

Bacterial identification using PCR

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- Conventional PCR assays are suited to detect the presence or absence of the target genes.
- NOT their function or expression.
 - Rapid detection
 - Confirm species identity because biochemical and phenotypic tests do not always produce correct species differentiation.
 - Detect and identify either live or dead bacteria.
 - Various PCR based bacterial identification

 DNA sequencing based
 PCR amplicon pattern of highly conserved genes



PCR amplification of 16s rRNA gene

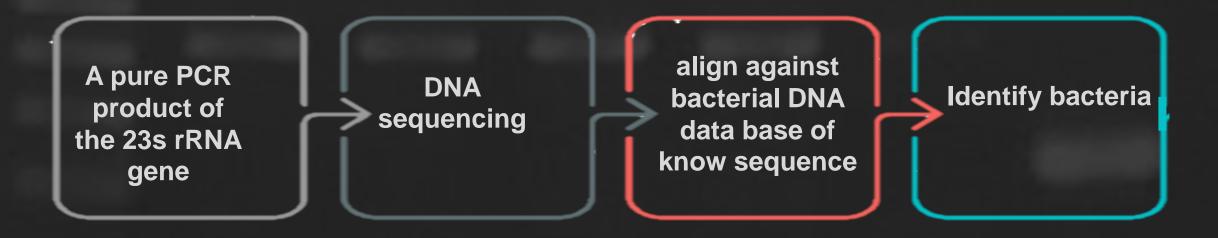
- widely used as a means to identify an unknown
- 16S rRNA
 - present in all bacterial species
 - \circ highly conserved sequences
 - \circ genus- or species-specific.



Fleming Fund PCR amplification of 23s rRNA gene

23s rRNA gene:

- \circ universal distribution
- \circ highly conserved sequences
- $\circ\,$ genus or species-specific.
- $\,\circ\,$ a greater length and sequence variations
- possibly better phylogenetic resolution
- the lack of established broad-range bacterial PCR amplification and sequencing primers.



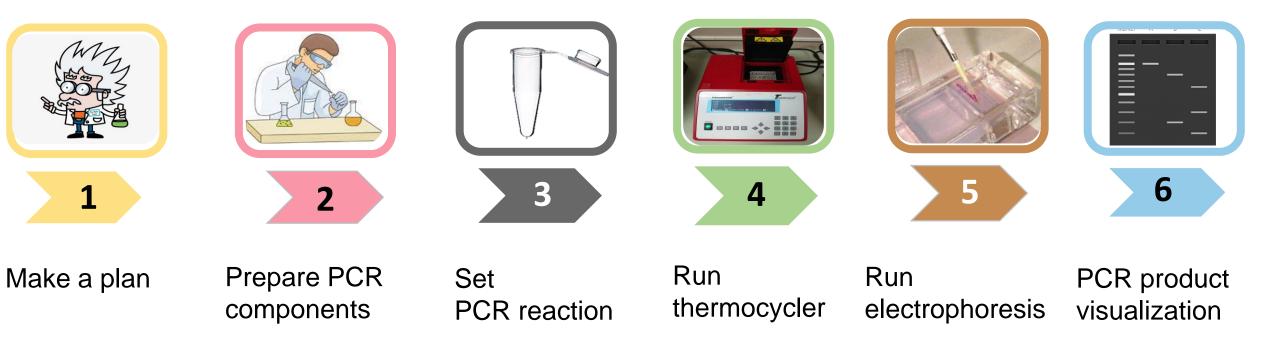


- Amplified 16S Ribosomal DNA Restriction Analysis (16S-ARDRA)
- real-time PCR Salmonella screening method (invA gene)
- Amplification of sodA (superoxide dismutase) gene and ddl (D-alanine-D-alanine ligase) gene for *E. faecium & E. faecalis* identification

• etc



Flow of conventional PCR





A well-designed and optimized PCR assay provides the highest specificity and yield.

- What is or are the purpose (s) of your PCR?
- What are the DNA sequence of your target gene and surroundings?
 - What is or are your target gene (s)?
- What materials are needed?



Materials

- Molecular marker (Ladder 100bp)
- Electrophoresis buffer (TAE or TBE)
- $\circ~$ Tips (filter) for pipettes 1 μL to 1000 μL
- \circ Agarose
- o PCR components
- \circ TE buffer
- o Tris HCI buffer
- o Crushed ice
- Mineral oil (if necessary)
- \circ etc

Equipment

- PCR thermocycler
- \circ Pipettes for 1 µL to 1000 µL
- Eppendorf tubes
- o PCR tubes
- Electrophoresis unit
- Microwave
- o Autoclave
- Eppendorf centrifuge (PCR tubes)
- o Photo camera
- UV-transilluminator
- o Water bath





