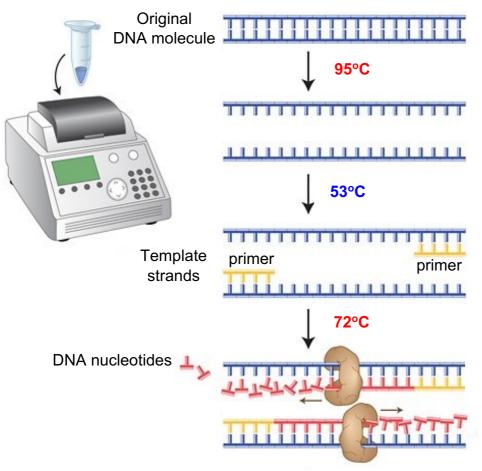
A. POLYMERASE CHAIN REACTION (PCR)

- Used to amplify the amount of DNA.
- A machine replicates DNA over many cycles.
- Used to amplify DNA for **forensic science** and **diagnosing disease**.

Ingredients needed

- DNA molecule
- DNA nucleotides
- Primers
- Taq DNA polymerase



Denaturation = strand separation

Temperature is increased to 95°C to separate the DNA strands

Binding of primers

Temperature is reduced to 53°C to allow primers to bind to the ends of the template strands by complementary base pairing.

Primers allow **Taq DNA polymerase** to start replication.

Extension

Temperature is increased to 73°C as this is the optimum temperature for Taq DNA polymerase.

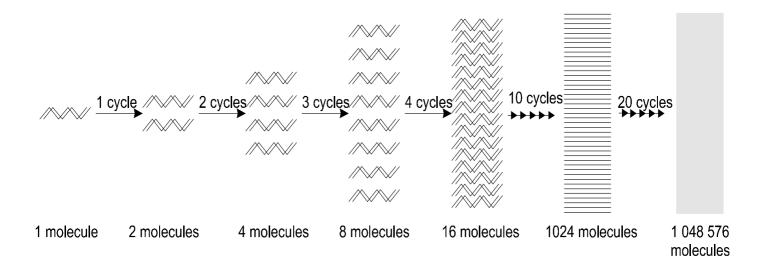
Taq DNA polymerase adds new complementary nucleotides to the new DNA strand.

Two identical DNA molecules are produced.

The process is then repeated.

Taq DNA polymerase is from a bacterium (*Thermophilus aquaticus*) that lives in volcanoes.
 This enzyme does not denature at high temperatures.

What Each Cycle Produces



Number of DNA molecules produced = 2ⁿ Where **n** is the number of cycles

What This Looks Like Graphically

Number of DNA molecules stays the same as the DNA nucleotides or primers have been used up As DNA molecules are doubled with time, there is an exponential increase 140 as the starting number is now significantly large 120 Number 100 of DNA 80 molecules/ Initially, quite flat as thousands 60 there is a very low number of molecules 40 that are being doubled 20 0-3 5 9 11 13 15 19 Number of complete PCR cycles

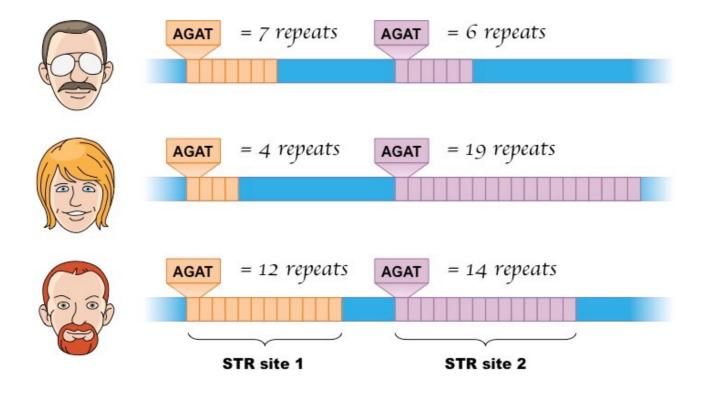
B. DNA FINGERPRINTING

Principle Behind It

- Some of our DNA base sequences do not code for proteins (they are called 'introns').
- Some are just short base sequences that are repeated many times.
- These are called **short tandem repeats** (STRs).
- The same STRs are found on the same chromosome position in different people, but:

