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Extraction of DNA and RNA

By Dr. Dalia Fouad

Work shop of extraction of DNA and RNA 4-5/08/1438



What is DNA?

DNA, or deoxyribonucleic acid, is the hereditary material in humans and almost all other organisms. Nearly every cell in a person's body has the same DNA.

Most DNA is located in the cell nucleus (where it is called nuclear DNA), but a small amount of DNA can also be found in the mitochondria (where it is called <u>mitochondrial</u> <u>DNA</u> or mtDNA).

The information in DNA is stored as a code made up of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T).

Human DNA consists of about 3 billion bases, and more than 99 percent of those bases are the same in all people.

The order, or sequence, of these bases determines the information available for building and maintaining an organism, similar to the way in which letters of the alphabet appear in a certain order to form words and sentences.

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What is DNA? (cont.)

DNA bases pair up with each other, A with T and C with G, to form units called base pairs.

Each base is also attached to a sugar molecule and a phosphate molecule.

Together, a base, sugar, and phosphate are called a nucleotide. Nucleotides are arranged in two long strands that form a spiral called a double helix.

The structure of the double helix is somewhat like a ladder, with the base pairs forming the ladder's rungs and the sugar and phosphate molecules forming the vertical sidepieces of the ladder.

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An important property of DNA is that it can replicate, or make copies of itself. Each strand of DNA in the double helix can serve as a pattern for duplicating the sequence of bases. This is critical when cells divide because each new cell needs to have an exact copy of the DNA present in the old cell.

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Why do people want to obtain genomic DNA?

There is a number of reasons.

For example, this DNA could be used to clone new genes or look for special regions of interest.

You could also obtain a number of different genomic DNA and make comparisons with them to identify genetic diseases.

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DNA Double Helix



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Watson and Crick 1953 article in Nature



The Roles of Nucleic Acids in heredity :

- There are two types of nucleic acids: <u>Deoxyribo</u> <u>Nucleic Acid</u> (<u>DNA</u>) and <u>R</u>ibo Nucleic Acid (<u>RNA</u>).
- DNA provides direction for its own replication.
- DNA also directs RNA synthesis and, through RNA, controls protein synthesis.
- **Organisms inherit DNA from their parents:**
- When a cell divides, its DNA is copied and passed to the next generation of cells.

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DNA Structure

- Prior to the 1950s, it was already known that DNA is a polymer of nucleotides, each consisting of three components:
 - ♦ a 5-carbon sugar called deoxyribose
 - ◆ a phosphate group (PO₄)
 - a nitrogenous base
 - adenine, thymine, cytosine, guanine

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Watson and Crick reasoned that there must be <u>additional specificity of pairing</u> <u>Each base pair</u> forms a different number of hydrogen bonds • Adenine (A) and thymine (T) form two bonds, cytosine (C) and guanine (G) form three bonds

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Figure 4.6 2-Deoxyribose is the sugar in DNA and ribose is the sugar in RNA. The carbon atoms are numbered as indicated for deoxyribose. The sugar is connected to the nitrogenous base via position 1'.



Figure 4.11 Complementary base pairing involves the formation of two hydrogen bonds between A and T, and of three hydrogen bonds between G and C. No other pairs form in DNA.



DNA Structure

Nucleotides are connected to each other to form a long chain

- phosphodiester bond: bond between adjacent nucleotides
 - formed between the phosphate group of one nucleotide and the 3' –OH of the next nucleotide

The chain of nucleotides has a 5' to 3' orientation.







DNA Structure

The double helix consists of:

- 2 sugar-phosphate backbones
- nitrogenous bases toward the interior of the molecule
- bases form hydrogen bonds with complementary bases on the opposite sugar-phosphate backbone
- G binds C by three hydrogen bonds
- A binds T by two hydrogen bonds

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General tips for conducting a safe and successful experiment.

1. Always keep the work area clean of any unwanted tubes, beakers and dirty dishes.

2. All reagents should be marked clearly with reagent name and concentration.

3. All samples should be numbered and labeled correctly with the names and dates.

4. Make sure that after use the reagents and chemical are placed in the fridge or freezer as required.

5. In bacterial cultures make sure the reagents and dishes are autoclaved properly and label using autoclave taps.

6. Always mark the bottom of the bacterial culture dishes and not the lid, as the lids can easily be mixed up.

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DNA extraction protocol

There are different protocols and several commercially available kits that can be used for the extraction of DNA from whole blood. This procedure is one routinely used both in research and clinical service provision and is cheap and robust. It can also be applied to cell pellets from dispersed tissues or cell cultures.

Theory

Successful nucleic acid isolation protocols have been published for nearly all biological materials. They involve the physical and chemical processes of tissue homogenisation, cell permeabilisation, cell lysis, protein degradation and removal of nucleases, protein precipitation, solubilisation of nucleic acids and finally various washing steps.

