

Polymerase Chain Reaction (PCR)=DNA Photocopier

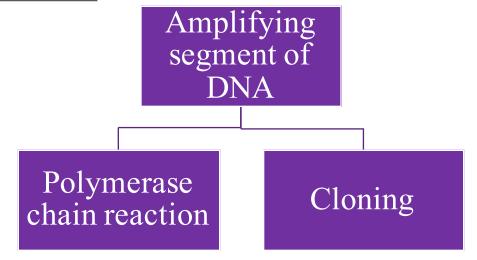


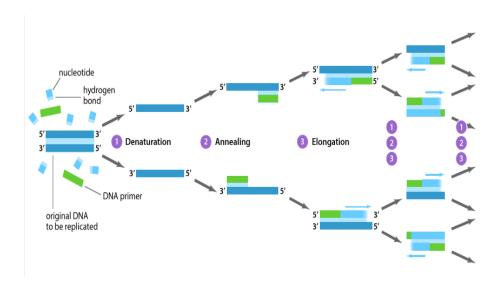
DNA amplification:

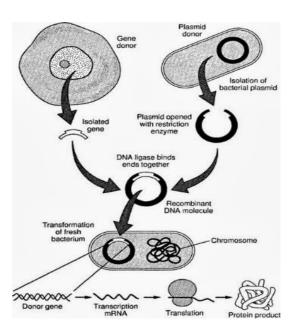
- In a crime scene, a sample of DNA was found, however **amount of DNA was not enough to** be analyzed.
- After DNA extraction, the scientist want to study a specific **part of a gene** to do sequencing.
- How scientist solve these problem?

■ The solution is to do amplification of parts of DNA!!

Mainly there are two methods:



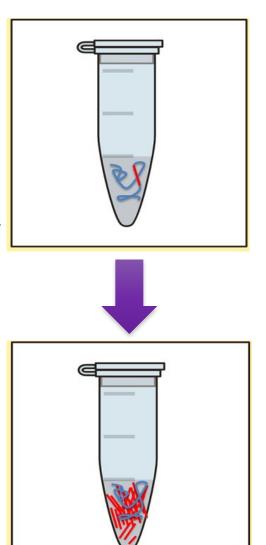




PCR-Polymerase Chain Reaction:

- PCR is a means to amplify a particular piece of DNA.
 - → <u>Amplify=</u> making numerous copies of a segment of DNA.
- PCR can make billions of copies of a target sequence of DNA in short time.

- It is a <u>laboratory version</u> of DNA <u>Replication</u> in cells.
- → The laboratory version is commonly called "in vitro" since it occurs in a test tube while "in vivo" signifies occurring in a living cell.



- So...
- → How the amplification will be done?
- → How you will determine your target sequence?
- → How the amplification will be specific for certain segment?

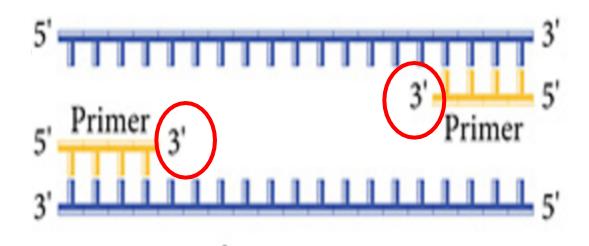
You must to understand these questions

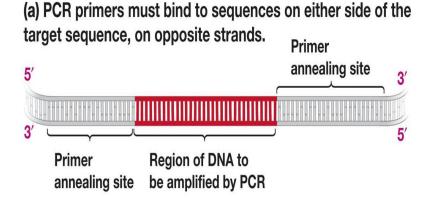
Amplification of a specific target sequence:

- PCR does not copy all of the DNA in the sample. It copies only a very specific sequence of genetic code from a template DNA, targeted by PCR primers.
- It does require the knowledge of some DNA sequence information which flanks the fragment of DNA to be amplified (target DNA).

