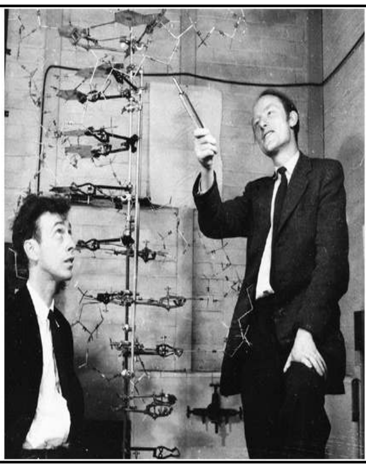
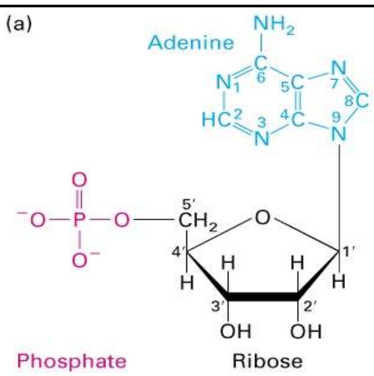


1

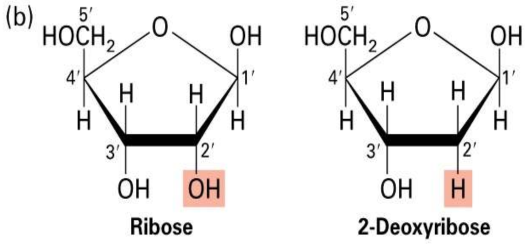
Figure 1.1 A brief history of genetics.

1865	Genes are particulate factors
1903	Chromosomes are hereditary units
1910	Genes lie on chromosomes
1913	Chromosomes contain linear arrays of genes
1927	Mutations are physical changes in genes
1931	Recombination is caused by crossing over
1944	DNA is the genetic material
1945	A gene codes for a protein
1953	DNA is a double helix
1958	DNA replicates semiconservatively
1961	Genetic code is triplet
1977	DNA can be sequenced
1997	Genomes can be sequenced



Adenosine 5′-monophosphate (AMP)

3



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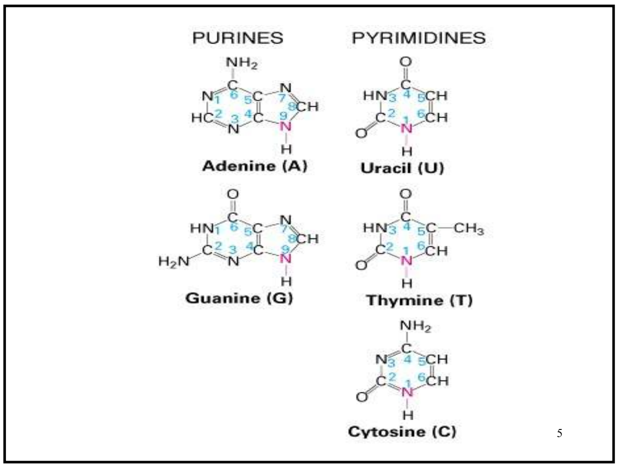
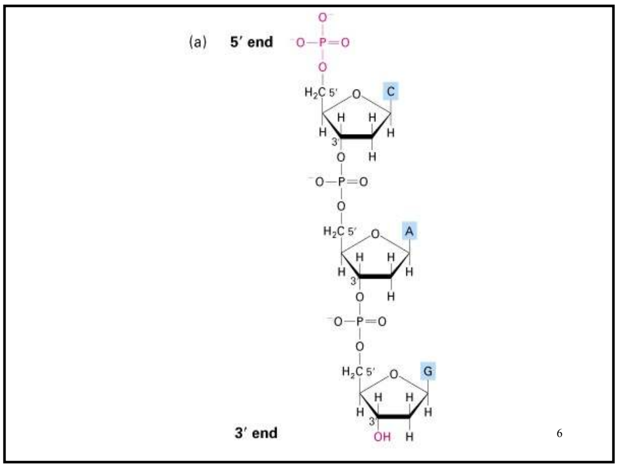
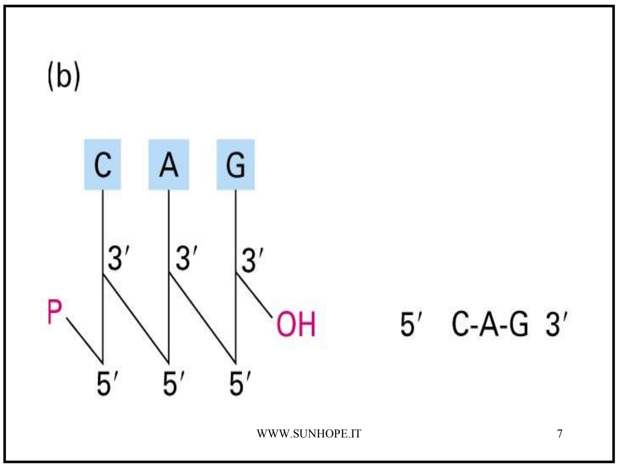
4