Different people have STRs of different lengths – some have more repeats than others

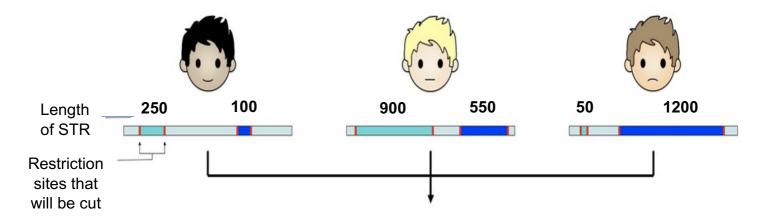
DNA fingerprinting exploits the fact that STRs are different base lengths in different people



How It Is Done

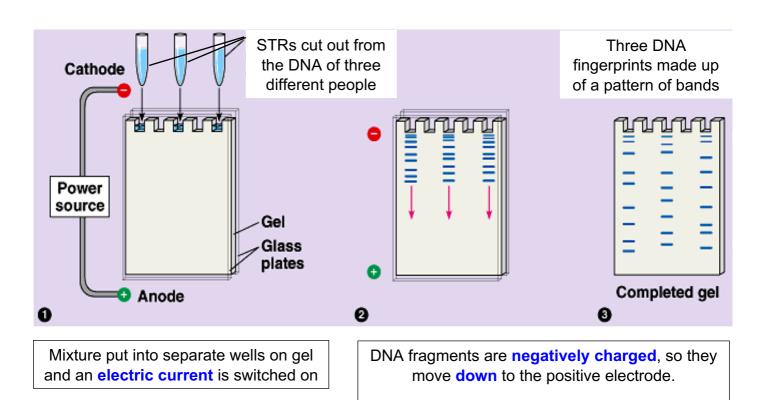
1. DNA Extraction & Digestion

- Collect cheek cells and extract DNA.
- Restriction enzymes are used to cut out the STR base sequences from the DNA.
- Restriction enzymes are specific different ones cut out different base sequences.



• This will produce different lengths of DNA fragments (STRs) for different people.

2. Separation Of DNA Fragments By Gel Electrophoresis



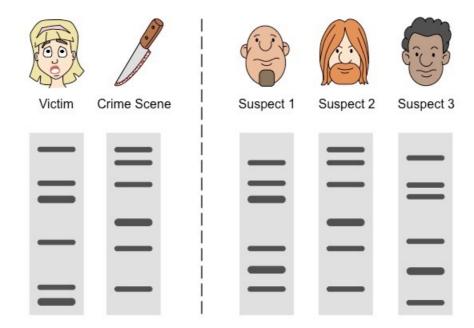
Shorter DNA fragments move faster and **further**.

3. Addition Of Radioactive Probes

- The bands on the gel (which show the different STRs) are not yet visible to the eye.
- Special man-made lengths of DNA called **probes** are added to the gel.
- Probes have complementary base sequences to the STRs and are radioactively-labelled.
- All probes are given time to attach to their specific STRs
- Any unbound probes are then washed away.

4. Autoradiography

- An X-ray film is taken and the radioactive probes show up as dark bands.
- This **indirectly** shows us where the corresponding **STRs** are located.

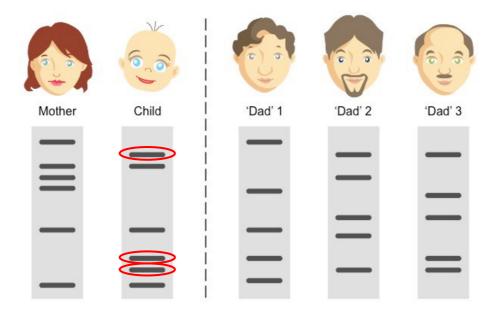


- In this example, we can deduce that **Suspect 2 was present at the crime scene**.
- However, more evidence is needed to prove that he committed the crime.