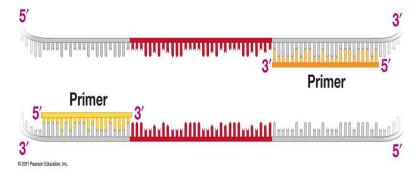


• From this information <u>two synthetic oligonucleotide primers</u> may be chemically synthesised each complementary to a stretch of DNA to the 3' side of the target DNA, one oligonucleotide for each of the two DNA strands (DNA polymerase can add a nucleotide only onto a **preexisting 3'-OH group**).

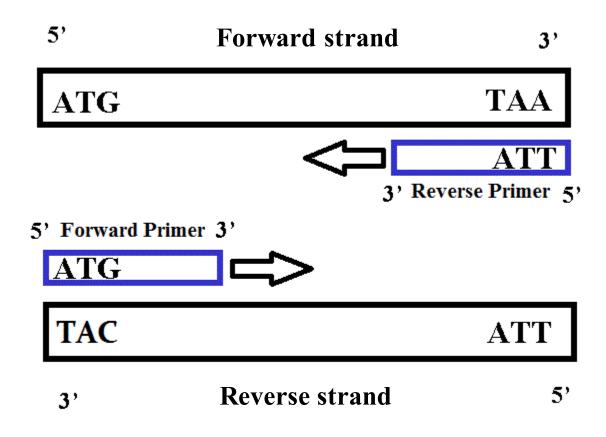




(b) When target DNA is single stranded, primers bind and allow DNA polymerase to work.



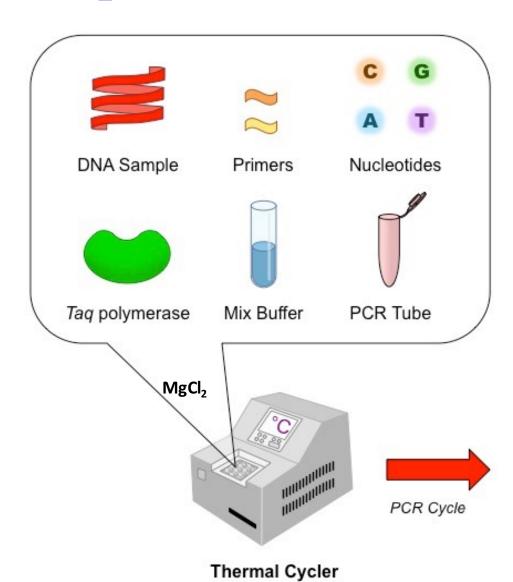
Why we need two primers P



- In a PCR reaction you need **two primers** to amplify the target sequence:
- →One called: Forward primer, which have the same sequence of <u>forward DNA</u> strand and bind to the complementary reverse strand.
- → The second called: Reverse primer, which have the same sequence of <u>reverse DNA</u> strand and bind to the complementary forward strand.

^{*}If there is only one primer, only one strand of the double stranded DNA will be amplified in the PCR reaction.

Components of PCR



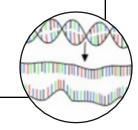
Additional reagents may included

The PCR Cycle:

• PCR proceeds in **THREE** distinct steps Governed by **Temperature**:

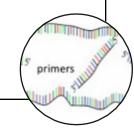
• The double-stranded template DNA is denatured by heating, typically to 95°C, to separate the double stranded DNA.

Denaturation: (95°C)



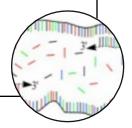
• The reaction is rapidly cooled to an annealing temperature to allow the oligonucleotide primers to hybridize to the template.

**Annealing: (50-65°C)



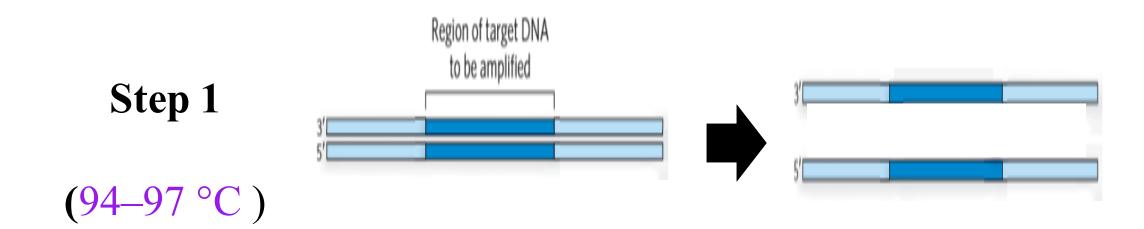
• The reaction is heated to a temperature, typically 72°C for efficient DNA synthesis by the thermostable DNA polymerase.