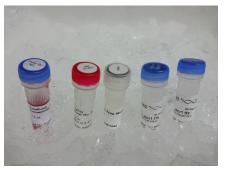








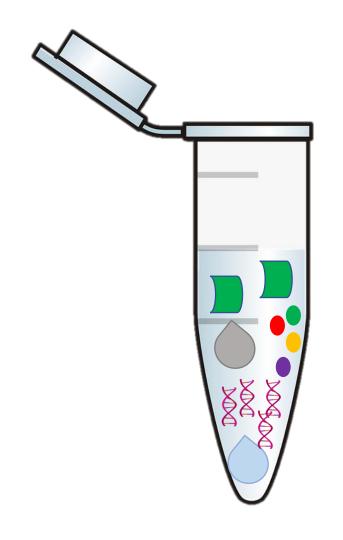




etc





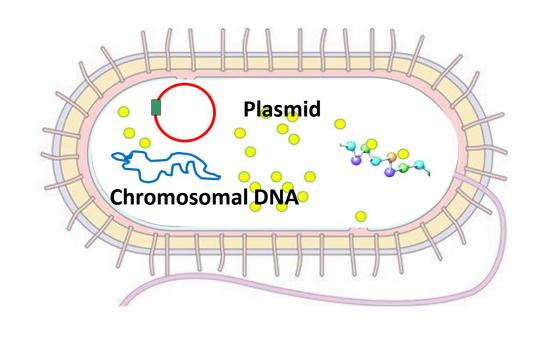


- Template DNA
- Thermostable DNA polymerase
- Primers
- dNTPs
- PCR grade water
- Buffer and salts (KCI, MgCl₂)
- Optional: DMSO, Formamide





- ✓ Any DNA sources
 - Genomic DNA (gDNA)
 - Plasmid DNA
 - DNA fragments
 - Complementary DNA (cDNA)



Template DNA properties:

- highly purified
- o free from chemical contaminants
 - and other DNA contaminants.
- with 50% to 55% GC content
- A starting amount in a 50 μ L PCR,
 - 0.1–1 ng of plasmid DNA
 - 5–50 ng of gDNA
- Optimization of DNA amounts
 - \circ \uparrow Amounts, \uparrow Nonspecificity
 - \downarrow Amounts, \downarrow PCR product yields





DNA preparation

 Purifying DNA by using physical and/or chemical methods from a sample

Conventional methods

Alkaline lysisPhenol chloroform extraction

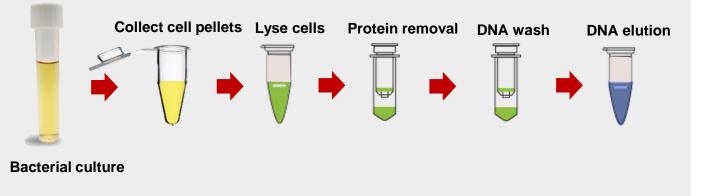
Commercial kits

Pure DNA if used properlyPhenol chloroform extraction

Boiling methods

- Whole cell DNA
- Simple, reproducible, rapid and economical
- Contain protein, enzyme etc







2

Preparation of DNA template by whole cell boiling method



 \checkmark Suspend a loopful of culture in 100 µl of sterile DW.



Boiled 10 min at 100°C



✓ Place on ice





Centrifuged 5 min at 12,000-13,000xg

✓ Store at -20°C

Transfer supernatant to a new tube





Assessing the quality of DNA by spectrometry:

- Absorption peak for DNA
 - = at ~260 nm. (A₂₆₀)
- Absorption peak for protein
 - = at ~280 nm. (A₂₈₀)
- DNA sample purity
 - $= A_{260}/A_{280}$ ratio
 - = ~1.8 for dsDNA
- A ration of < 1.7
 - = protein contamination.

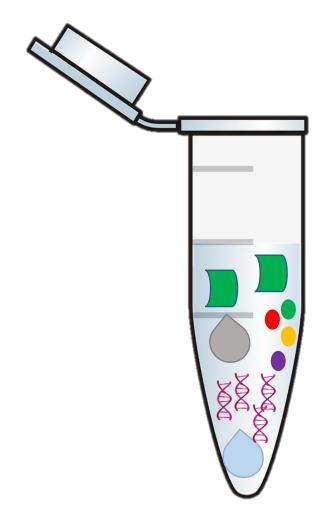
Assessing the quality of DNA DNA by spectrometry:

- One A260 unit is the amount of nucleic acid contained in 1 mL and producing an OD of 1.
- Conversion factors:
 - \circ 1 A260 unit dsDNA = 50 µg
 - \circ 1 A260 unit ss DNA = 33 µg
 - \circ 1 A260 unit ssRNA = 40 µg
- Example,
 - If A260 of a DNA sample is = 2.5

$$\therefore \text{ dsDNA amount} = 2.5 \times 50$$
$$= 125 \,\mu\text{g}$$









- Template DNA
- Thermostable DNA polymerase

• Primers

• dNTPs

- PCR grade water
- Buffer and salts (KCI, MgCl₂)
- Optional: DMSO, Formamide

Fleming Fund Thermostable DNA polymerase Regional Grants



Taq Polymerases

a thermostable enzyme from hyperthermophilic *Thermus aquaticus*.