How DNA fingerprinting is used in paternity cases

A child can only inherit its STRs from its natural mother and father

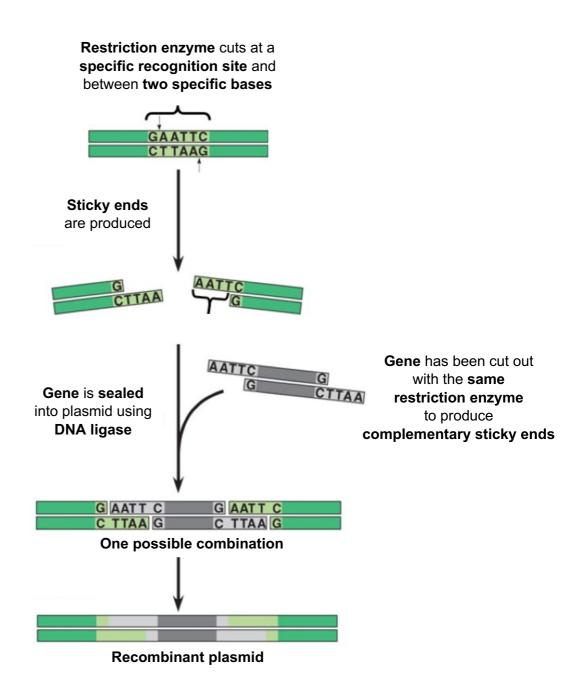
Look at the **bands** that the child did **not** receive from its **mother**Only the **real father** could have passed **these bands** on
Half of the **child's bands** will match the **real father**.



- Dad 3 is the biological father of this child as he has all STRs that the child did not receive from its mother.
- Scientists look at many STRs (usually 13) when doing this not just five or six!

C. RESTRICTION ENZYMES

- Each restriction enzyme cuts a specific DNA base sequence.
- They **break phosphodiester bonds** between the **deoxyribose** sugar and **phosphate** (of the sugar-phosphate backbone).



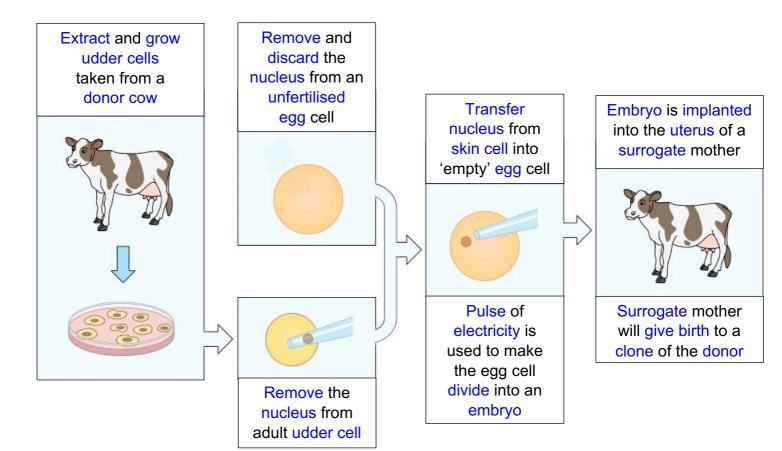
- Bacteria can be infected with virus.
- Restriction enzymes occur naturally in bacteria and they are designed to cut viral DNA to prevent infection.
- We have exploited their natural use in genetic engineering.

Outline the application of DNA fingerprinting to determine paternity.

