

POLYMERASE CHAIN REACTION



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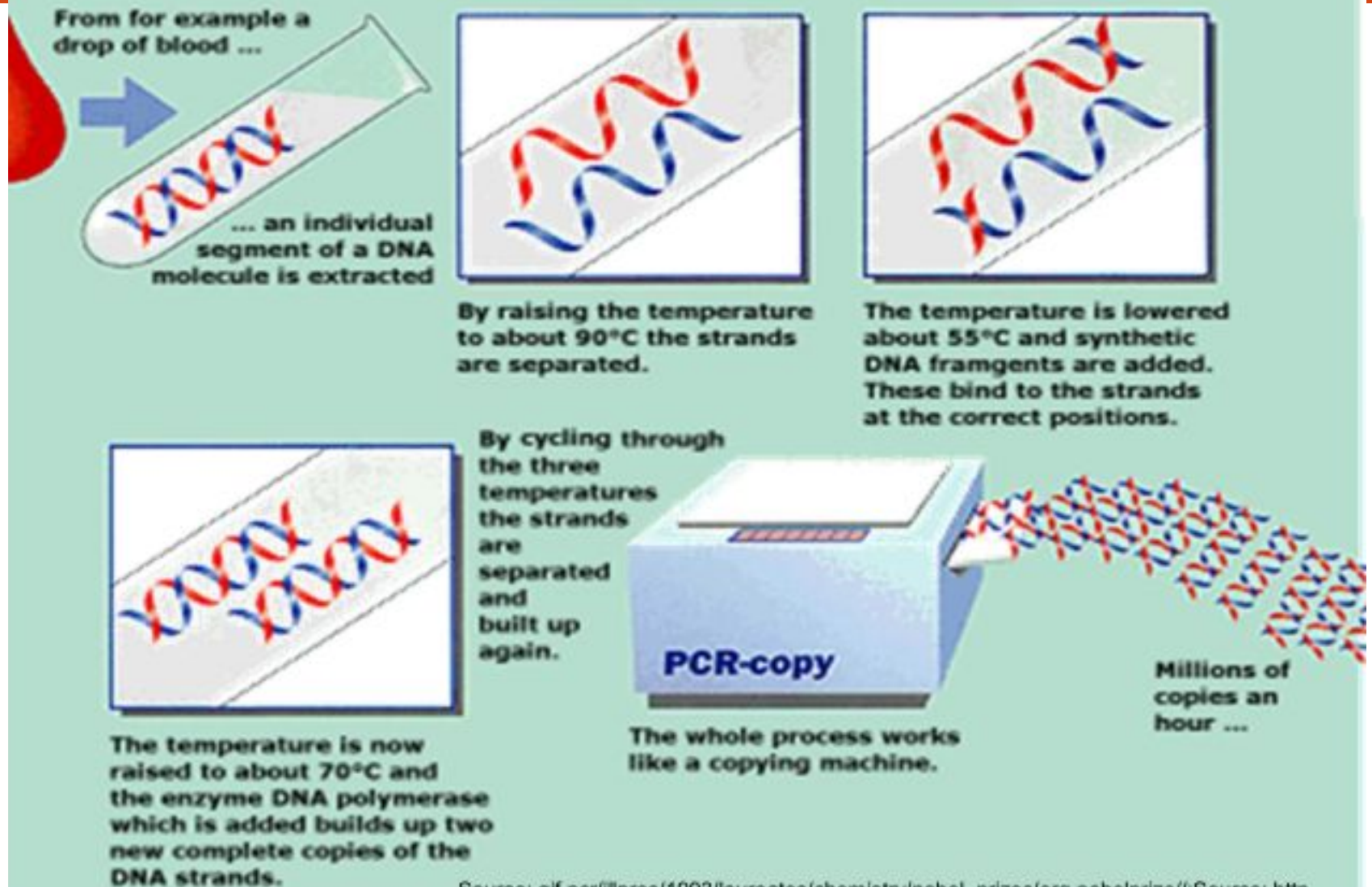


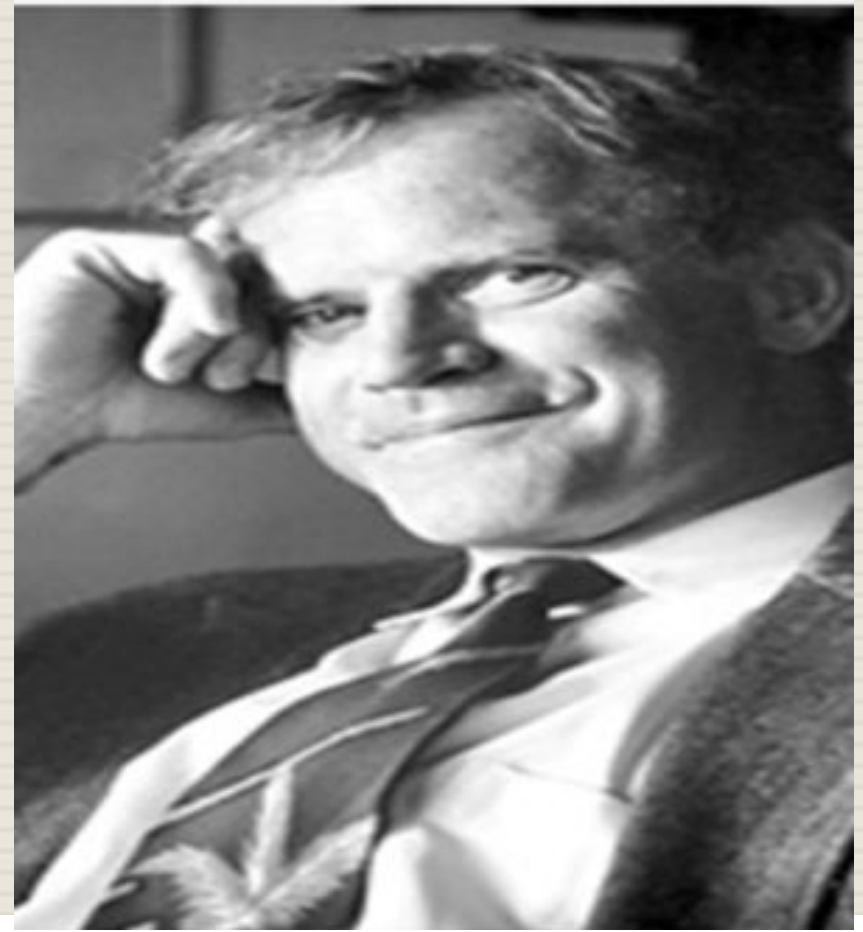
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POLYMERASE CHAIN REACTION

Nobel prize 1993





- Coping Machine for DNA Molecule**
- Invented by Kary Mullis and his colleagues in the 1983**

Polymerase Chain Reaction

- **PCR**: Technique for in vitro (test tube) amplification of specific DNA sequences via the temperature mediated. DNA polymerase enzyme by simultaneous primer extension of complementary strands of DNA.
- **PCR**: This system for DNA replication that allows a "target" DNA sequence to be selectively amplified, several million-fold in just a few hours.

PCR

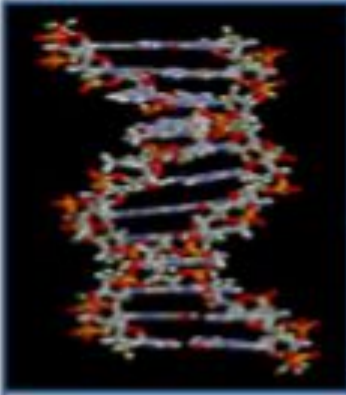
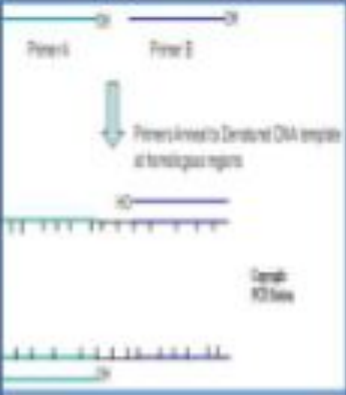