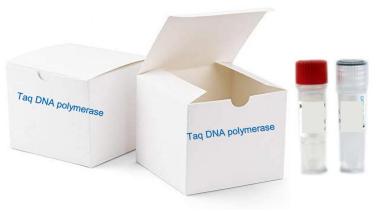
Most active around 70-72°C.

incorporates \approx 1,000 bp per a min

makes an error in approx. every 125,000 nucleotides

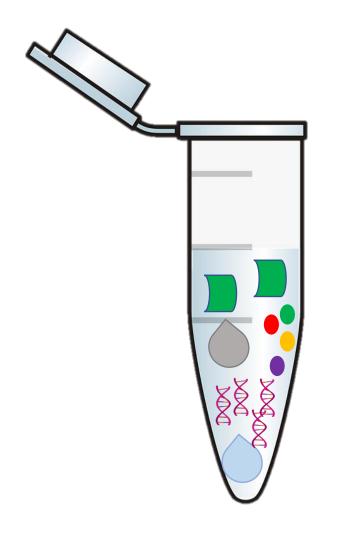
0.5–2 units of DNA polymerase are sufficient in a typical 50 μ L reaction.













Template DNA

• Thermostable DNA polymerase

• Primers

dNTPs

- PCR grade water
- Buffer and salts (KCI, MgCl₂)
- Optional: DMSO, Formamide





 A piece of single-stranded DNA that matches the sequences at the ends of or within the target DNA in such a way that the 3' end of it is available to serve as the starting point for the new DNA.

Template (target) DNA

TAGCTGGATCGACCCATC





Primer criteria :

- Optimal length = 18-25 bases long (up to 30)
- Best to have G or C (≤3 base) at least 5 bases from 3' end
- Should contain 40-60% G + C content
- Primers should have approximately equal melting temperatures (within 5°C)
- No self-complementary sequence between primers

• No inverted repeat sequence (Max. 3 bp)

How to get primers

 Design primers (Manual design & Computer-assisted design)

 Send for custom oligo synthesis

Prepare and use

Fleming Fund Melting temperature (Tm)

2

What is Tm?

The temperature at which one-half of the DNA duplex will dissociate to become single stranded.

What is annealing temperature (Ta)?

- Temperature that primers bind to template DNA
- Annealing temperature is <u>about 5°C below the</u> <u>T_m of the primers.</u>
- Optimal annealing temperatures give the highest product yield of the correct amplicon.

- If T_a is too low

 nonspecific PCR amplification
- If T_a is too high
 = reduced yield of
 PCR amplicons





Tm calculation

1.	Tm = 2AT + 4GC	5	5' - G T G C T	GGATCGACCCTAC-3'
	Good for 15-20 bp primersHigh ionic strength solvent		T _m	= $2AT + 4GC$ = $(2 \times 7) + (4 \times 11)$ = 58
Ar	nnealing temperature (Ta) = T	m - 5	T _a	= Tm - 5 = 58 - 5 = 53 = 53

- 2. $Tm = 81.5 + 16.6(logK^+) + 0.41[\%(G+C)] (675/n)$
 - N = primer lengthK = concentration of cations (nM)
- Good for 14-70 bp primers
- Cation concentration of $\leq 4M$

Fleming Fund Melting temperature (Tm)



Tm calculation

3. Online software

Popular Applicatio	ons & Techniques Shop All Products Ser	vices Support	Quick		
Search All	Search by catalog number, product nam	e, keyword, application			
Home > Brands > Then	mo Scientific → Molecular Biology → Molecular I	Biology Resource Library > Thermo Scientific Web Tools > Tm Ca	alculator		
T _m Calcula	ator				
)=)	This tool calculates the T _m of primers and estimates an appropriate annealing temperature when using different DNA polymerases. How to use this calculator >				
	Quickly find the right annealing temperature Tm Calculato version 1.13.0	re for Platinum SuperFi DNA polymerase (also works for Supe	rScript IV One-Step RT-PCR Kit),	€ BioLabs ⊕ Feedbac	
	Use the NEB Tm Calculator to estimate an appropriate annealing temperature when using NEB PCR products. Instructions • Select the product group of the	Product Group Q5 Polymerase/Kit Q5 High-Fidelity DNA Polymerase Primer Concentration (nM) 500	✓ ✓ Reset concentration	Anneal at	
	 polymerase or kit you plan to use. Select the polymerase or kit from the list of products. If needed, modify the recommended primer concentration. 	Primer 1 Primer 1 SEQUENCE Primer 2 Primer 2 Primer 2 SEQUENCE		Primer 1 nt % GC Tm:*C	
	Enter primer sequences (with up to 3 ambiguous bases). Spaces allowed. Note that an anealing temperature will only be displayed if both primer sequences are entered.	Switch to batch mode	Clear Use example input	Primer 2 nt % GC Tm:°C	

Melting Temperature (Tm) Calculation

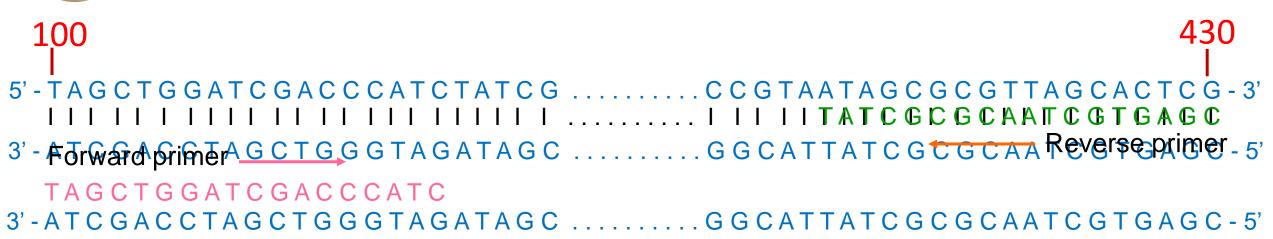
GTATGTGTGTATATATATGT		Compute Tm
LENGTH C+G% Molecular weight:	20 25 6272.715	
Basic Tm Degenerated nucleotides ar	e allowed	
 <u>Base-Stacking Tm</u> Degenerated nucleotides ar 	e NOT allow	red
Primer concentration:	200	nM
Salt concentration:	50	mM
Mg ²⁺ concentration:	0	mM
Tm: Enthalpy: -145.6 Entropy: -430.95	41.3 °C	
		http://insilico.ehu.e







