.genetics tutorial.

http://learn.genetics.utah.edu/content/molecules/transcribe/
Now use this table to answer the questions on the next slide.

<table>
<thead>
<tr>
<th>First letter</th>
<th>Second letter</th>
<th>Third letter</th>
<th>Key:</th>
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</thead>
<tbody>
<tr>
<td>U</td>
<td>U</td>
<td>U</td>
<td>Ala = Alanine (A)</td>
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<td>U</td>
<td>C</td>
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<td>Arg = Arginine (R)</td>
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<td>A</td>
<td>Asn = Asparagine (N)</td>
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<td>Asp = Aspartate (D)</td>
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<td>Cys = Cysteine (C)</td>
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<td>Gln = Glutamine (Q)</td>
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<td>Met = Methionine (M)</td>
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<td>Phe = Phenylalanine (F)</td>
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<td>Pro = Proline (P)</td>
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<td>Trp = Tryptophan (W)</td>
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<td>C</td>
<td>G</td>
<td>Tyr = Tyrosine (Y)</td>
</tr>
<tr>
<td>U</td>
<td>G</td>
<td>G</td>
<td>Val = Valine (V)</td>
</tr>
</tbody>
</table>

n.b. You just have to be able to use the table. You do not have to memorize which codon translates to which amino acid.
1. Deduce the codon(s) that translate for Aspartate.

2. If mRNA contains the base sequence CUGACUAGGUCCGGA
   a. deduce the amino acid sequence of the polypeptide translated.

   b. deduce the base sequence of the DNA antisense strand from which the mRNA was transcribed.

3. If mRNA contains the base sequence ACUAUAC deduce the base sequence of the DNA sense strand.
1. Deduce the codon(s) that translate for Aspartate.

2. If mRNA contains the base sequence CUGACUAGGUCCGGA
   a. deduce the amino acid sequence of the polypeptide translated.
   b. deduce the base sequence of the DNA antisense strand from which the mRNA was transcribed.

3. If mRNA contains the base sequence ACUAUAC deduce the base sequence of the DNA sense strand.
1. Deduce the codon(s) that translate for Aspartate.

   **GAU, GAC**

2. If mRNA contains the base sequence CUGACUAGGUCCGGA
   a. deduce the amino acid sequence of the polypeptide translated.

   **Leucine + Threonine + Lysine + Arginine + Serine + Glycine**

   b. deduce the base sequence of the DNA antisense strand from which the mRNA was transcribed.

   **GACTGATCCAGGCCT** *(the antisense strand is complementary to the mRNA, but remember that uracil is replaced by thymine)*

3. If mRNA contains the base sequence ACUAAC deduce the base sequence of the DNA sense strand.

   **ACTAAC** *(the sense strand is the template for the mRNA the only change is that uracil is replaced by thymine)*
2.7. S1 Use a table of the genetic code to deduce which codon(s) corresponds to which amino acid.

**Transcribe** this DNA strand into mRNA:

DNA:  ACGTTACGGGATTACAGTCCCCAAACTAC

mRNA:
Transcribe this DNA strand into mRNA:

**DNA:** ACGTTACGGGATTACAGTCCCCAAACTAC

**mRNA:** UGCAAUUGCCUAUUUGUCAUGGGGUUUGAUG

Don't forget: on mRNA, **Uracil** takes the place of Thymine

**Uracil** is complementary to Adenine
2.7.S1 Use a table of the genetic code to deduce which codon(s) corresponds to which amino acid.

Now translate the mRNA into a polypeptide:

DNA: ACGTTACGGGATTACAGTCCCCAATACTAC

mRNA: UGCAAUGCCUAUGUCAGGGUUUGAUG

Remember: the 'Met' codon is 'Start'

There are 20 amino acids and a Stop codon:

- Phe
- Leu
- Ile
- Met
- Val
- Ser
- Pro
- Thr
- Ala
- Tyr
- His
- Gln
- Asn
- Lys
- Asp
- Glu
- Cys
- Trp
- Arg
- Gly
- Stop

http://learn.genetics.utah.edu/units/basics/transcribe/
How many amino acids in the polypeptide?:

DNA: ACGTTACGGATTACAGTCCCAAACTAC

mRNA: UGCAAUUGCCUAUAUGUCAGGGGUUUGAUG

Met Pro Asn Val Arg Val Stop

The 'Met' codon is always the first.

There are 20 amino acids and a Stop codon:

Phe Leu Ile Met Val Ser Pro Thr Ala Tyr
His Gln Asn Lys Asp Glu Cys Trp Arg Gly Stop
2.7. S1 Use a table of the genetic code to deduce which codon(s) corresponds to which amino acid.

Things to remember about the genetic code:

DNA: ACGTTACGGATTACAGTCCCCAAACTAC

this gene = 21 base pairs

giving 7 codons

mRNA: UGC AAU GCC UAA UAG CAG GGU UU UGA AUG

Met Pro Asn Val Arg Val

6 amino acids in the polypeptide

plus stop

The 'Met' codon is always the first.

Number of amino acids = codons - 1

or = (base pairs/3) - 1

There are 20 amino acids and a Stop codon:

Phe  Leu  Ile  Met  Val  Ser  Pro  Thr  Ala  Tyr

His  Gln  Asn  Lys  Asp  Glu  Cys  Trp  Arg  Gly  Stop
Diabetes in some individuals is due to destruction of cells in the pancreas that secrete the hormone insulin. It can be treated by injecting insulin into the blood. Porcine and bovine insulin, extracted from the pancreases of pigs and cattle, have both been widely used. Porcine insulin has only one difference in amino acid sequence from human insulin and bovine insulin has three differences. Shark insulin, which has been used for treating diabetics in Japan, has seventeen differences.

Despite the differences in the amino acid sequence between animal and human insulin, they all bind to the human insulin receptor and cause lowering of blood glucose concentration. However, some diabetics develop an allergy to animal insulins, so it is preferable to use human insulin. In 1982 human insulin became commercially available for the first time. It was produced using genetically modified E. coli bacteria. Since then methods of production have been developed using yeast cells and more recently safflower plants.

2.7.A2 Production of human insulin in bacteria as an example of the universality of the genetic code allowing gene transfer between species.

- All living things use the **same bases** and the **same genetic code**.
- Each **codon** produces the **same amino acid** in transcription and translation, regardless of the species.
- So the sequence of amino acids in a **polypeptide remains unchanged**.
- Therefore, we can take genes from one species and insert them into the genome of another species.

"The Genetic Code is Universal"

We already make use of gene transfer in industrial production of insulin:
Restriction enzymes ‘cut’ the desired gene from the genome.

E. coli bacteria contain small circles of DNA called plasmids.

These can be removed.

The same restriction enzyme cuts into the plasmid.

Because it is the same restriction enzyme the same bases are left exposed, creating ‘sticky ends’

Ligase joins the sticky ends, fixing the gene into the E. coli plasmid.

The recombinant plasmid is inserted into the host cell. It now expresses the new gene. An example of this is human insulin production.
Bibliography / Acknowledgments

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