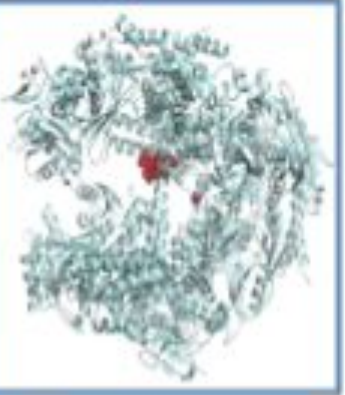
→

1 **ACG GCC CTC ATC ACC TTC TTT CAC TTT TTG TTT TTG** TGT AGG TGA GTC AAT TGC GTG TGG
61 CCT TCA AGT ATT TCG TAT TGT AAC AAT ATT CGA TCG GCA TCC AAA CAA AGG TGC ATG TAC
121 GGT TCC TAA GGG ATA CAA TTT TGT CTT AAA TCA TCG AGA AAG A TT AAG GTA AGT TGA TAG
181 GCG CGA TCT CGT ACC TAA CAC ATA CTC TCT AAA TAT TGA AGA A CT TGC ATG CGG CCT TCA
241 AGC CAC AAC GCG GTA TGA GTT CTT TGT TTG GGG GCT GCT TGC C CC TTC GCG TCG ACA AGG
301 AAA CTG AGG ACG ACA ATG G **CA CC**

←

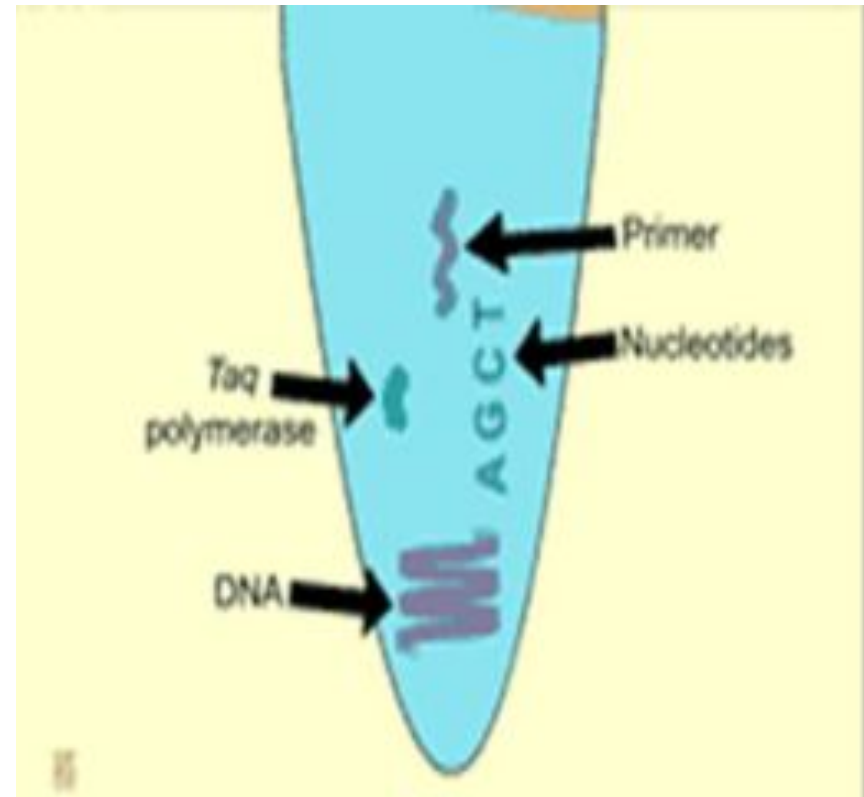


PCR reaction components

				
Template	Two primers (forward and reverse)	Four (dNTPs) A, G, C, T	Buffer system containing magnesium Mg^{2+}	DNA polymerase
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PCR reaction components

- DNA template
- Two primers
- Four normal deoxynucleosides triphosphates
- Buffer system
- DNA polymerase I



DNA Template

Integrity

- **High molecular weight**

Purity

- **Pure**

Amount

- **Human genomic DNA should be up to 500ng**
- **Bacterial DNA 1-10ng**
- **Plasmid DNA 0.1-1ng**

Primers

- Typical primers are 18-28 bases in length,
- Having 40- 60% GC composition,
- Have a balanced distribution of G/C and A/T rich domains,
- The calculated T_m for a given primer pair should be balanced (difference no more than 5 °C),
- Primer concentration between 0.1 and 0.6 μM are generally optimal,
- Contain no internal secondary structure,
- Have a cytosine and guanine at the 3'-end because they form three hydrogen bonds with the matrix molecules, making a more stable hybridization

Four Normal Deoxynucleosides Triphosphate

- Final concentration of dNTPs should be 50-500 μM (each dNTP). Usually included at conc. of 200 μM for each nucleotide.
- Always use balanced solution of all four dNTPs to minimize polymerase error rate.

Buffer System Containing Magnesium

The standard PCR buffer contains:

- ❑ **Tris-HCl 10mM (10-50mM)** for dissolution of nucleic acids
pH 8.3 (pH 8.3-8.8 at 20C°)
- ❑ **KCl 50mM** promotes specificity of hybridization
- ❑ **MgCL2 1.5mM (0.5-10mM)** for stabilizing of complex between primers and matrix and for increasing of exit the special product of PCR
- ❑ **Gelatin or Bovine Serum Albumin 100 µg/ml**
frequent unfreezing-freezing at the temperature -20C

DNA Polymerase

- ❑ **The most widely characterized polymerase is that from *Thermus aquaticus* (Taq), Thermophilic bacterium lives in hot springs and capable of growing at 70 -75 C°,**
- ❑ **Consist of a single polypeptide chain has a molecular weight of 95 Kd, and has an optimum polymerization temperature of 70 – 80 C° (72 C°).**
- ❑ **0.5 – 2 units/50µl reaction. Too little will limit the amount of products, while too much can produce unwanted non specific products.**

Enhance The Specificity and or Efficiency of a PCR

Betadine

(antiseptic)

Bovine serum albumin

(for stabilizing of enzymes)

Dimethylsulfoxide

for inhibition of reannealing of initial

molecules of DNA

Glycerol

Pyrophosphate

Spermidine, Detergent, Gelatin,....

Calculation of Melting Temperature

$$T_m = 2 \text{ C}^\circ \times (\text{number of A and T bases}) + 4 \text{ C}^\circ \times (\text{number of G and C bases}).$$

Optimal annealing temperature are 5-10 C ° lower than T_m values of the primers .

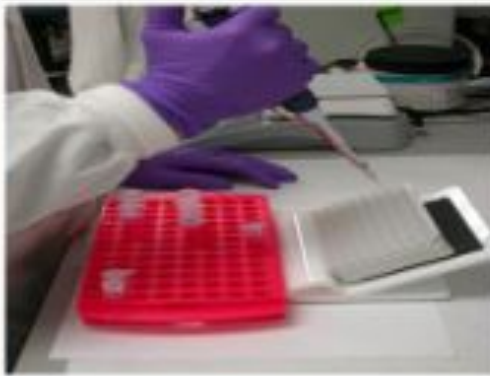
STANDARD PCR REACTION

		Vol./tube	final cons.
10 X	PCR buffer	5 ul	1 x
25 mM	MgCl ₂	4 ul	2mM
10 mM	dATP	1 ul	0.2 mM
10 mM	dTTP	1 ul	0.2 mM
10 mM	dCTP	1 ul	0.2 mM
10 mM	dGTP	1 ul	0.2 mM
Taq	polymerase (5U/ul)	0.3 ul	1.5 units
Forward	primer (50 ng/ul)	2 ul	100 ng
Reverse	primer (50 ng/ul)	2 ul	100 ng
Template DNA	(100 ng)	3 ul	100 ng

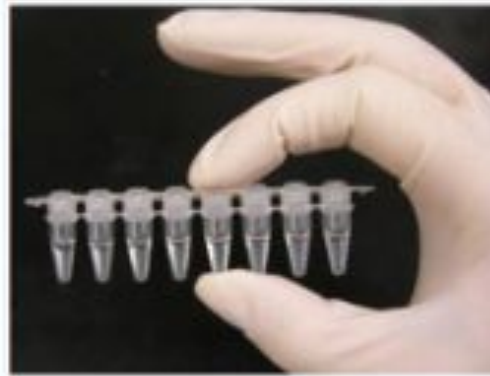
Add sterile H₂O to 50 ul and 30 ul mineral oil

Component	Amount	Your Reaction
10X PCR Buffer	5 μ L	
25 mM MgCl ₂	4 μ L	
10 μ M forward primer	5 μ L	
10 μ M reverse primer	5 μ L	
10 mM dNTP (mix)	1 μ L	
100 ng template DNA (genomic DNA)	x μ L	
Taq DNA polymerase (1U/ μ L) (add last)	1.0 μ L	
dH ₂ O (use whatever volume y is correct to bring total reaction volume to 50 μ L)	y μ L	
TOTAL	50 μL	

PCR



All one has to do is to mix the contents in the test tube and



Seal the tube and then place it in a thermal cycler.