Manual design



PCR amplicon size = 330 bp

Fleming Fund Internet software for primer design egional Grants



Designing Primers

- NCBI
- Primer3 (Whitehead Institute for **Biomedical Research**, MIT)
- GenScript
- GeneFisher2 (Bielefeld University)
- FastPCR (PrimerDigital, Helsinki, Finland)
- PerlPrimer (Owen Marshall)
- Primer Design Assistant (Division of Biostatistics and Bioinformatics, NHRI)
- Beacon Designer (PREMIER Biosoft • International)*

Checking Primer Specificity

Basic Local Alignment Search Tool (BLAST; NCBI)

Checking for Existing PCR Primers

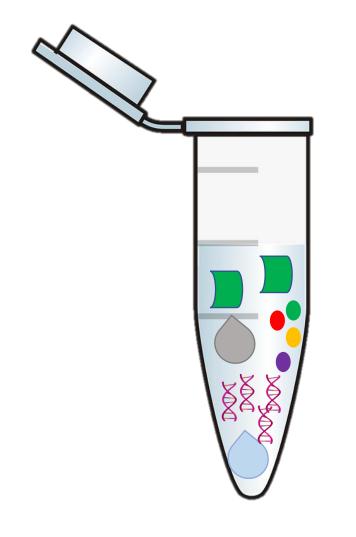
- PrimerBank (Massachusetts General Hospital)
- RTPrimerDB
- Quantitative PCR Primer Database (QPPD; NCI)
- Choosing a Target Sequence

Assessing Primer Properties

- OligoAnalyzer 3.1 (Integrated DNA) **Technologies**)
- NetPrimer (PREMIER Biosoft International)
- Gene Walker (CyberGene AB)
- Oligo Calc: Oligonucleotide Properties Calculator (Northwestern University)







- Template DNA
- Thermostable DNA polymerase

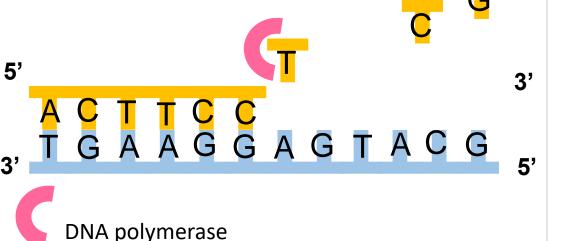
• Primers

dNTPs

- PCR grade water
- Buffer and salts (KCI, MgCl₂)
- Optional: DMSO, Formamide

^{The} Fleming Fund Deoxynucleotide Triphosphates (dNTPs) 2

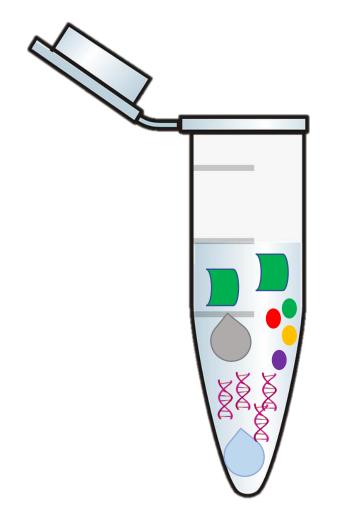




- **Four** nucleotides are typically added to the PCR reaction in equimolar amounts for optimal base incorporation.
- Incorporate into a new DNA strand by DNA polymerase
- For efficient incorporation by DNA polymerase, free dNTPs should be present in the reaction at a concentration of **no less** than 0.010–0.05 mM.
- In most PCR applications, the recommended final concentration of each dNTP is generally 200 µM.







- Template DNA
- Thermostable DNA polymerase
- Primers
- dNTPs
- PCR grade water
- Buffer and salts (KCI, MgCl₂)
- Optional: DMSO, Formamide





 Must free of all DNA, RNase and DNase contamination.

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- purified
- double-distilled
- deionized
- autoclaved.

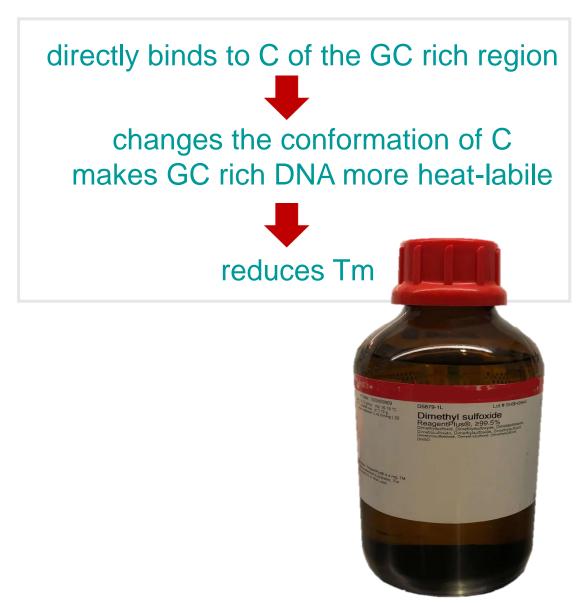






Dimethyl sulfoxide (DMSO)

- an organosulfur compound with a high polarity and high dielectric constant
- can greatly reduce the activity of *Taq* polymerase.
- benefit for longer and high GC rich DNA that are hard to amplify with basic PCR components and normal PCR protocol
- test a variety of DMSO concentrations between 1-10% w/v to find the best balance.