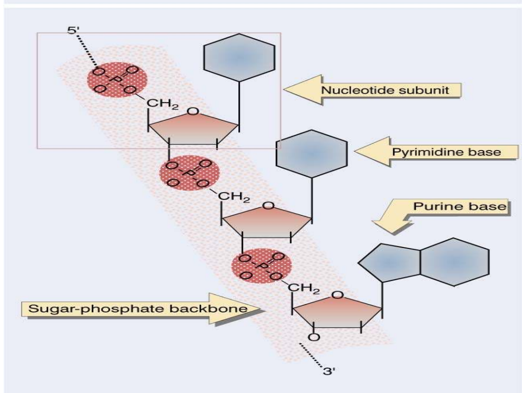


Figure 1.5 A polynucleotide chain consists of a series of 5'-3' sugar-phosphate links that form a backbone from which the bases protrude.

Figure 3.1 DNA content of the haploid genome is related to the morphological complexity of lower eukaryotes, but varies extensively among the higher eukaryotes. The range of DNA values within a phylum is indicated by the shaded area.

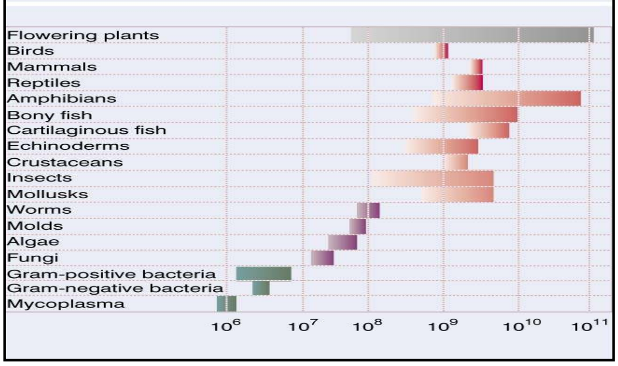


Figure 3.2 The minimum genome size found in each phylum increases from prokaryotes to mammals.

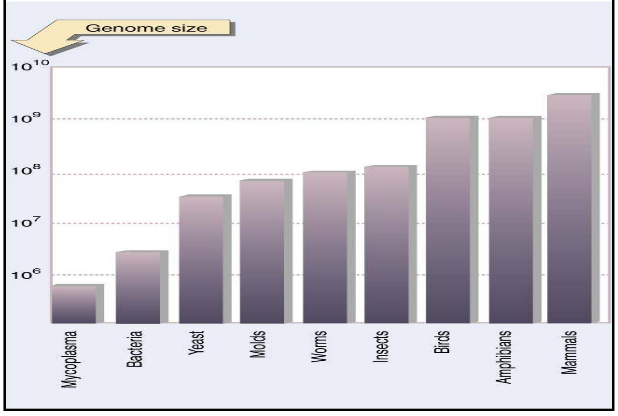


Figure 1.6 The double helix maintains a constant width because purines always face pyrimidines in the complementary A–T and G–C base pairs. The sequence in the figure is
T–A
C–G
A–T
G–C