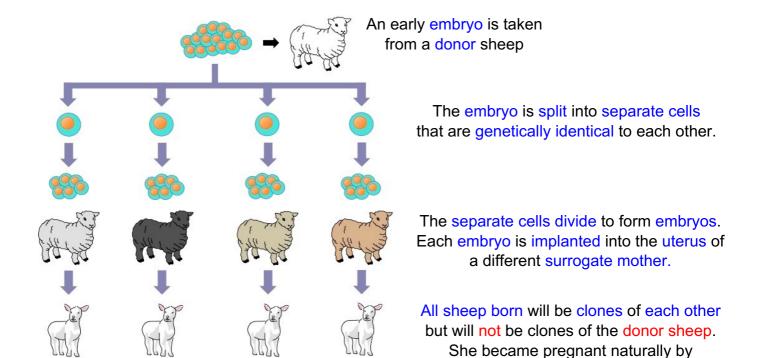
- DNA from child, mother and possible father(s) used
- DNA copied/amplified using PCR
- DNA cut using restriction enzymes
- To cut out short tandem repeats/STRs
- (Gel) electrophoresis used to separate DNA fragments/STRs
- Pattern of bands is produced (in gel)
- (Bands) analysed for matches between child with mother and possible father
- (About) half the child's bands will match the father
- (Biological) father will have all bands the child did not receive from its mother

D. CLONING ANIMALS USING DIFFERENTIATED BODY CELLS

Clones are groups of genetically identical organisms, derived from a single original parent cell



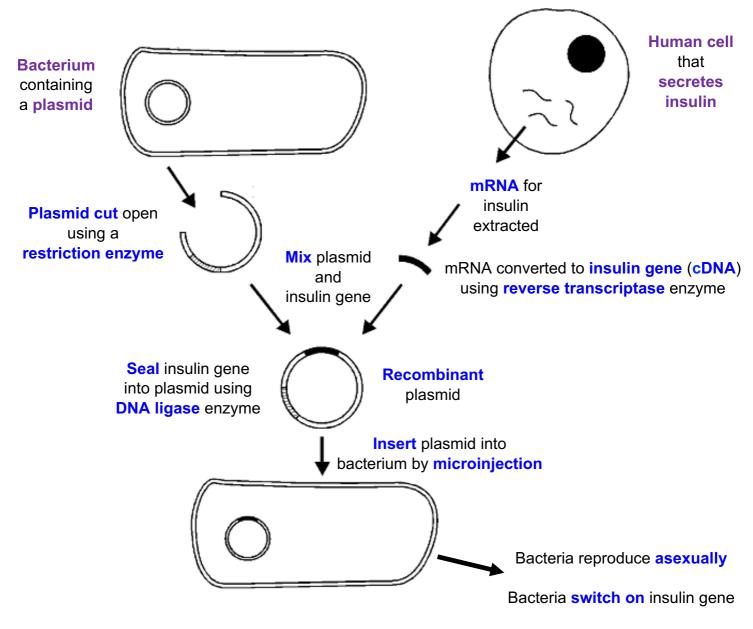
- Be aware that an older, and less reliable technique, called 'embryo splitting', was first used to produce clones.
- All cells in an embryo are genetically identical.



sexual reproduction.

E. USING GENETIC ENGINEERING TO PRODUCE HUMAN INSULIN

- Human insulin is used to treat diabetes.
- Many years ago, it was extracted from the dead or other animals.
- This gave a **low yield** of insulin, which could contain **contaminants**.
- Nowadays, the human insulin gene is transferred into bacteria, so they produce human insulin.
- This works because the **genetic code** is **universal** the **same codons** code for the **same amino acids** in **all organisms**.



The insulin gene and cut plasmid fit together because they have complementary sticky ends

Insulin is **secreted** into fluid

Insulin is **extracted** and **purified**

 Sticky ends are made by adding extra G nucleotides to the ends of the gene and extra C nucleotides to the ends of the cut plasmid.