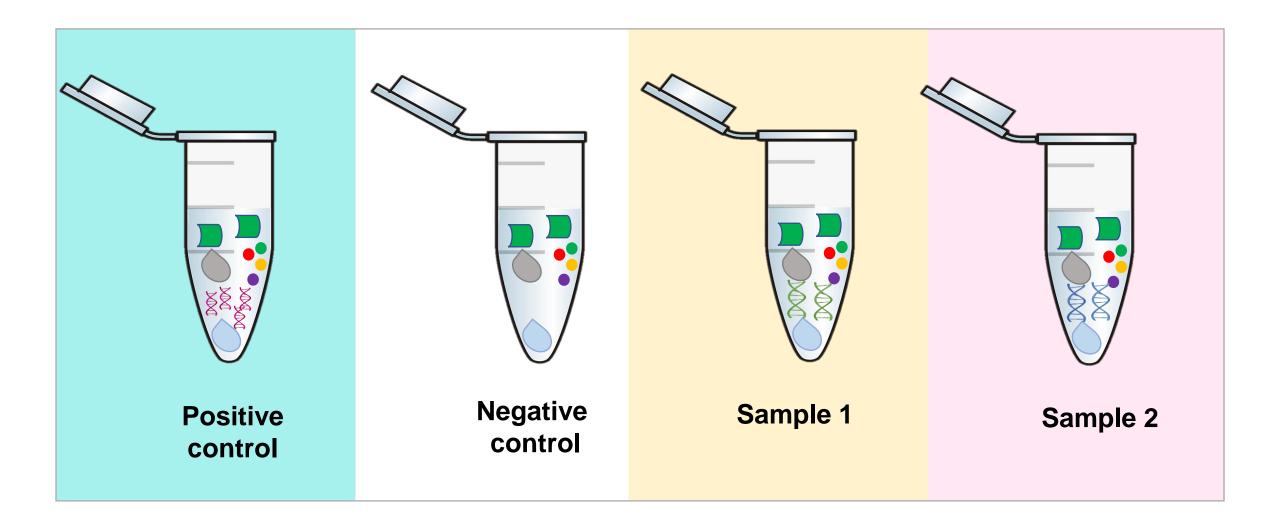
A traditional PCR reaction (50 μ l)

Component	Concentration range	Stock concentration	A PCR standard reaction
Sterile DW	Add to 50 µl		Add to 50 μl
PCR buffer	10x	10x	1x
dNTPs	200-250 µM	10mM	200 μM
MgCl2	0.1-5 mM	25mM	1.5 mM
Forward primer	0.1-0.5 μM	20 pmol/μl (20 μM)	20 pmol
Reverse primer	0.1-0.5 μM	20 pmol/μl (20 μM)	20 pmol
Taq polymerase	0.5 – 2.5 units	5 unit/μl	0.5 units
DNA template	1 pg to 1 µg	25 ng/μl	10 ng
DMSO	1 to 10% w/v		



These PCR conditions are suitable for products ranging up to 3 kb in length. PCRs that result in longer products may require optimization of the dNTP and primer concentrations and the use of special DNA polymerase kits.

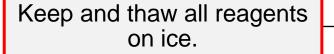




Fleming Fund Setting up traditional PCR reaction







Assemble reaction mix into 50 μ L volume in a thin walled 0.2 mL PCR tubes.

Add reagents in following order:

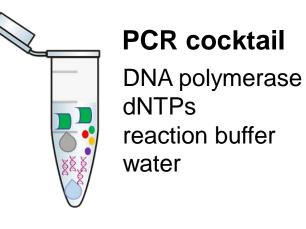
Water \rightarrow buffer \rightarrow dNTPs \rightarrow MgCl₂, \rightarrow template DNA \rightarrow primers \rightarrow Taq polymerase.

Gently mix by tapping tube. Briefly centrifuge to settle tube contents. Prepare negative control reaction without template DNA Prepare positive control reaction with template of known size and appropriate primers.

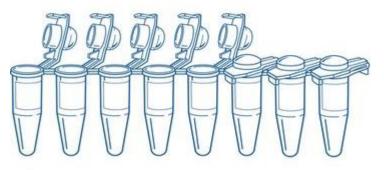


- PCR cocktail is good for multiple PCR experiments.
- assemble a mixture of reagents common to all reactions (i.e., Master Mix).
- The amount of each reagent added to the cocktail is equivalent to the total number plus one whole reaction.