Thermal cycler

AVOIDING CONTAMINATION



Sample Handling

- ❑ Use sterile techniques and always wear fresh gloves,
- ❑ Always use new or sterilized glassware, plasticware and pipettes to prepare the PCR reagents and template DNA,
- ❑ Autoclave and sterilize all reagents and solution,
- ❑ Have your own set of PCR reagent and Solution (store in small aliquots),
- ❑ Positive and negative control should be included.

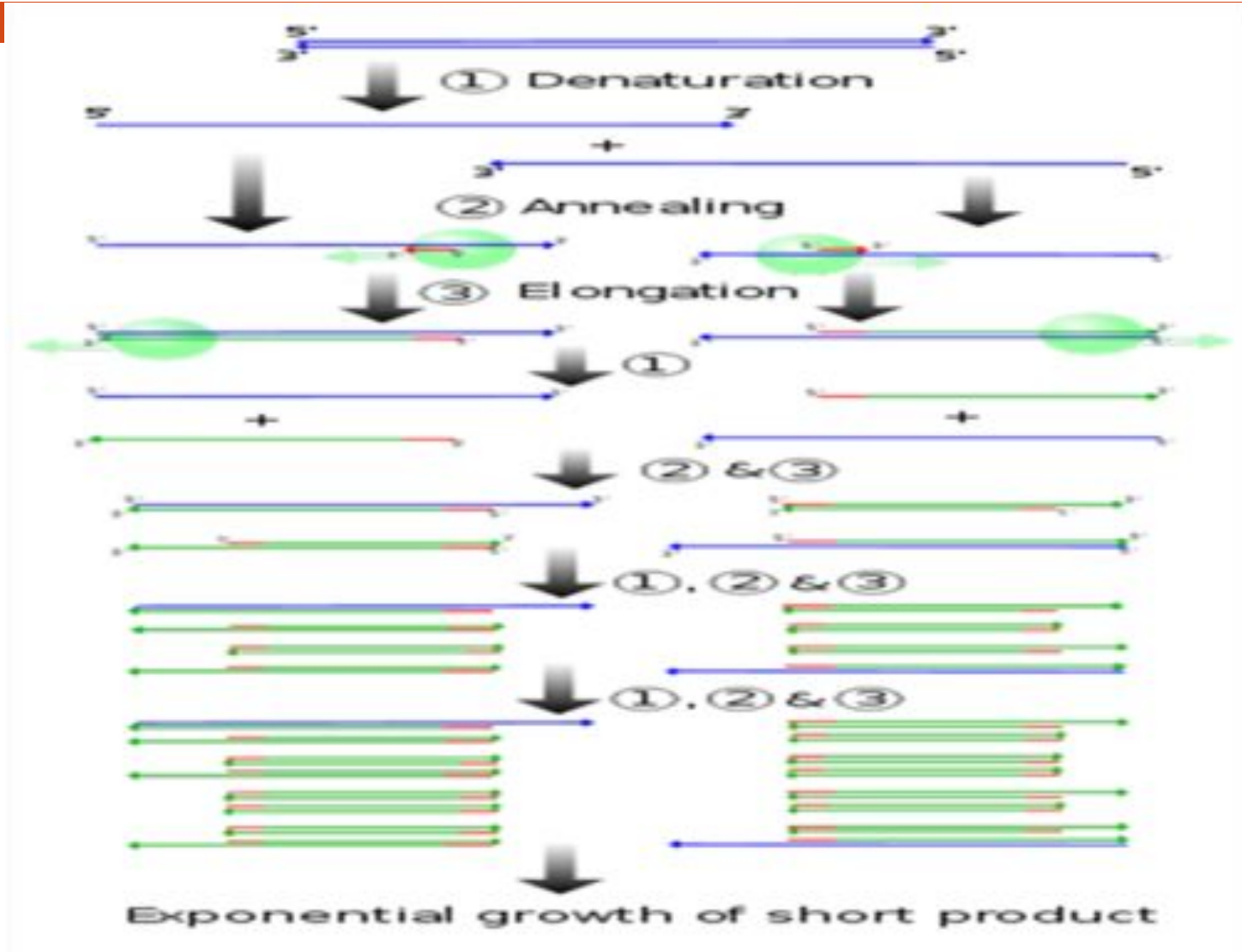
Laboratory Facilities

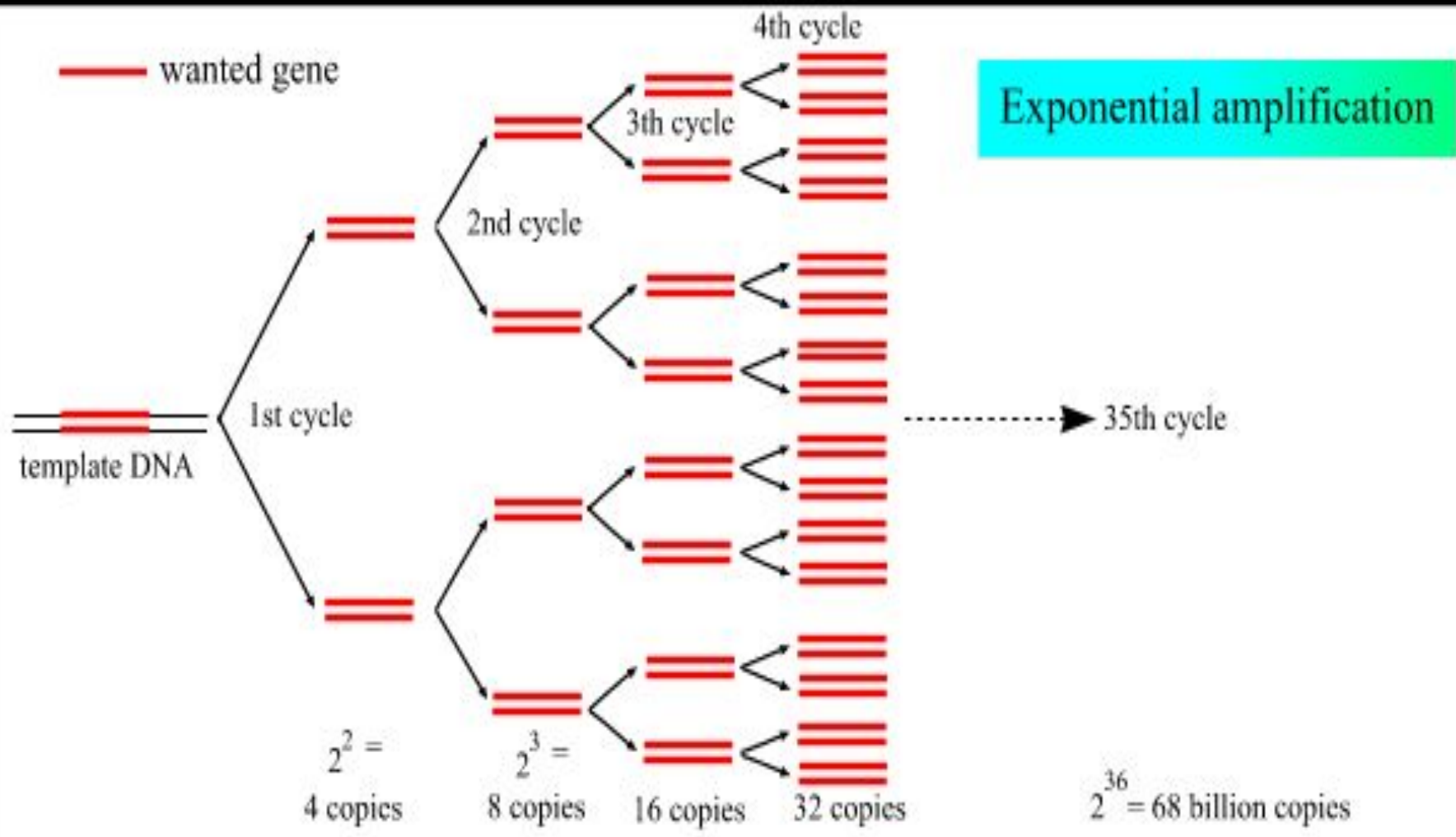
- ❑ Set up physically separated working places for:
 - Template preparation
 - Setting up PCR reactions
 - Post PCR analysis
- ❑ Use PCR only pipettes, micro-centrifuges and disposable gloves
- ❑ Use aerosol resistant pipette tips
- ❑ PCR reaction under a fume hood equipped with UV
- ❑ LIGHT.

Working with RNA

- Do not touch a surface after putting the gloves to avoid reintroduction of RNase to decontaminated material.
- Designate a special area for RNA work only.
- Treat surface or benches and glassware with commercially available RNase inactivating agents.