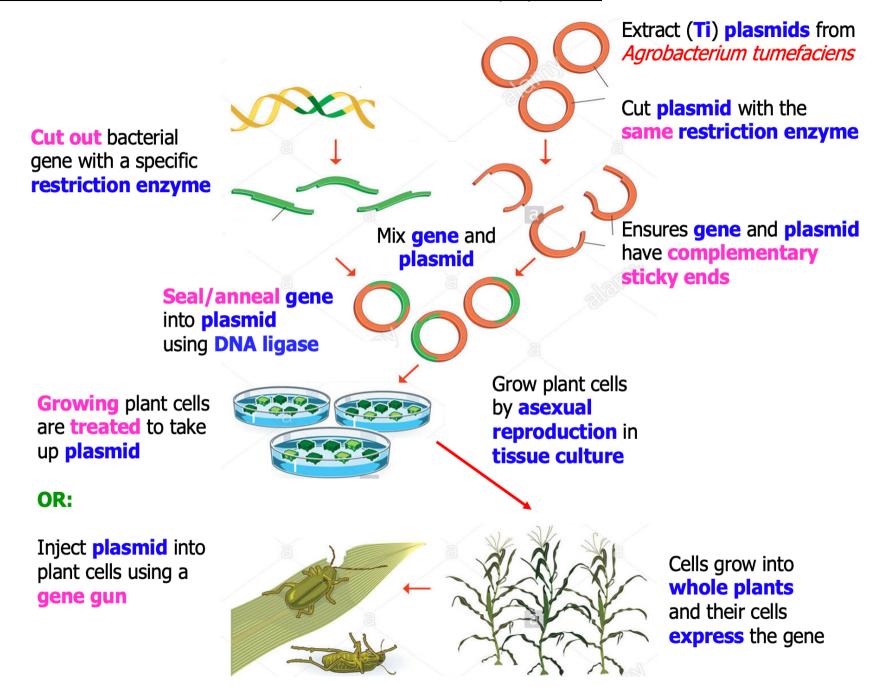
Why extract mRNA for insulin, rather than its gene (DNA)?

- There are more copies of mRNA than the gene (DNA) in the cell
- **Difficult to find one gene** among all the genes in the nucleus
- mRNA already has the introns removed so the cDNA will not contain introns

Why use bacteria?

- They **reproduce rapidly** can double in number every 20 minutes!
- They can reproduce asexually so all offspring will contain the human insulin gene.
- They are easy to genetically manipulate.

F. USING GENETIC ENGINEERING TO PRODUCE GENETICALLY MODIFIED (GM) PLANTS



G. BENEFITS AND RISKS OF GENETICALLY MODIFIED CROPS

The bt gene from a bacterium (Bacillus thuringiensis) that codes for the Bt toxin (poison) has been transferred into crop plants, such as corn or maize (Zea Mays).

It is designed to kill insects that feed on the crop plant.

Specific Example From The IB Syllabus

Possible benefits of Bt Maize	Possible harmful effects of Bt Maize
	Insects that are not pests could be killed (e.g. bees are pollinators)
Higher crop yields and more food for humans	Maize pollen containing the Bt toxin can be blown onto other plants, which monarch caterpillars eat.
	These caterpillars can be killed even though they do not feed on maize.
Less use of insecticides so: o less expensive o less disruption of food webs o less harm to wildlife	The gene may be transferred to unwanted plants such as weeds by cross-pollination
Less land needed for crop production so: some areas could be used for wildlife conservation	Insects many develop resistance to the toxin over time

Other General Points

Benefits	Possible Concerns
Increased resistance to herbicides/insects/disease/drought	Harmful effects if eaten by humans
Increased nutritional content e.g. golden rice: - has a high content of beta-carotene - which our body converts to vitamin A - prevents malnutrition in poorer countries (and night-blindness)	Long term effects are not yet known
Increased shelf life / less food spoilage	Reduced genetic variation so many may be killed by the same disease

H. THE HUMAN GENOME PROJECT

Scientists have found the **DNA base sequence** of **all human chromosomes**This allows **identification** of **all human genes**

In the future, it may be possible to:

- find out the **structure** and **function** of **proteins** (that the genes code for)
- find evidence for evolutionary relationships with other species
- find mutations that cause genetic diseases
- find mutations that increase the risk of getting a disease (e.g. cancer or heart disease)
- develop tests that can screen for more genetic diseases
- develop new drugs that are tailored to the specific genes carried by a person