Aliquot into PCR tubes



Add DNA as the last step



Example of a PCR cocktail for 10 DNA samples (11 50 μ l-reactions)

Component	Stock conc.	Volume in 1 rxn	No of rxn	Volume in cocktail (11rxn)	Final conc. in 1 rxn (50 ul)
Sterile DW		36.5	11	401.5	
PCR buffer	10x	5 μl	11	55	1x
dNTPs	10mM	1 µl	11	11	200 μM
MgCl2	25mM	3 μl	11	33	1.5 mM
Forward primer	20 pmol/μl (20 μM)	1 µl	11	11	20 pmol
Reverse primer	20 pmol/μl (20 μM)	1 μl	11	11	20 pmol
Taq polymerase	5 unit/μl	0.5 μl	11	5.5	2.5 units
DNA template	25 ng/μl	2 µl	11	22	50 ng
Total		50 μl		550	

48 μl

+ 2 μl - DNA template







1. MASTERMIX

- Sterile Water
- 10X PCR Buffer
- MgCl₂
- dNTP's
- DNA Polymerase

2. Primers (Forward + Reverse)

3. DNA Template

WHY?

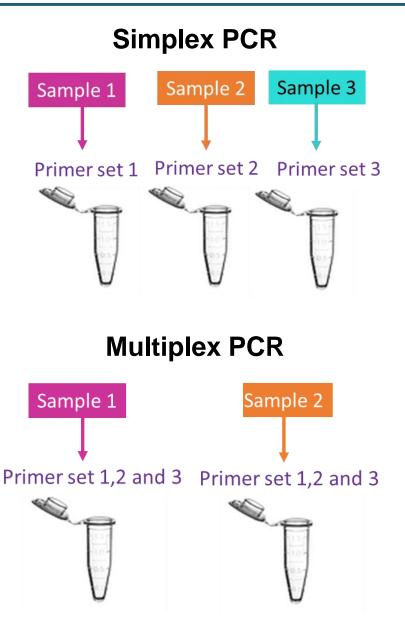
- reduce pipetting error
- Reduce risk of contamination
- convenient
- saves time
- prevent possible errors in mixing
- Improve consistency





Simplex PCR amplifies a single gene.

Component	A PCR standard reaction
Sterile DW	Add to 50 µl
PCR buffer	1x
dNTPs	200 μM
MgCl2	1.5 mM
Forward primer	20 pmol
Reverse primer	20 pmol
Taq polymerase	0.5 units
DNA template	10 ng
DMSO	



Multiplex PCR amplifies multiple target DNA simultaneously

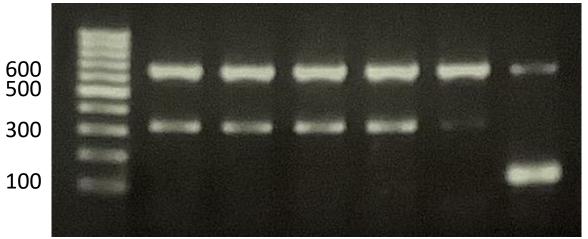
- several target DNA fragments are amplified simultaneously with different primers.
- The products must be of different sizes and can be visualized by gel electrophoresis.
- Often designed to detect different genes, all relating to the same resistance phenotype
 - detection of ESBL genes
 - detect genus and species of bacteria



Detection of Campylobacter spp.

Reagents	Volume used (µl)	Final conc.
10X PCR buffer	10	1X
25 mM MgCl ₂	3	1.5 mM
10 mM dNTPs	1	200 µM
DNA template	5	100-500 nM
CJF (10 µM)	2.5	0.5 µM
CJR (10 µM)	2.5	0.5 µM
CCF (20 µM)	2.5	1.0 µM
CCR (20 µM)	2.5	1.0 µM
CLF (20 µM)	2.5	1.0 µM
CLR (20 µM)	2.5	1.0 µM
23SF(10 µM)	1	0.2 µM
23SR (10 µM)	1	0.2 µM
Tag polymerase	1	5 units
dH ₂ O	13	
Total	50	