Polymerase Chain Reaction





(Andy Vierstraete 1999)

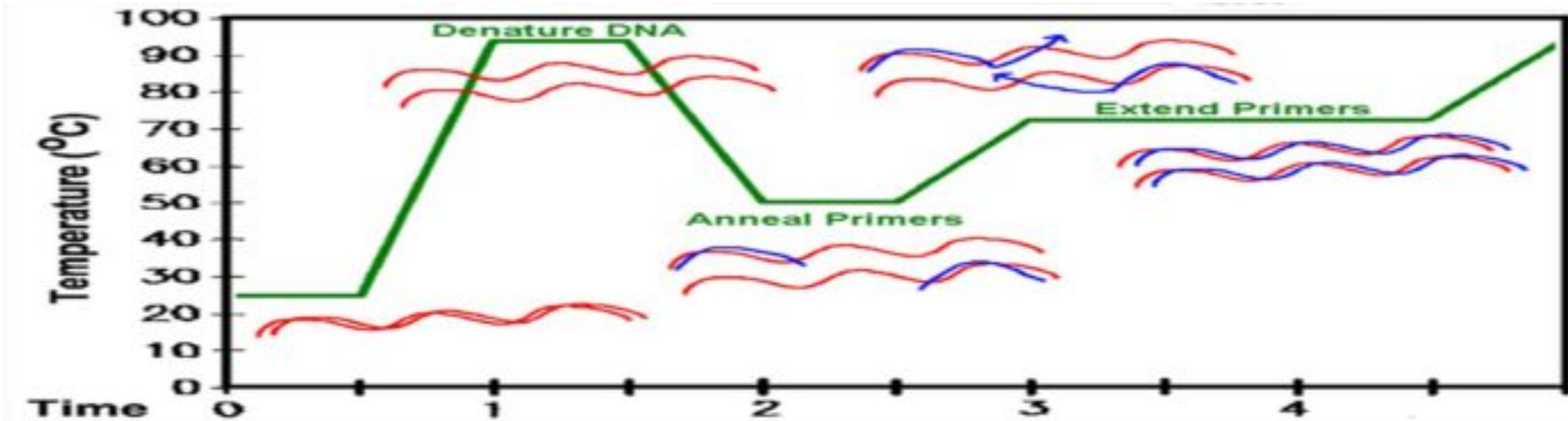
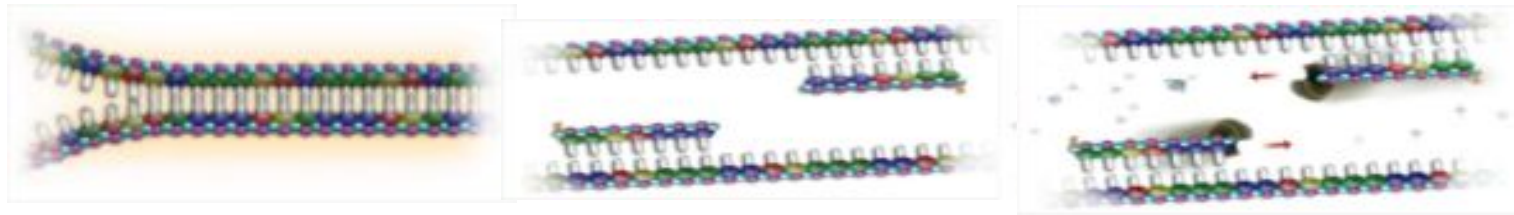
Thermal Cycling Profile for Standard PCR

- ❑ **Initial Denaturation:**
- ❑ Initial heating of the PCR mixture at 94- 95C within 2 min. is enough to completely denature complex genomic DNA.
- ❑ **Each cycle includes three successive steps:** Denaturation, annealing and extension.
- ❑ **Post extension and holding:**
- ❑ Cycling should conclude with a final extension at 72 C° for 5 -15 minute to promote completion of partial extension products and then holding at 4 C°.

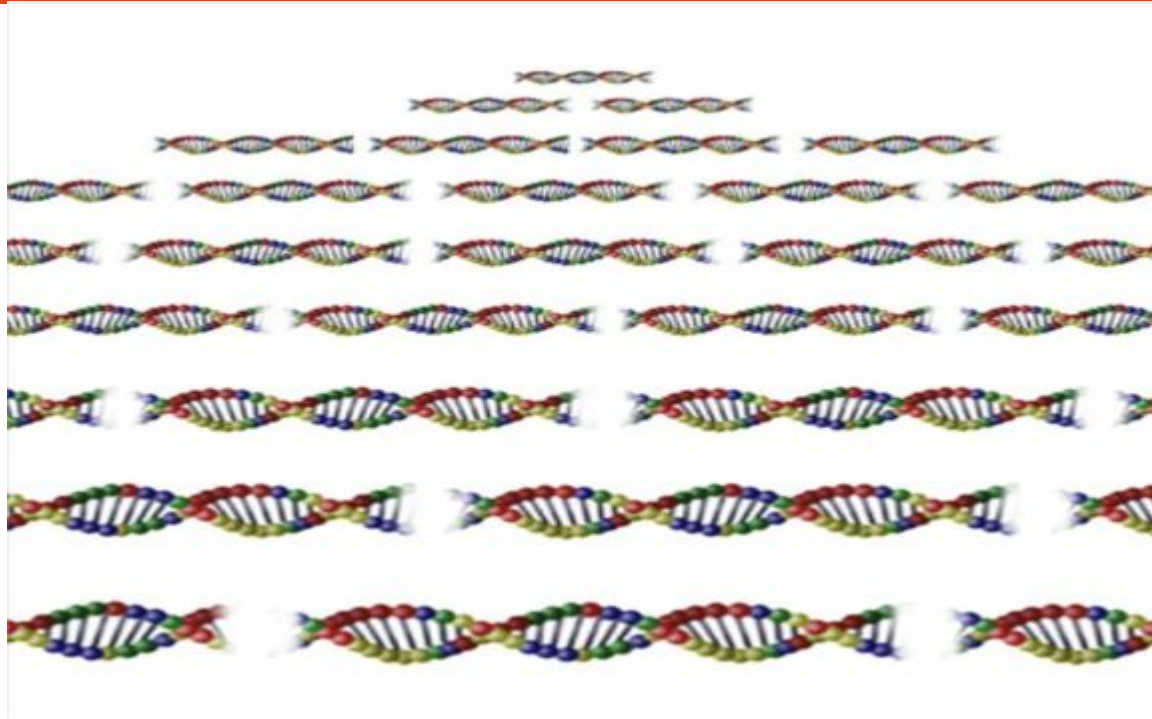
Each cycle includes three successive steps:

Denaturation	94C° 15sec-one minute	The DNA is denatured into single strands.
Annealing	34-72C° 30sec-two minute	The primers hybridize or "anneal" to their complementary sequences on either side of the target sequence.
Extension	72C° 1.5-3 minute	The polymerase binds and extends a complementary DNA strand from each primer

PCR



Exponential Amplification



As amplification proceeds, the DNA sequence between primers doubles after each cycle.

(The amplification of the target sequence proceeding in an exponential fashion ($1 \rightarrow 2 \rightarrow 4 \rightarrow 8 \rightarrow 16 \dots$) up to million of times the starting amount until enough is present to be seen by gel electrophoresis.)