Extension: (72°C)



1. Denaturation:

- The double-stranded template DNA is denatured by heating, typically to 95°C, to separate the double stranded DNA (why?).
- Breaking the _____ bonds.



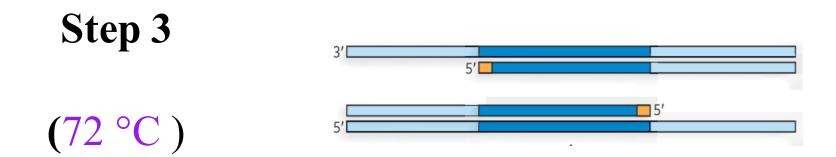
2. Annealing:

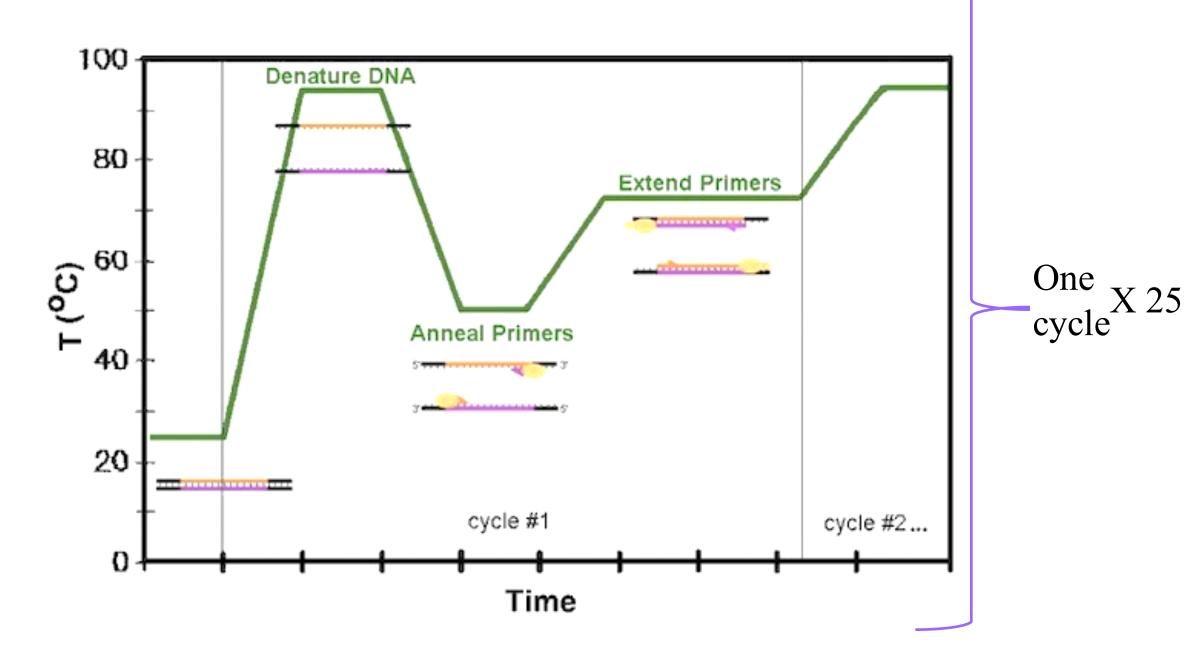
- The reaction is rapidly cooled to the primer annealing temperature (50-65 °C) to allow the oligonucleotide primers to hybridize to single stranded template.
- Primer will anneal only to sequences that are complementary to them (target sequence).
- What is the type of the bond?