Cell permeabilisation may be achieved with the help of non-ionic (non DNA-binding) detergents such as SDS and Triton.

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Transcription





Central Dogma of Gene Expression.

Through the production of mRNA (transcription) and the synthesis of proteins (translation), the information contained in DNA is expressed.

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RNA (Ribonucleic acid)

<u>Structure:</u> Similar to that of DNA except:

- 1- it is single stranded polunucleotide chain.
- 2- Sugar is ribose
- 3- Uracil is instead of thymine

There are 3 types of RNA:

- 1- Ribosomal RNA (rRNA)
- 2- Messenger RNA (mRNA)
- 3- Transfer RNA (tRNA)

RNA are copies from DNA sequences formed by a process called

" transcription". After transcription some modifications occur to obtain the three types of RNA.

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Types of cellular RNA molecules

Туре	Relative amount (%)	Sedimentation coefficient (S)	Mass (kd)	Number of nucleotides
Ribosomal RNA (rRNA)	80	23	1.2×10 ³	3700
		16	0.55×10^{3}	1700
		5	3.6×10^{1}	120
Transfer RNA (tRNA)	15	4	2.5×10^{1}	75
Messenger RNA (mRNA)	(5)		Heterogeneous	Correction of the second se

- All RNA in E. coli (a bacterium) is made by one RNA polymerase

mRNA encodes proteins

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Types of RNA

There are three main types of RNA

1-messenger RNA

mRNA is transcribed from the DNA template and carries the <u>coding</u> informations to the site of protein synthesis.

It is the RNA which helps to carry the informations produced by the DNA during protein synthesis in all higher organisms such as humans, animals etc



1- Ribosomal RNA (rRNA):

- 80 % of total RNA in the cells are rRNA.
- rRNA are found in combination with several proteins (about 82 proteins) as component of the ribosome Which is the site of protein synthesis.
- In Eucaryotic (mammals). There are 4 size types of rRNA (5S, 5.8S, 18Ss and 28S)



Schematic model of Ribosome

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<u>rRNA</u> :- (Ribosomal RNA) is
the central component of
ribosomes. The important
function of rRNA is to <u>decode</u>
the mRNA to form amino
acids and then relate to tRNA
during translation

 It catalysis the ribosomal activity during translation phase of protein synthesis such as humans, animals etc.



3- Transfer RNA (tRNA): tRNA represents 15% of total RNA in the cell. Structure:

1- <u>Amino acid attachment site or amino</u> <u>acid acceptor</u>: which terminates with the triplet CCA.

- 2- Anticodon loop or anticodon triplet
- 3- <u>D loop and T loop</u>: contain unusual bases e.g. dihydrouracil,
 - ribothymidine or methyl

guanine



Funtions of tRNA

Structure of tRNA

RNA Synthesis



DNA & RNA Purification Quantitation

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DNA Purification Requirements

- Many applications require purified DNA.
- Purity and amount of DNA required (and process used) depends on intended application.
- Example applications:
- Tissue typing for organ transplant
- Detection of pathogens
- Human identity testing
- Genetic research

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DNA Purification Challenges

- 1. Separating DNA from other cellular components such as proteins, lipids, RNA, etc.
- 2. Avoiding fragmentation of the long DNA molecules by mechanical shearing or the action of endogenous nucleases.

Effectively inactivating endogenous nucleases (DNase enzymes) and preventing them from digesting the genomic DNA is a key early step in the purification process. DNases can usually be inactivated by use of heat or chelating agents.

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Quality is Important

- Best yields are obtained from fresh or frozen materials.
- Blood/Tissues must be processed correctly to minimize destruction of DNA by endogenous nucleases.
- DNA yield will be reduced if endogenous nucleases are active.
- Prompt freezing, immediate processing or treatment with chelating agents (such as EDTA) minimizes nuclease effects.

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Nucleic Acid Purification

There are many DNA purification methods. All must:

- 1. Effectively disrupt cells or tissues (usually using detergent)
- 2. Denature proteins and nucleoprotein complexes (a protease/denaturant)
- 3. Inactivate endogenous nucleases (chelating agents)

Purify nucleic acid target away from other nucleic acids and protein
 (could involve RNases, proteases, selective matrix and alcohol precipitations)

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Disruption of Cells/Tissues

Most purification methods disrupt cells using lysis buffer containing:

- Detergent to disrupt the lipid bilayer of the cell membrane
- Denaturants to release chromosomal DNA and denature proteins

Additional enzymes are required for lysis of some cell types:

- Gram-positive bacteria require lysozyme to disrupt the bacterial cell wall.
- Yeasts require addition of lyticase to disrupt the cell wall.
- Plant cells may require cellulase pre-treatment.