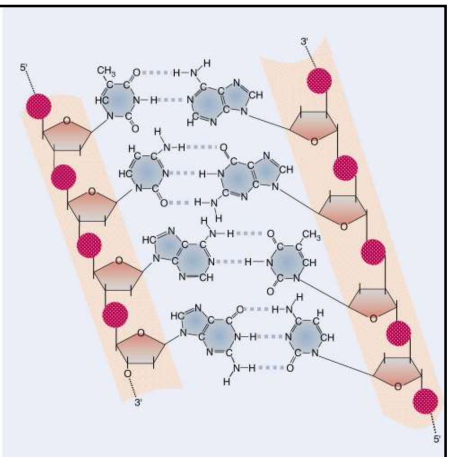
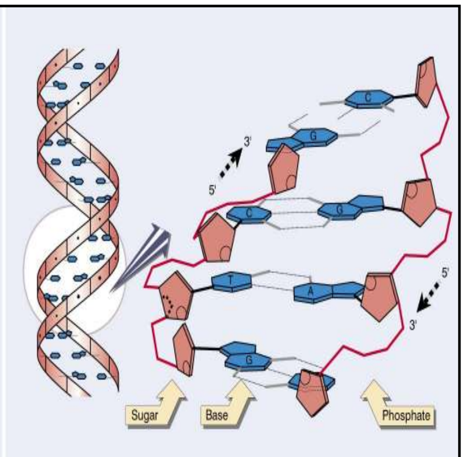
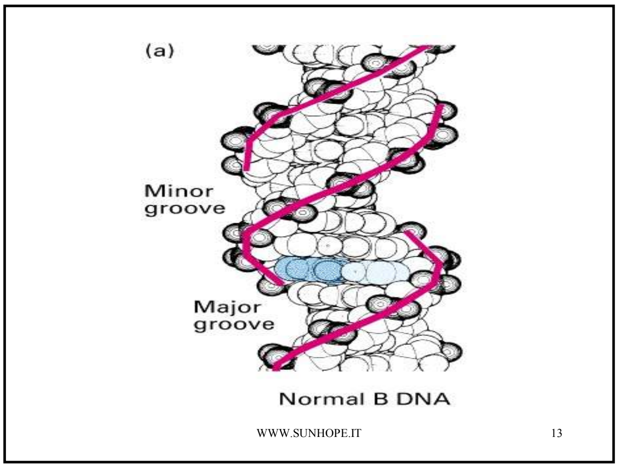


Figure 1.7 Flat base pairs lie perpendicular to the sugar-phosphate backbone.