Number of Cycles

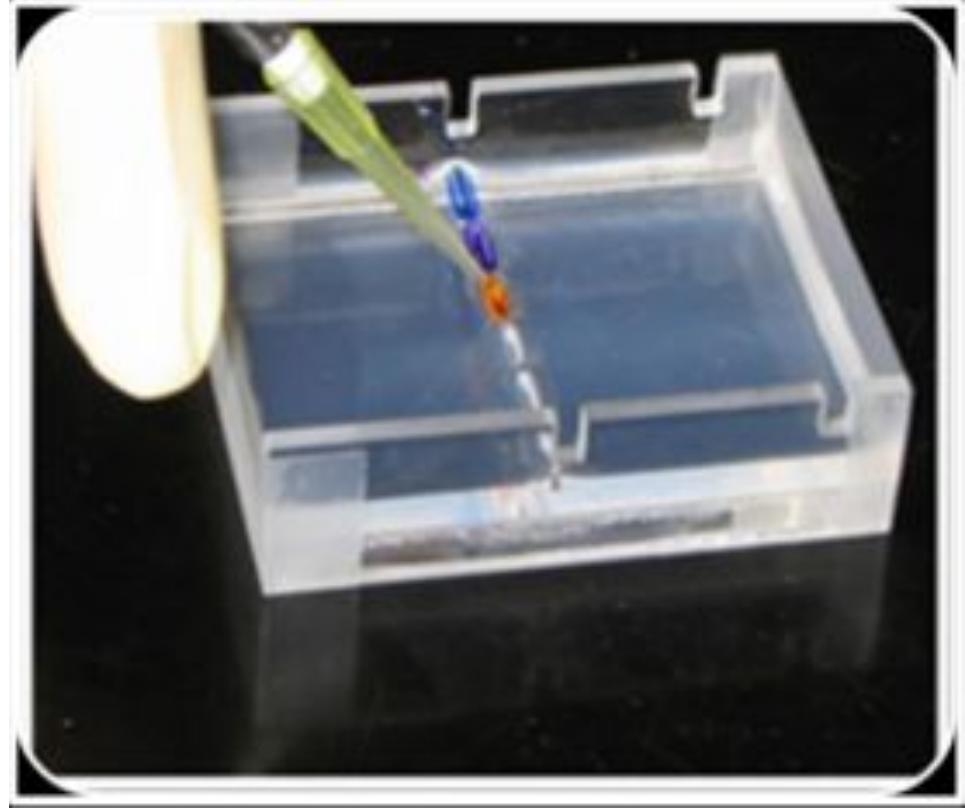
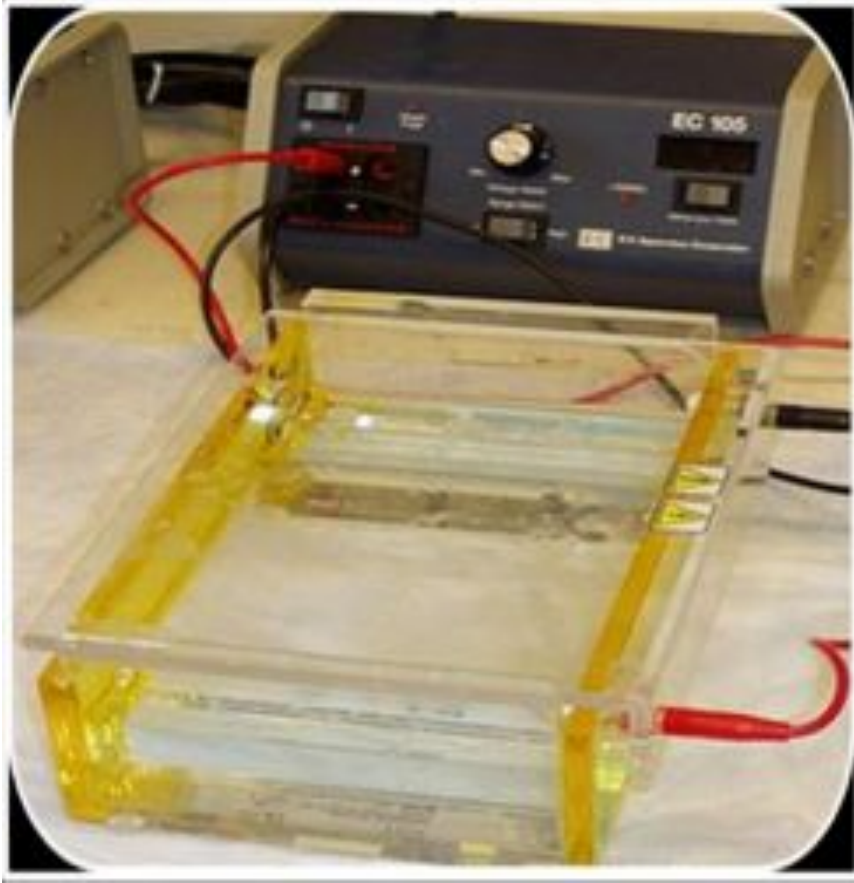
- The number of cycles required for optimum amplification varies depending on the amount of the starting material.
- Most PCR should, therefore, include only **25 – 35** cycles. As cycle increases, nonspecific products can accumulate.
- After **20- 40 cycles** of heating and cooling build up over a million copies of original DNA molecules.

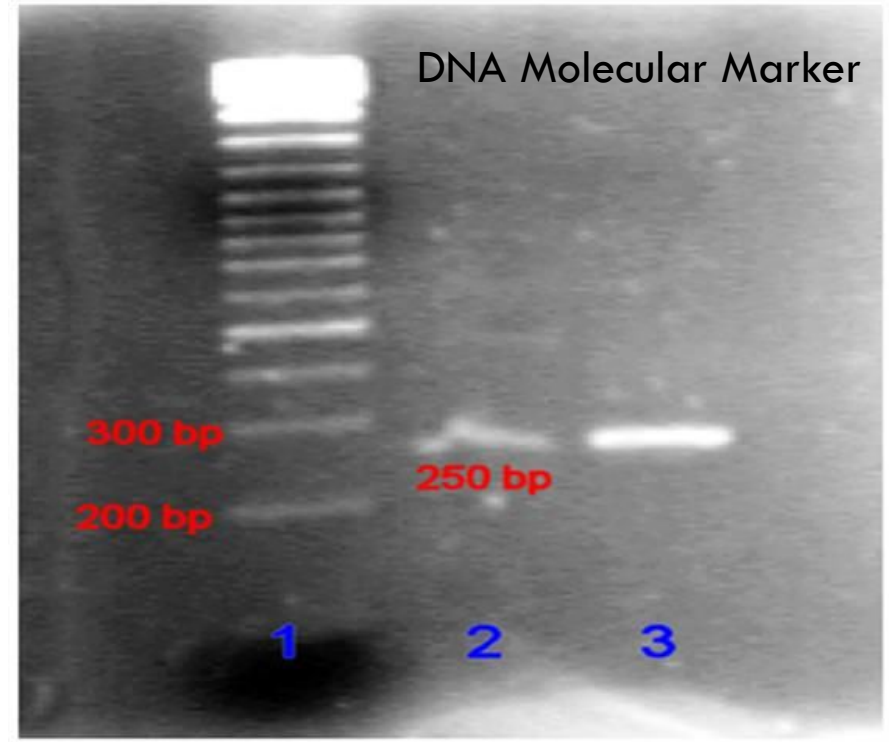
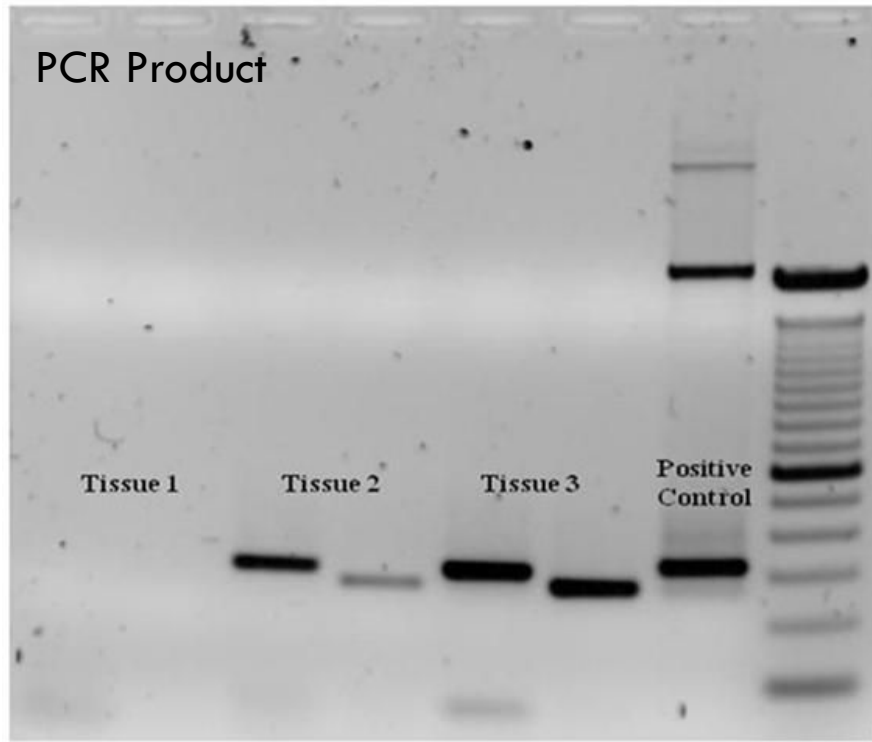
GEL ELECTROPHORESIS

Agarose Gel Electrophoresis

- ❑ It is a method used in **biochemistry** and molecular **biology** to separate **DNA**, or **RNA** molecules based upon charge, size and shape.
- ❑ Agarose is a polysaccharide derivative of agar.