Step 2 (50–65 °C)

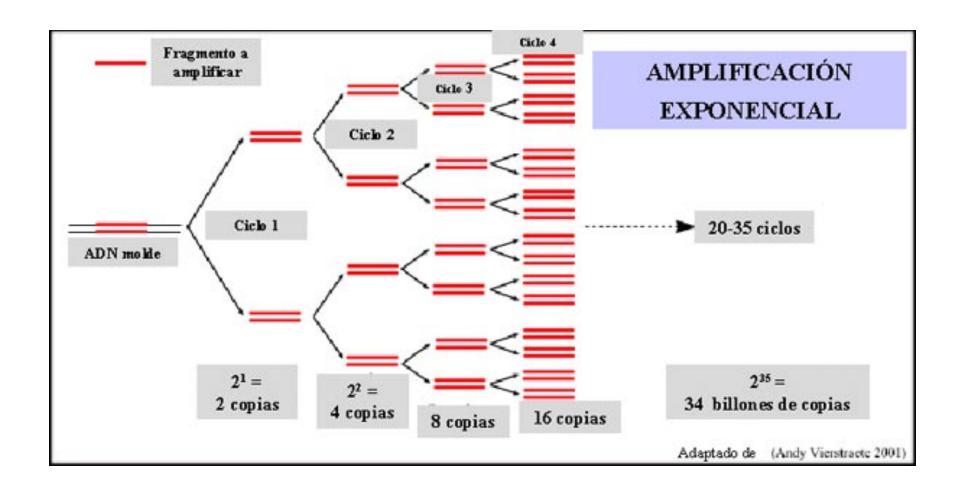
3. Extension:

- The reaction is heated to a temperature depends on the DNA polymerase used.
- Commonly a temperature of 72°C is used with this enzyme.
- This means that 72°C is the optimum of DNA polymerase.
- At this step the DNA polymerase synthesizes a new DNA strand complementary to the DNA template

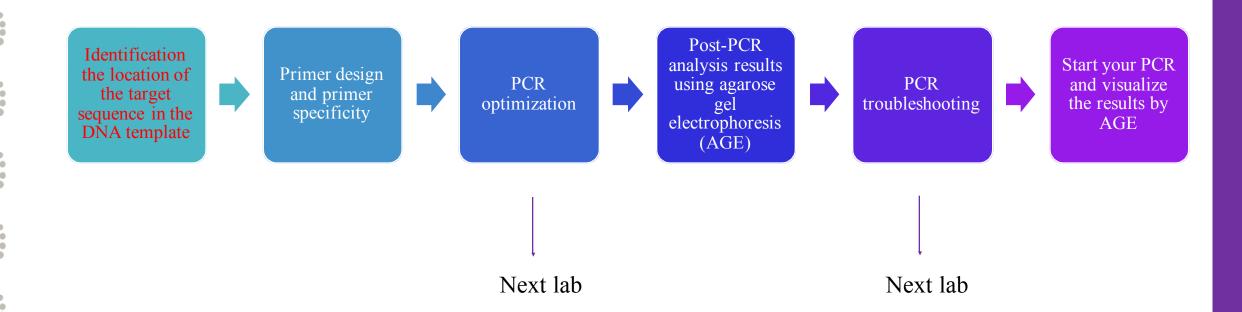




- At the end of the PCR reaction, the **specific sequence** will be accumulated in billions of copies (amplicons).
- In only 20 cycles, PCR can product about a million (2^{20}) copies of the target.



Performing PCR steps:



Example:

- You want to study a mutation in a DLG3 gene and how it relate to memory:
 - 1. Find the sequence of the gene from any website, eg.Ensebmle.
 - 2. Determine your target region.