(a)
Minor groove
Major groove
Normal B DNA
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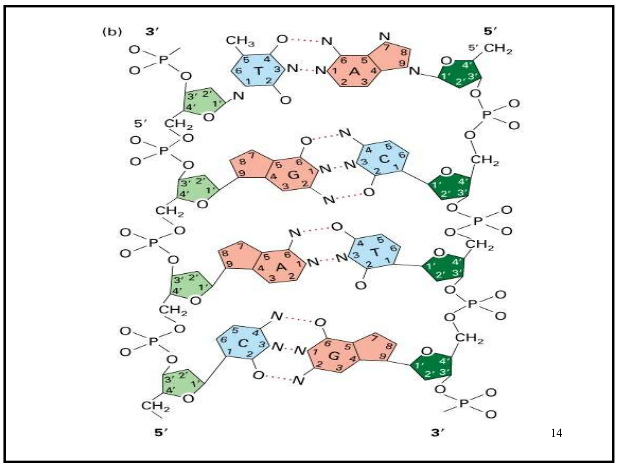
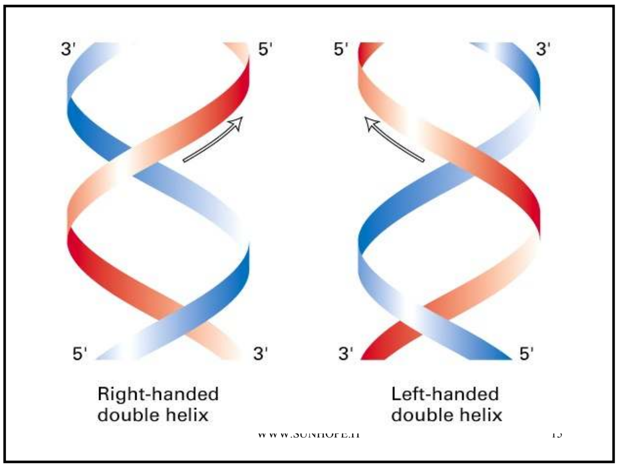
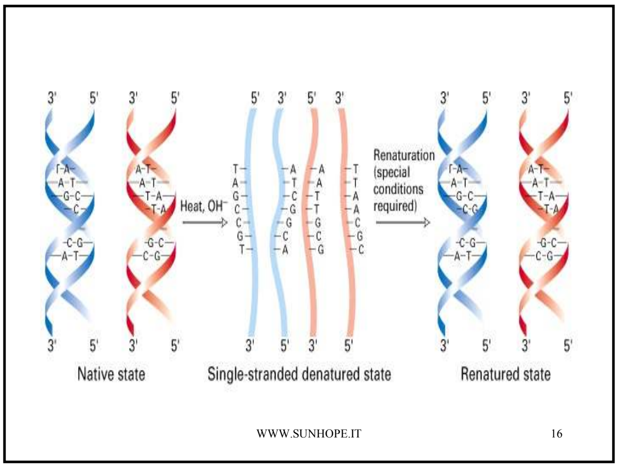
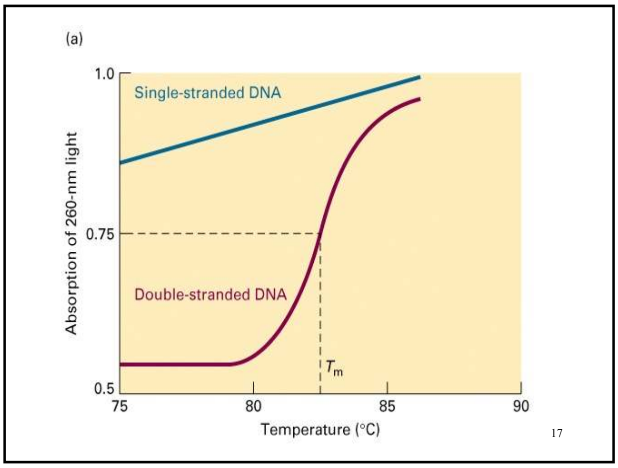

(b)
3′
5′
5′
3′
14


3'
5'
5'
3'
Right-handed double helix
Left-handed double helix


Heat, OH⁻
Renaturation (special conditions required)
Native state
Single-stranded denatured state
Renatured state
WWW.SUNHOPE.IT 16



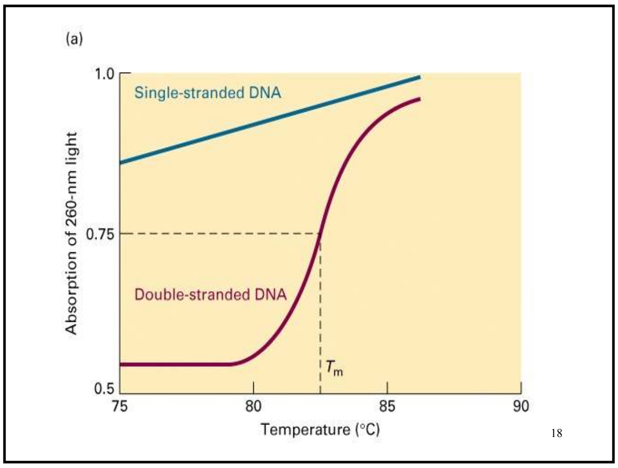


Figure 3.4 A DNA reassociation reaction is described by the $C_0t_{1/2}$

Rate of reaction

The reaction follows the second order equation

$$\frac{dC}{dt} = -kC^2$$

C is the concentration of DNA that is single-stranded at time t
k is a reassociation rate constant.

Progress of reaction

Integrate the rate equation between the limits:
initial concentration of DNA = C_0 at time $t = 0$;
concentration remaining single stranded = C after time t

$$\frac{C}{C_0} = \frac{1}{1 + k.C_0t}$$

Critical parameter is $C_0t_{1/2}$

When the reaction is half complete at time $t = 1/2$

$$\frac{C}{C_0} = \frac{1}{2} = \frac{1}{1 + k.C_0t_{1/2}}$$

Therefore $$C_0t_{1/2} = \frac{1}{k}$$

Figure 3.5 Rate of reassociation is inversely proportional to the length of the reassociating DNA.