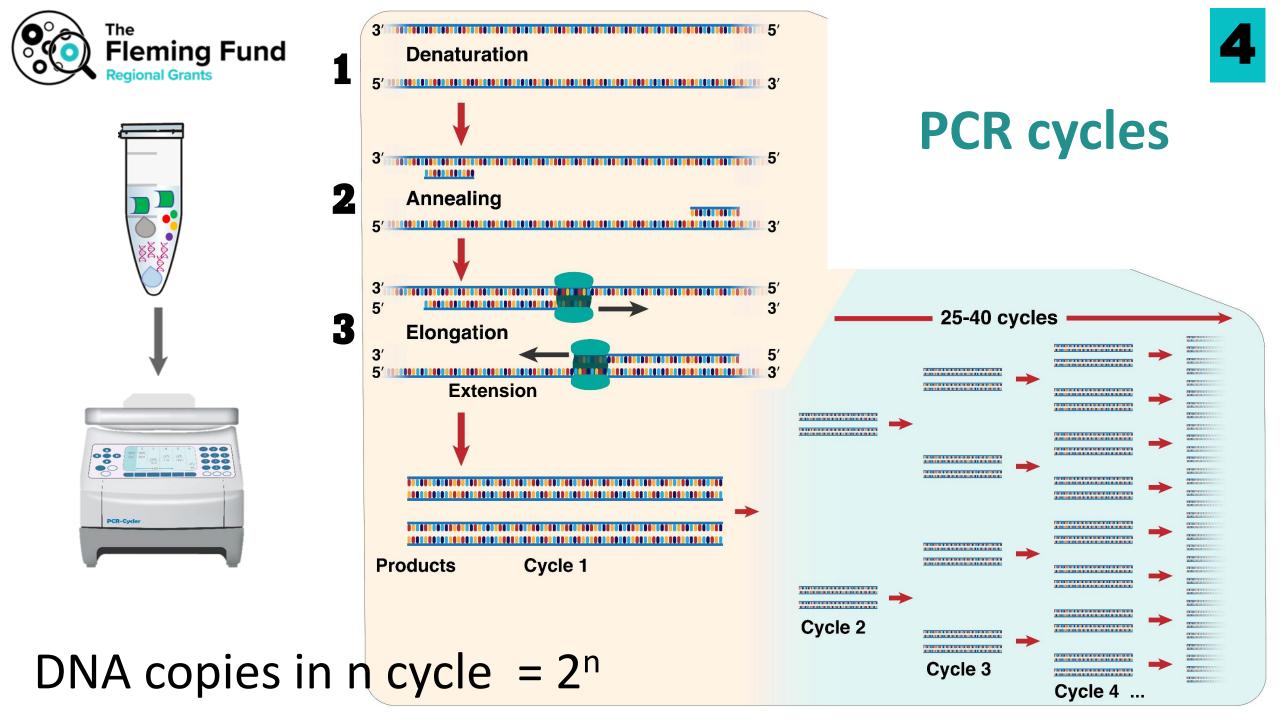
Campylobacter	650 bp
C. jejuni	323 bp
C. coli	126 bp

1. 2

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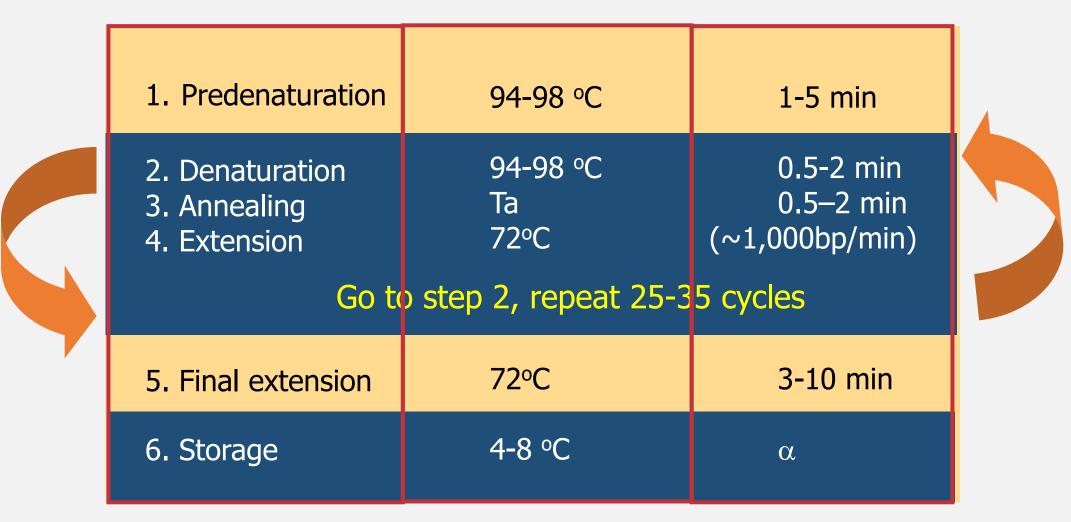
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Wang et al 2002





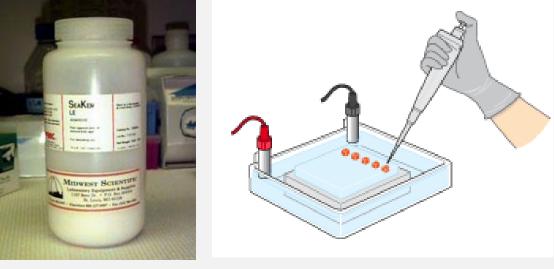






Gel Electrophoresis

- A method that separates macromolecules-either nucleic acids or proteins-on the basis of size, electric charge, and other physical properties.
- Gel is made from "Agarose" that is a linear polysaccharide and made up of the basic repeat units of agarobiose







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- Decide what percentage of agarose to use
- Agarose concentration should be appropriate for molecular size of interest.
- If there are a wide range of sizes to be separated on a gel, it is recommended to start with a 1.20% agarose gel concentration.

Agarose % (w/v)	Resolution	
0.50%	1,000 – 30,000 bp	
0.70%	800 – 12,000 bp	
1.00%	500 – 10,000 bp	
1.20%	400 – 7,000 bp	
1.50%	200 – 3,000 bp	
2.00%	50 – 2,000 bp	





able to conduct electricity & working at 1X



Tris acetate EDTA (TAE)

10x Stock

- 48.5 g tris
- 11.4 mL glacial acetic acid
- 20 mL 0.5M EDTA (pH 8.0)
- Adjust volume to 1 L.