The segment that you want to amplified is in the red square

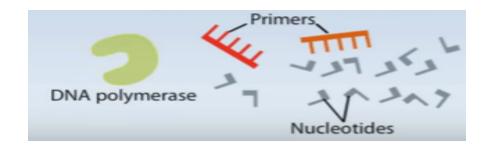
- 5'CATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT 3'
- 3° GTACGCTATTCTCACTAACTCCA GGTGGTACAATAGTACGCTATTCTCACTAACTCCA GGTGGTACAATAGTACGCTATTCTCACTAACTCCA 5°
 - 3. Design the primers using primer design tool, eg.Primer3, then send them to any company who will synthesize them.
 - 4. Make sure that the area that you want to study is **between the primers** (the region to be studied should be between the forward and reverse primer).
 - 5. Check primer specificity by BLAST.
 - 6. Optimize your PCR and trouble shooting.
 - 7. Start PCR.

1. Denaturation:



5' CATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT 3

3° GTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCA



2. Annealing:



5' CATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT 3

3' GGTGGTACAATAGTACGCTATT 5'

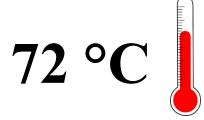
5' CCACCATGTTATCATGCGA' 3'

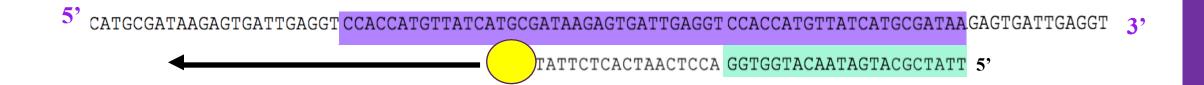
3' GTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCA

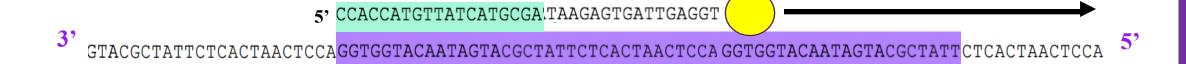
Forward primer: 5' CCACCATGTTATCATGCGA 3'

Reverse primer: 3' GGTGGTACAATAGTACGCTATT 5'

3. Extension:





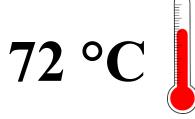


Taq DNA polymerase



3. Extension:





- 5' CATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT
- 3° GTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCA GGTGGTACAATAGTACGCTATT 5°

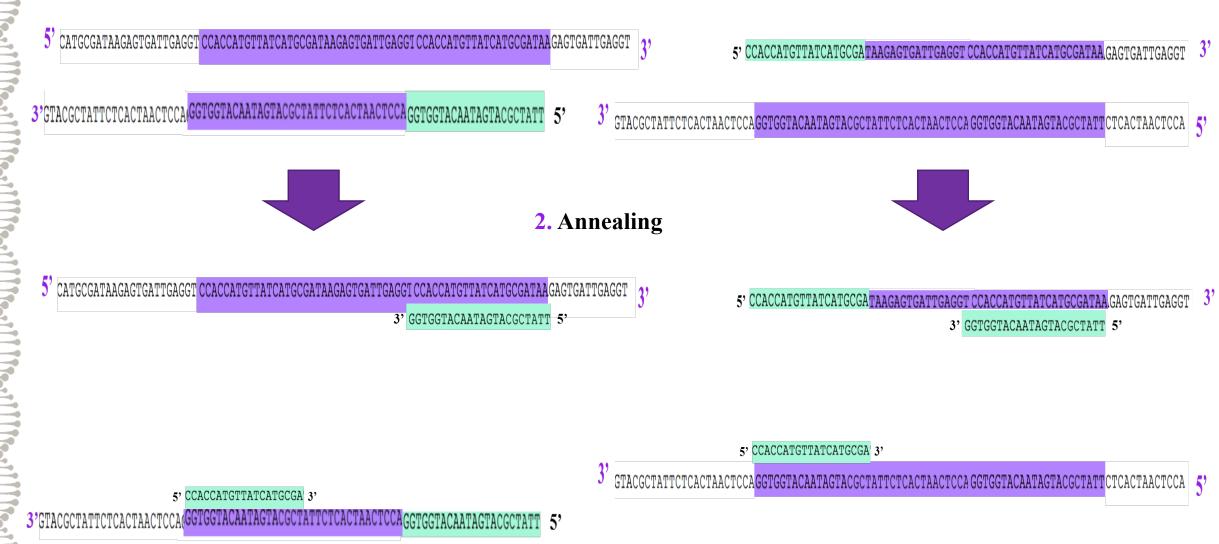
- 5' CCACCATGTTATCATGCGALTAAGAGTGATTGAGGT CCACCATGTTATCATGCGATAAGAGTGATTGAGGT 3'
- 3° GTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCAGGTGGTACAATAGTACGCTATTCTCACTAACTCCA 5°