Gel Tray/ Loading





- ❑ **Amplified fragments** can be visualized easily following staining with a chemical stain such as ethidium bromide.
- ❑ The DNA fragments are separated by charge and the relative sizes of fragments are determined by comparing to a standard DNA ladder

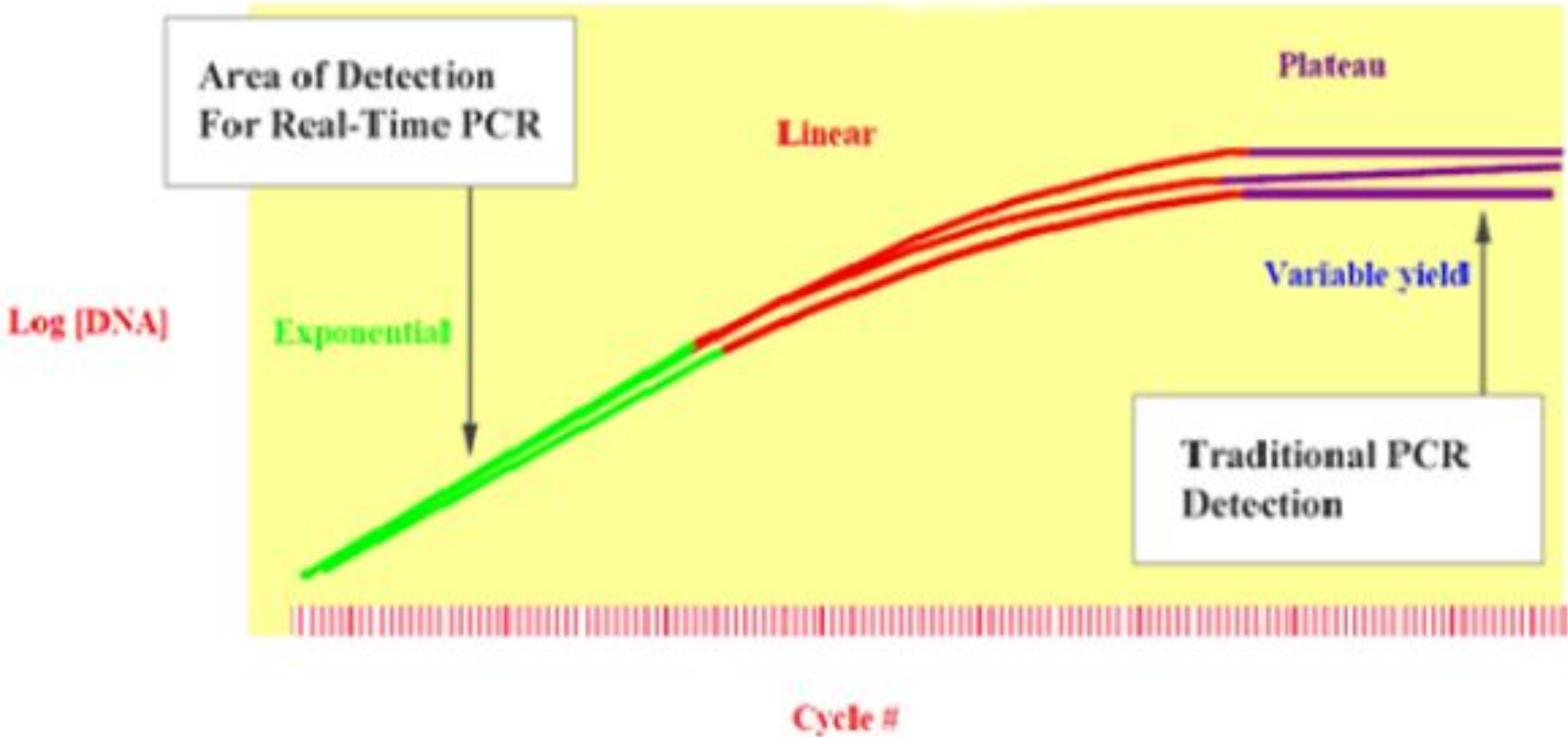
» Factors, affect the mobility of molecules in gel

- Charge
- Size
- Shape
- Buffer conditions
- Gel concentration and
- Voltage

PCR: Three Phases

- **Exponential:** Exact doubling of product is accumulating at every cycle (assuming 100% reaction efficiency). The reaction is very specific and precise.
- **Linear:** The reaction components are being consumed; the reaction is slowing, and products are starting to degrade.
- **Plateau:** The reaction has stopped; no more products are being made and if left long enough; the PCR products will begin to degrade.

PCR Phases



Polymerase Chain Reaction

□ **Advantages of PCR**

- Useful non- invasive procedure.
- Simplicity of the procedure.
- Sensitivity of the PCR

□ **Disadvantages of PCR**

- False positive results (cross contamination).
- False negative results

Variant PCR

- Reverse transcriptase-PCR.
- Nested-PCR.
- Hot-start PCR.
- Quantitative PCR.
- Multiplex-PCR.
- Mutagenesis by PCR.
- Allele specific PCR.
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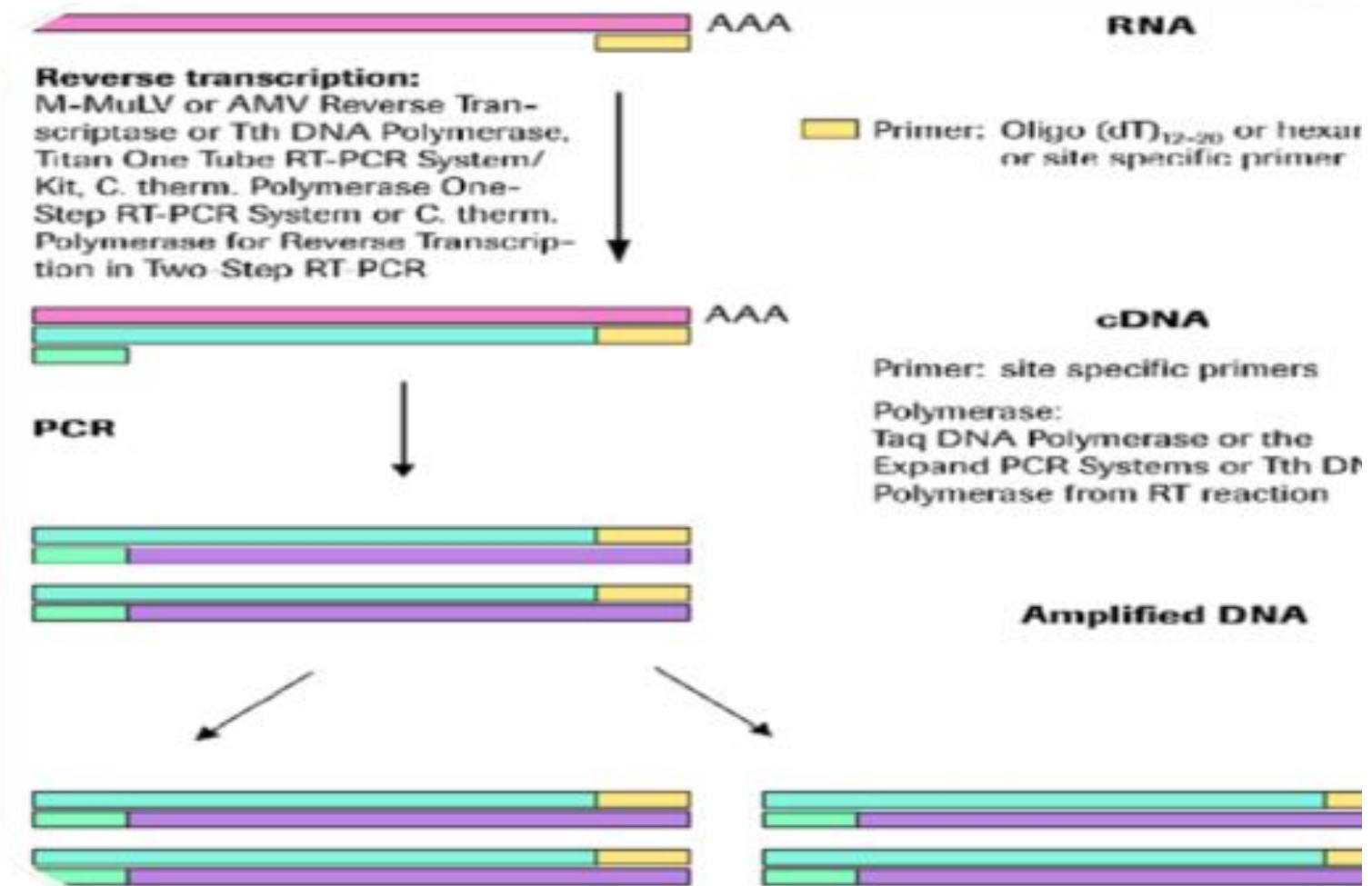
Reverse Transcriptase - PCR

RT-PCR, one of the most sensitive methods for the detection and analysis of rare mRNA transcripts or other RNA present in low abundance.