Tris borate EDTA (TBE)

10X Stock

- 108 g tris base
- 55 g boric acid
- 900 ml double-distilled H_2O
- 40 ml 0.5 M EDTA solution (pH 8.0)
- Adjust volume to 1 L.

NOTE

- TBE gives a better conductive medium than TAE and is less prone to overheating.
- use TBE for long runs
- Use TBE for <2kb DNA fragments
- Use TAE for isolating the DNA for downstream enzymatic steps.



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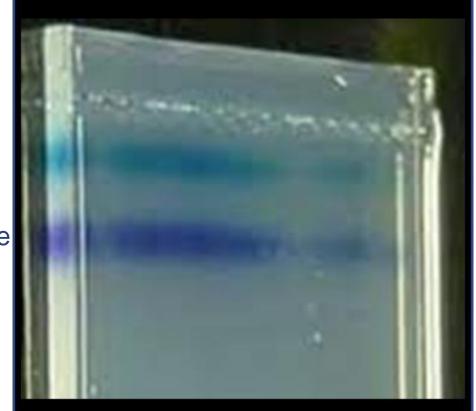
- Used to prepare DNA markers and DNA samples for **loading** on agarose **gels.**
- Used as a tracking dye during electrophoresis allowing the user to monitor the progress of molecules moving through the gel

Common recipe

- o Bromophenol blue
- Ficoll 400
- \circ water
- Optional Xylene cyanol, Tris and EDTA, sucrose, glycerol)

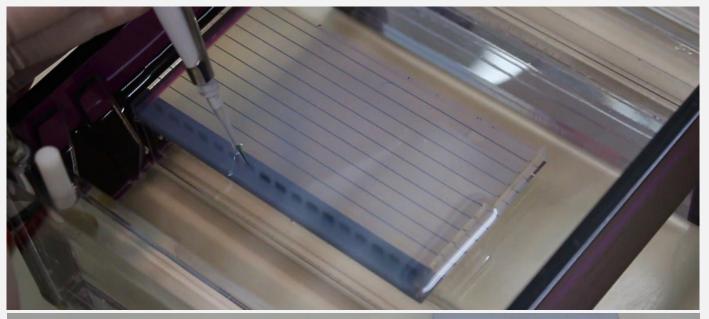
Xylene cyanol

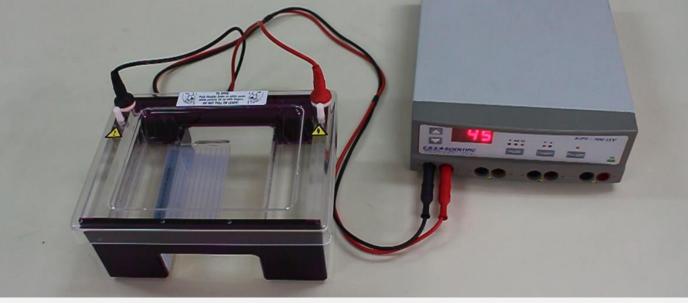
Bromophenol blue



Fleming Fund DNA loading & running gel electrophoresis 5

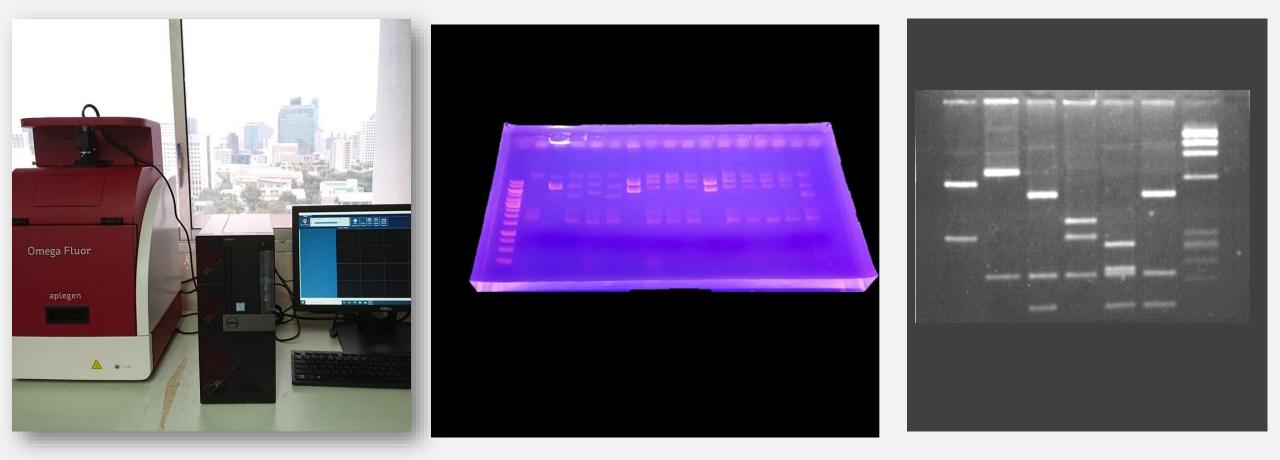
- Mix DNA with loading dye
- Load to a gel.
- Apply electricity (Run DNA on gel)
- Staining
- Visualize DNA
- PCR products are visible as different "bands".











UV transilluminator





UKaid

from the British people

Thank you









กรมวิทยาศาสตร์การแพทย์ Department of Medical Sciences

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