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Inactivation of Nucleases

- Chelating agents, such as EDTA, sequester Mg²⁺ required for nuclease activity.
- Proteinase K digests and destroys all proteins, including nucleases.
- Some commercial purification systems provide a single solution for cell lysis, protein digestion/denaturation and nuclease inactivation.

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Removal of RNA

- Some procedures incorporate RNase digestion during cell lysate preparation.
- In other procedures, RNase digestion is incorporated during wash steps.

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Separation of DNA from Crude Lysate

DNA must be separated from proteins and cellular debris.

Separation Methods

- Organic extraction
- Salting out
- Selective DNA binding to a solid support

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Separation by Organic Extraction

- DNA is polar and therefore insoluble in organic solvents.
- Traditionally, phenol:chloroform is used to extract DNA.
- When phenol is mixed with the cell lysate, two phases form. DNA partitions to the (upper) aqueous phase, denatured proteins partition to the (lower) organic phase.
- DNA is a polar molecule because of the negatively charged phosphate backbone.
- This polarity makes it more soluble in the polar aqueous phase.

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Separation by Salting Out

- Salts associate with charged groups.
- At high salt concentration, proteins are dehydrated, lose solubility and precipitate. Usually sodium chloride, potassium acetate or ammonium acetate are used.
- Precipitated proteins are removed by centrifugation.
- DNA remains in the supernatant.

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Ethanol Precipitation of DNA

- Methods using organic extraction or salting-out techniques result in an aqueous solution containing DNA.
- The DNA is precipitated out of this solution using salt and isopropanol or ethanol.
- Salt neutralizes the charges on the phosphate groups in the DNA backbone.
- The alcohol (having a lower dielectric constant than water) allows the sodium ions from the salt to interact with the negatively charged phosphate groups closely enough to neutralize them and let the DNA fall out of solution.

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Separation by Binding to a Solid Support

Most modern DNA purification methods are based on purification of DNA from crude cell lysates by selective binding to a support material.

Support Materials

- Silica
- Anion-exchange resin

Advantages

- Speed and convenience
- No organic solvents
- Amenable to automation/miniaturization





DNA purification column containing a silica membrane

Silica

- DNA binds selectively to silica in the presence of high concentrations of chaotropic salts (e.g., guanidinium HCl).
- Protein does not bind under these conditions.
- Silica membranes or columns are washed with an alcohol-based solution to remove the salts.
- DNA is eluted from the membrane with a low-ionic-strength solution, such as a low-salt buffer or water.

Advantages

- Fast purification
- Amenable to automation
- No centrifugation required (can use vacuum)
- No organic solvents or precipitation steps

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DNA Quantitation

Once DNA is purified, it is usually quantified. Typical quantities are in the milligrampicogram range

- gram (g)
- milligram (mg) = 10⁻³ g; 0.001g
- microgram (μ g) = 10⁻³ mg; 0.00001g
- nanogram (ng) = $10^{-3} \mu g$; $10^{-6} mg$; 0.00000001g
- picogram (pg) = 10⁻³ ng; 10⁻⁶ μg; 10⁻⁹ mg; 0.000000000001g

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Quantification Methods

Spectrophotometry: Use of light absorbance to measure concentration. Many biological substances absorb light. The spectrophometer measures absorbance of light at specific wavelengths

Most commonly used method
 DNA concentration can be calculated absorbance at 260 nm:

 A = ε × c × l (Beer-Lambert Law)
 A = absorbance
 ε = extinction coefficient
 c = concentration
 l = path length



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Summary

DNA purification methods all do the following: Disrupt cells and denature/digest of proteins Separate DNA from proteins, RNA and other cellular components Prepare a purified DNA solution **Older methods relied on laborious organic extraction** and precipitation procedures. Newer methods are faster, using selective binding of DNA to silica or magnetic beads, and are amenable to automation and miniaturization.

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Nucleic Acid Storage Requirements: Storage of DNA Specimens



Not recommended

Recommended for long-term storage in ethanol

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Quantity from UV Spectrophotometry

- DNA and RNA absorb maximally at 260 nm.
- Proteins absorb at 280 nm.

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Quality from UV Spectrophotometry

 A_{260}/A_{280} = measure of purity $(A_{260} - A_{320})/(A_{280} - A_{320})$ 1.7 - 2.0 = good DNA or RNA <1.7 = too much protein or other contaminant (?)

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Quality from Agarose Gel Electrophoresis

Genomic DNA:

- 0.6% to 1% gel, 0.125 μg/mL ethidium bromide in gel and/or in running buffer
- Electrophorese at 70–80 volts, 45–90 minutes.

Total RNA:

 – 1% to 2% gel, 0.125 μg/ml ethidium bromide in gel and/or in running buffer

Electrophorese at 80–100 volts, 20–40 minutes.