RNA cannot serve as a template for PCR.

RNA must be first transcribed into cDNA with reverse transcriptase from Moloney murine leukemia virus or Avian myeloblastosis virus, and the cDNA copy is then amplified.

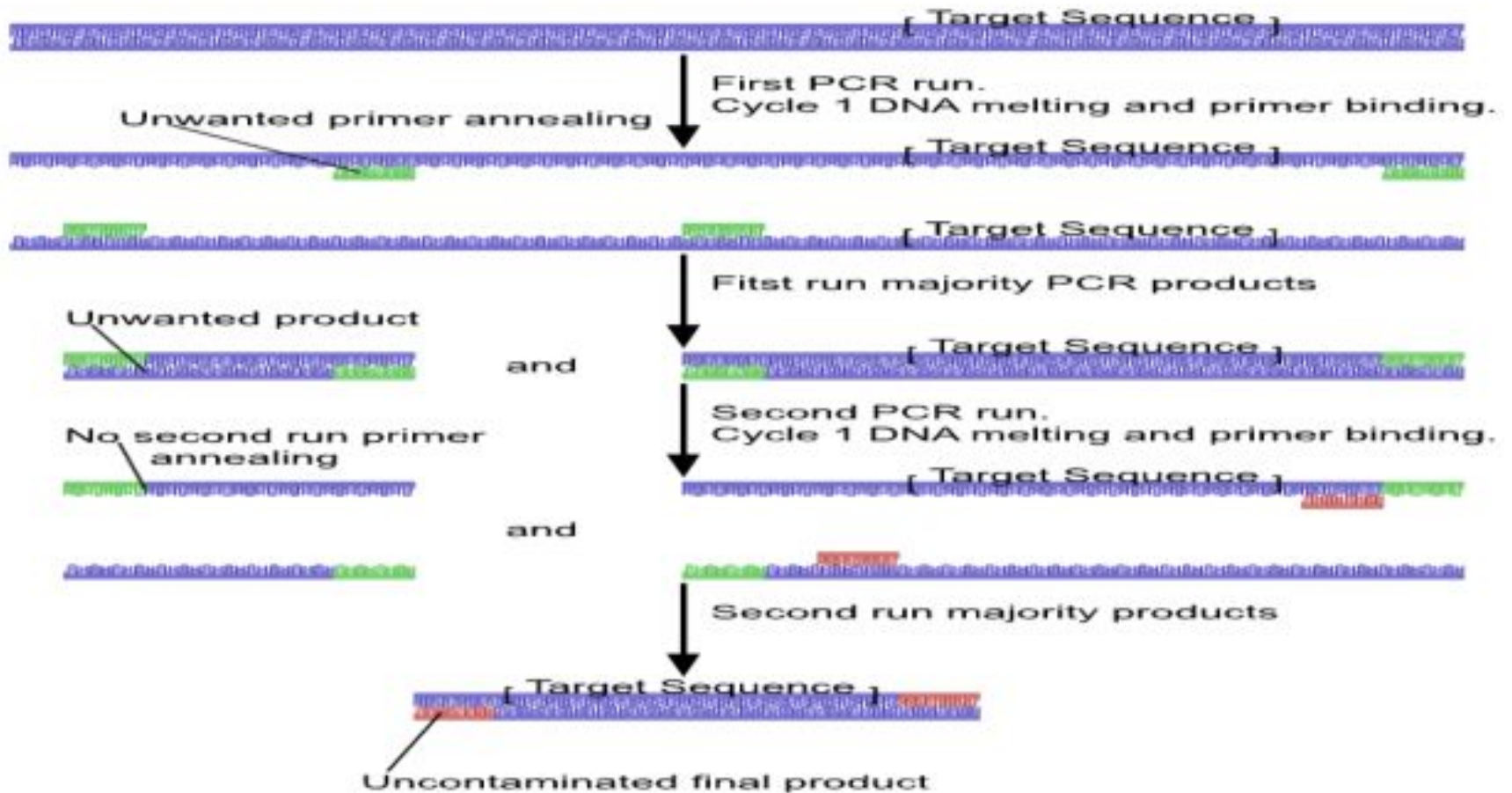
RT-PCR



Nested PCR

- Nested PCR is a very specific PCR amplification.
- Nested PCR use two pairs (instead of one pair) of PCR primers are used to amplify a fragment.

Nested - PCR

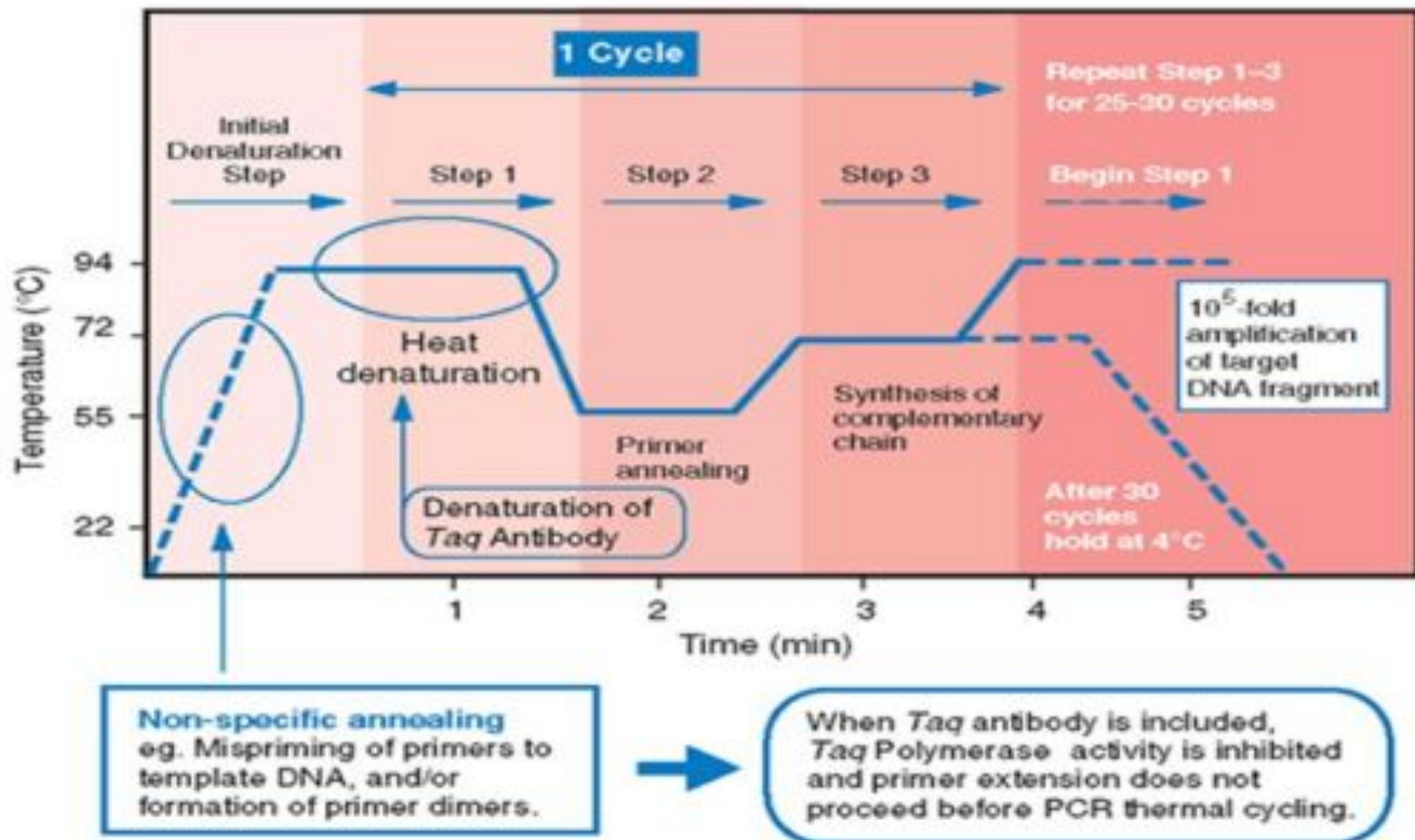


Hot - Start PCR

- Hot Start PCR significantly improves specificity, sensitivity and yield of PCR.
- The technique may be performed manually by heating the reaction components to the melting temperature (e.g., 95°C) before adding the polymerase. Specialized enzyme systems can be used.