Cycle # 1:

1 DNA amplified to 2 DNA

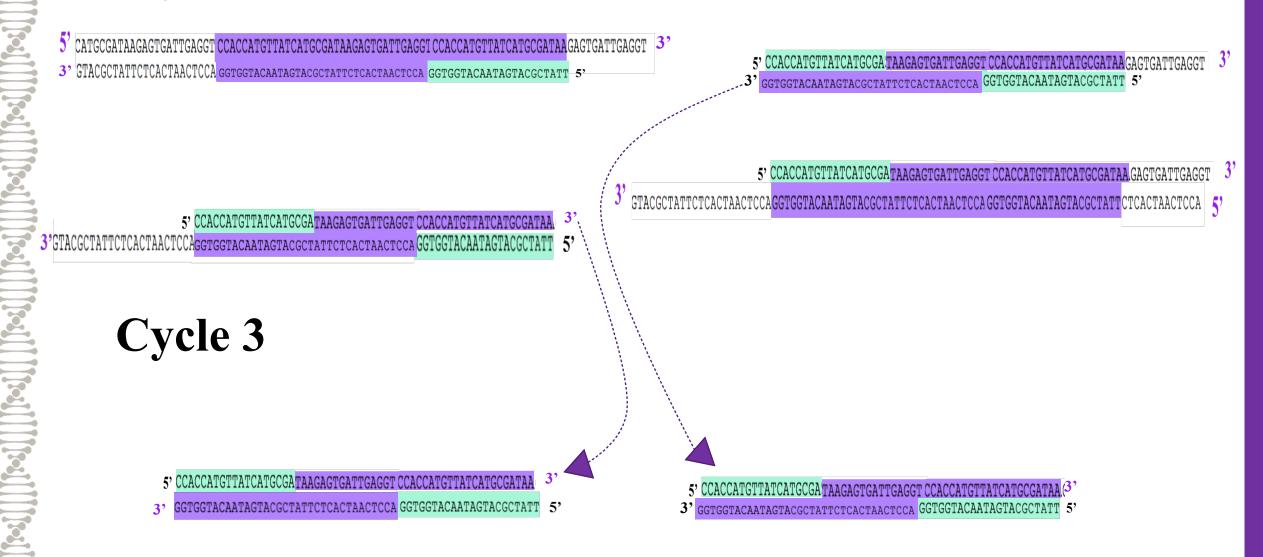
Cycle 2

1. Denaturation



Cycle 2

3. Extension



Target sequence

Appeared after three cycles and start to accumulate



After 30 cycles:

2³⁰ copy of target DNA!!

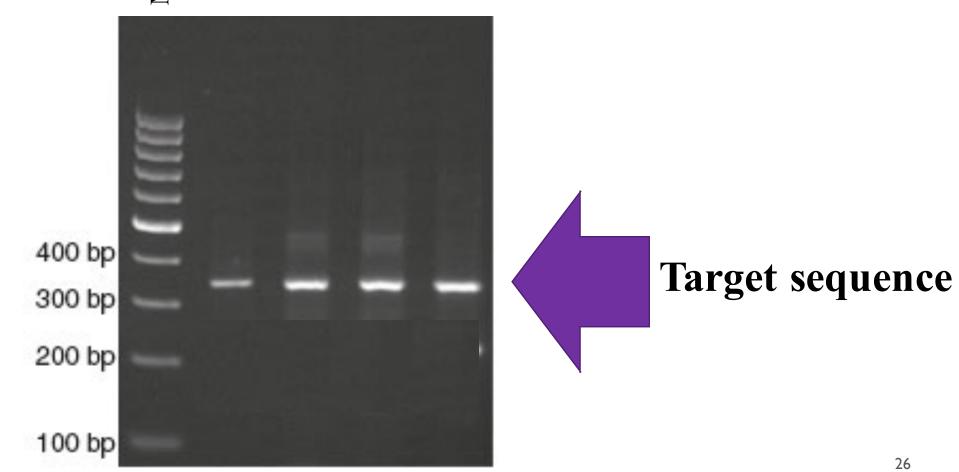
How you will make sure that you target sequence is amplified?