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DNA Size from Agarose Gel Electrophoresis: Compares unknown DNA to known size standards



DNA Quality from Agarose Gel Electrophoresis

Human Whole Blood DNA



Lambda DNA marker

> Lambda DNA cut with Hind III marker

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Whole blood genomic DNA

Cultured Cell DNA and RNA



100 50 25 ng Genomic DNA markers

Degraded RNA

mRNA = background smear high → low MW 5S rRNA, tRNA, and other small RNA molecules



Lavender or purple top tube, it contains <u>EDTA</u> (the potassium salt, or K₂EDTA). This is a strong anticoagulant. Lavender top tubes are generally used when whole blood is needed for analysis.



Pasteur Pipette



Permanent Marker



Centrifuge Tube 50 ml



Rack







Pipettes and Tips





Biohazard Bags





DNA Blood Kit- Qiagen















.ocated Primer Pairs								-	
55 Primary Pairs, 269 Located, 2 Alternates			_						
200 400	Upper Primer: 18-mer 5' CCGGAGG Lower Primer: 24-mer 5' CCCCAAC)	GCCATCAGTG ATCTACGTCCCC		10p0	Score 22.5	dTm 4.5	<u>Ta-Tm</u> 24.1	C Length 515bp	
	DNA 250 pM, Salt 50 mM	Upper Primer	Lower Primer		_	22.2	4.8	21.8	415bp
						21.5	1.5	24.5	670bp
	Primer Tm Brimer Overall Stability	58.3 ℃ -39.9 kc/m 59.,76	60.3 ℃ 47.5 koden			20.3	5.4	21.5	555bp
	Primer Location		11061083			17.5	1.2	24.3	739bp
						13.1	6.4	23.6	461bp
	Product Tm - Primer Tm	25.7	7 °C			12.2	10.4	27.7	816bp
	Primers Tm Difference	2.0	°C 1°C			11.9	4.8	22.2	408bp
	optimal Ameaning Temperature	01.4	+ 0			11.0	2.0	25.7	1.048Kb
	Product Length	104	8 bp			10.4	2.3	25.0	892bp
	Product Tm (%GC Method)	84.0)°C			9.6	5.6	27.9	823bp
	Product GC Content Product Tm at 6xSSC	60.3% 105.6 ℃			•••••••••••••••••••••••••••••••••••••••	8.9	11.8	29.6	838bp
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Primer Select program of DNA-Star Package



Sequencing data using Chromas program

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	1	Z	5		46	CAG	GGC	ACC	ATC	CAC	TTC	GAG	CAG	AAG	GAA	AAT	GGG	CCA	GTC	ATG	90
					16	Q	G	т	I	н	F	Е	Q	к	Е	N	G	P	v	м	30
					91 31	GTA V	TCG S	GGG G	TCC S	ATT I	TCA S	GGA G	TTG L	GCC A	GAA E	GGC G	GAT D	CAT H	GGA G	TTC F	135 45
10000					136 46	CAT H	GTC V	CAT H	CAG Q	TTT F	GGA G	GAT D	AAC N	ACA T	CAA Q	GGC G	TGT C	ACC T	AGT S	GCA A	180 60
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2500 2000	-				226	GAT	CAA	GAG	AGG	CAT	- GTT	- GGA	GAC	CTG	GGC	AAT	GTG	АСТ	GCT	GGC	270
1500				1500	76	D	Q	Е	R	н	v	G	D	L	G	N	v	т	А	G	90
1000	-		_	1000	271 91	AAA K	GAT D	GGT G	GTG V	GCC A	ATT I	GTG V	TCT S	ATT I	GAA E	GAT D	CCT P	GTG V	ATC I	TCA S	315 105
750	-		\equiv	700	316 106	CTC L	TCA S	GGA G	GAC D	CAT H	TCC S	ATC I	ATT I	GGC G	CGC R	ACA T	ATG M	GTG V	GTC V	CAT <u>H</u>	360 120
500	-			500 400	361 121	GAA E	AAA K	CCA P	GAT D	GAC D	TTG L	GGC G	AAA K	GGT G	GGA G	AAT N	GAA E	GAA E	AGT S	ACA T	405 135
250	-		-	300 200	406 136	AAG K	ACG T	GGA G	AAT N	GCT А	GGA G	AGT S	CGT R	CTG L	GCC A	TGC C	GGC G	GTG V	ATT I	GGG G	450 150
				100	451 151	ATC I	GCC A	CAA Q	ТАА *	gca	ttc	cct	agg	acg	tgg	tct	gag	tcc	tag	taa	495 165
					496	ctc	atc	tgt	tgt	ctt	gct	53	13								

PCR and Nucleotide sequence of the cloned gene and the predicted amino acid sequence and primary protein structure







2ry structure annotation sites of the cSOD1 sequence



Predicted 3D structure of the cSOD1





Thank you for your attention