Hot - Start PCR

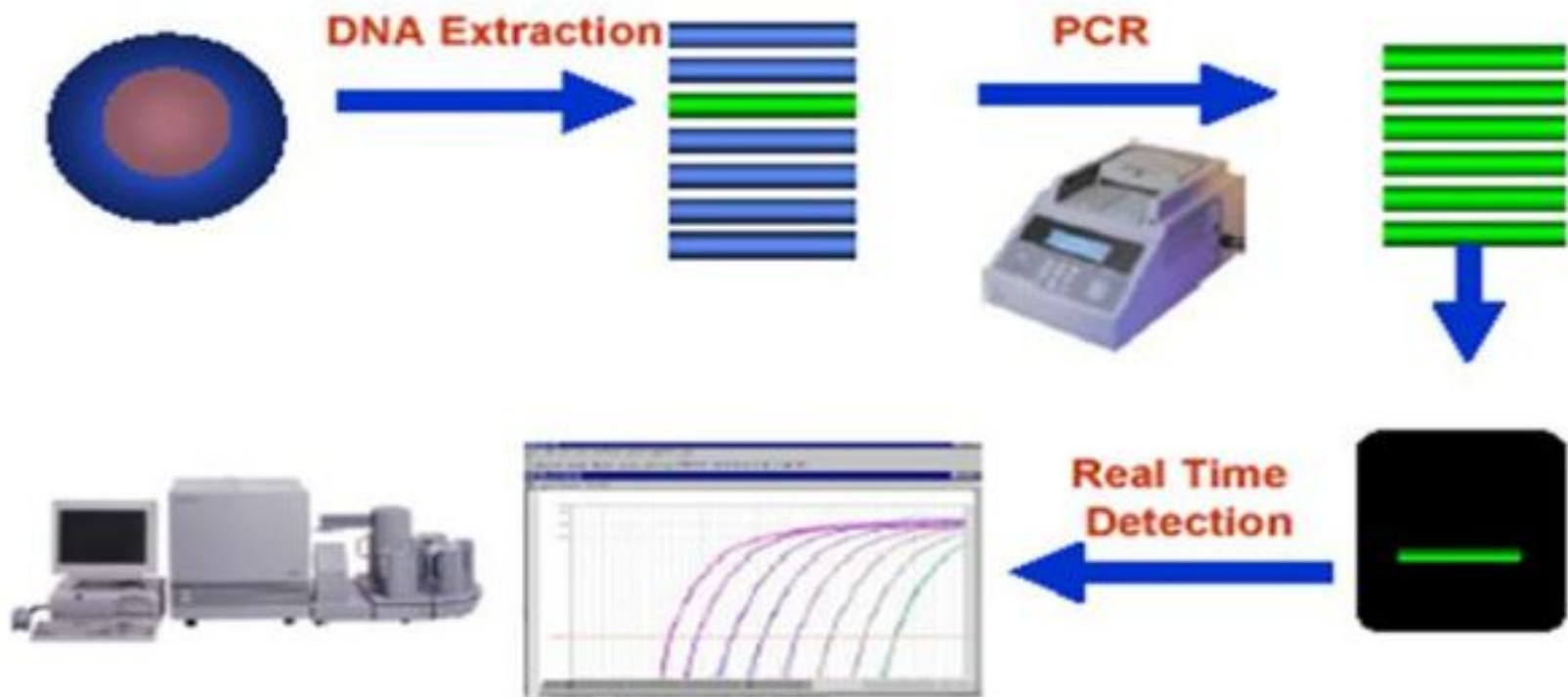
Profile of a Hot Start PCR Reaction



Real Time PCR

- Traditional PCR has advanced from detection at the end-point of the reaction to detection while the reaction is occurring (Real-Time).
- Real-time PCR uses a fluorescent reporter signal to measure the amount of amplicon as it is generated . This kinetic PCR allows for data collection after each cycle of PCR instead of only at the end of the 20 to 40 cycles.

Real Time PCR



POLYMERASE CHAIN REACTION: USES

- Molecular biology,
- Microbiology,
- Genetics,
- Diagnostics clinical laboratories,
- Forensic science,
- Environmental science,
-

Infectious Diseases/ Cancer

- Detection of infectious agents, such as Pathogenic bacteria, Viruses or Protozoa.
- **Cancer**
Detection of malignant diseases by PCR, Recurrence of hematological cancers has also been evaluated and
Detection of micro-metastasis in blood, lymph nodes and bone marrow.

Genetic Disease

- Single point mutations can be detected by modified PCR techniques such as the ligase chain reaction (LCR) and PCR-single-strand conformational polymorphisms (PCR-SSCP) analysis.
- Detection of variation and mutation in genes using primers containing sequences that were not completely complementary to the template.

Inherited disorders diagnosed using PCR protocols

- Alpha1 antitrypsin
- B thalassaemia
- Cystic fibrosis
- Duchenne muscular dystrophy
- Myotonic dystrophy
- Haemophilia A and B
- Huntington's chorea
- Phenylketonuria
- Sickle cell anaemia
- Familial adenomatous polyposis
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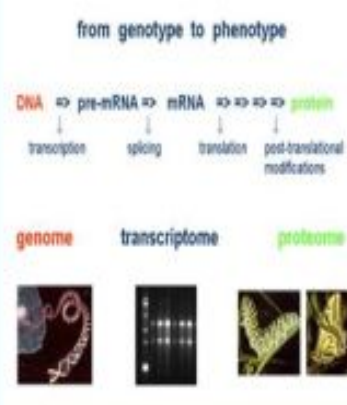
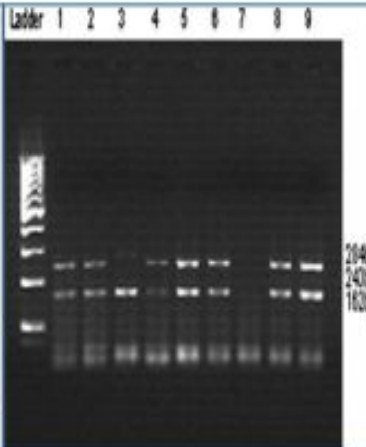
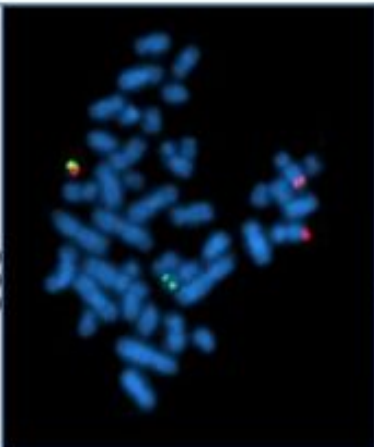

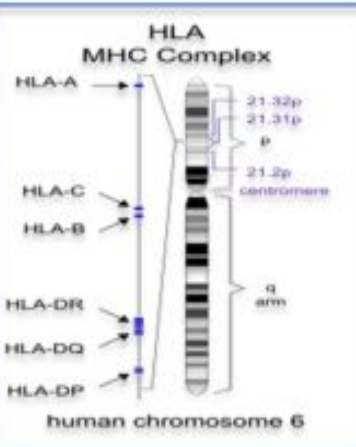
Prenatal Diagnosis

- **Prenatal sexing:** Often required in families with inherited sex-linked diseases.
- **Prenatal Diagnosis of diseases:** Prenatal diagnosis of many of the inborn errors of metabolism is possible by DNA markers.

Research

- PCR is used in research laboratories in DNA cloning procedures, Southern blotting, DNA sequencing, recombinant DNA technology.
- Major role in the human genome project.

Polymerase Chain Reaction

<p>from genotype to phenotype</p> <p>DNA → pre-mRNA → mRNA → protein</p> <p>transcription splicing translation post-translational modifications</p> <p>genome transcriptome proteome</p> 				
<p><u>Gene expression analysis</u></p>	<p><u>Multiplex PCR</u> ,</p> <ul style="list-style-type: none"> made it possible to compare two or more complex genomes, for instance to detect chromosomal imbalances. 	<p>Combining in situ hybridization with PCR</p> <ul style="list-style-type: none"> made possible the localization of single nucleic acid sequences on one chromosome within an eukaryotic organism. 	<p>Amplification of <u>archival</u> and <u>forensic</u> material.</p>	<p>HLA Typing</p> <ul style="list-style-type: none"> <u>Identify testing for transplantation.</u>

Clinical Microbiology

Viral load (HIV,HCV,HBV,...)

Bacterial load (Salmonella,
Mycobacterium,...)

Fungal load (Candida,
Cryptococcus, Aspergillus,....)

Food microbiology

Bacterial load (Listeria,
Salmonella, Campylobacter,...)

Clinical Oncology

Minimal residual disease

Chromosomal translocations

Single nucleotide
polymorphism (SNPs)

Gene therapy

Gene transfer estimation

Biodistribution of vector

Gene expression

Cytokines, receptors,.....