It is very important to know your product size, why?

→ Our target sequence size is 350 bp

AGE results

Marker



PCR advantages:

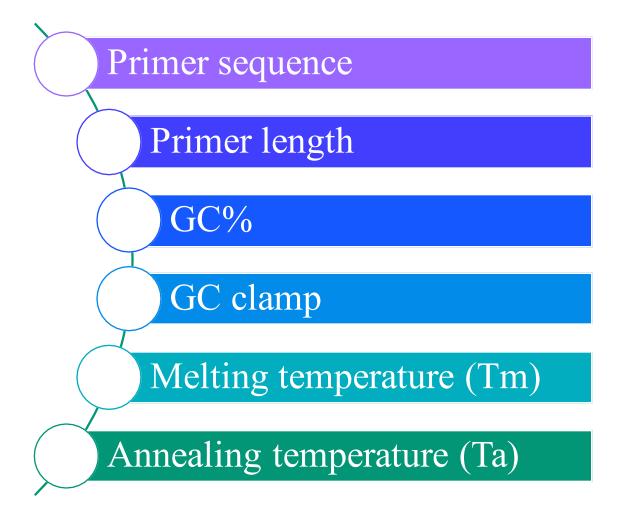
• Simplicity, easier methodology, sensitive, extensively validated standard operating procedure and availability of reagents and equipment

PCR application:

- > Genotyping.
- > RT-PCR.
- > Cloning.
- > Mutation detection.
- > Sequencing.
- > Microarrays.
- > Forensics.
- > Paternity testing.

PCR Optimization:

- There is no single set of conditions that is optimal for all PCR reactions.
- Next Lab.



1. Primer sequence:

- Must be complementary to flanking sequences of target region.
- Avoid:
- → Complementary sequences between primers.
- → Repeat (ex: ATATATAT) → misprime.
- → Runs (ex: AGCGGGGGAT) → misprime.
- → Mismatch at 3' end.
- → Cross Homology.

2. Primer length:

- It is generally accepted that the optimal length of primers is 18-25 bp.
- Not too long nor too short

3. GC content:

- GC% = Number of G's and C's in the primer as a percentage of the total bases.
- Should be 40-60%.

4. GC clamp:

- Presence of G or C bases within the last five bases from the 3' end of primers.
- Not more than 2 G's or C's.

5 '-caacataatagcgacaaca<mark>ctaga</mark>-3 '

5. Melting temperature (Tm):

- What is Tm?
- Melting temperatures in the range of 50-60 °C generally produce the best results.
- Maximum difference between primer pairs is 5°C.
- The Tm of the primer can be calculated by the following formula:

$$Tm = [(G + C) \times 4] + [(A + T) \times 2]$$

6. Annealing Temperature (Ta):

- The primer melting temperature is the estimate of the DNA-DNA hybrid stability and critical in **determining the annealing temperature.**
- Depends directly on **length** and **GC composition** of the primers.
- Too high Ta → produce insufficient primer-template hybridization.
- Too low Ta lead to non-specific products caused by a high number of base pair mismatches.

Now... you should be able to answer the following questions:

- How the amplification will be done?
- How you will determine your target sequence?
- How the amplification will be specific for certain segment?
- What are the requirements to carry PCR?

Home Work:

• Suppose you perform a PCR that begins with one double-strand of the following DNA template:

- A. Draw one cycle of PCR reaction below the following diagram.
 - B. Label the template DNA, the primers, and what is happening at each step.