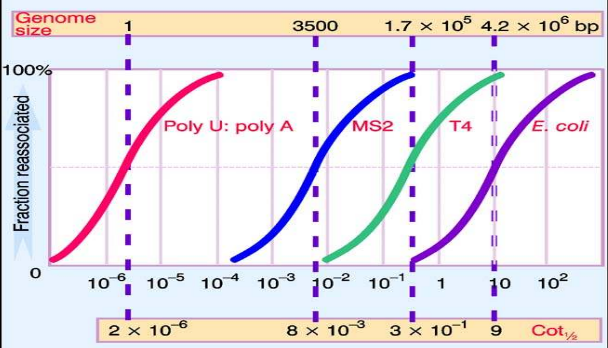
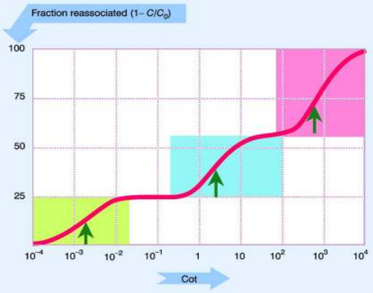
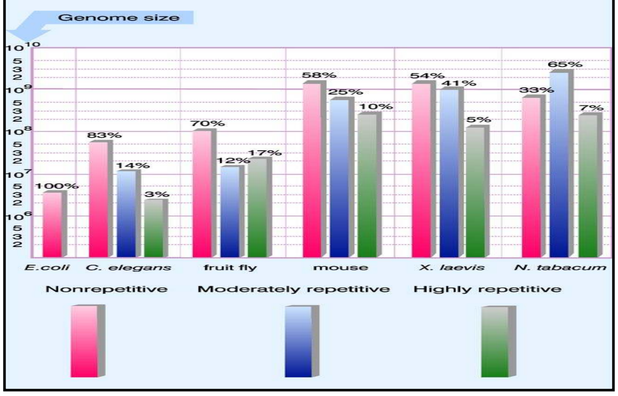


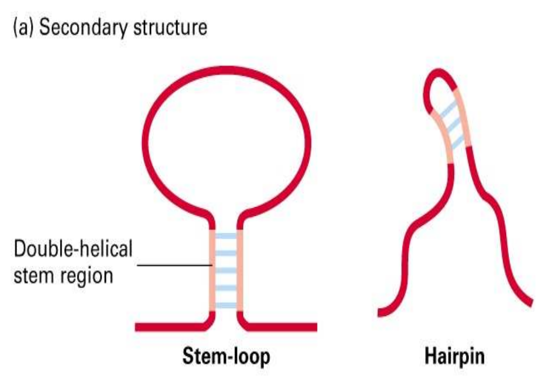
Figure 3.6 The reassociation kinetics of eukaryotic DNA show three types of component (indicated by the shaded areas). The arrows identify the $Cot_{1/2}$ values for each component.



	Fast component	Intermediate component	Slow component
Percent of genome	25	30	45
$Cot_{1/2}$	0.0013	1.9	630
Complexity, bp	340	6.0×10^5	3.0×10^8
Repetition frequency	500,000	350	1

Figure 3.8 The proportions of different sequence components vary in eukaryotic genomes. The absolute content of nonrepetitive DNA increases with genome size, but reaches a plateau at $\sim 2 \times 10^9$ bp.





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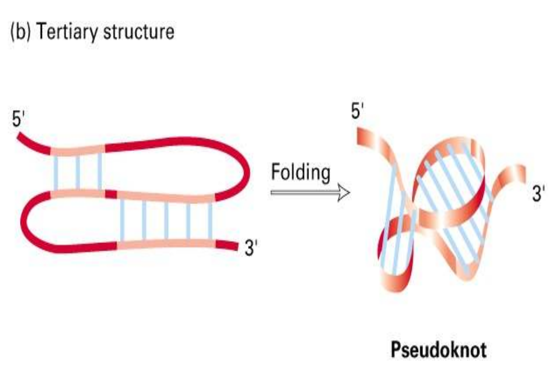
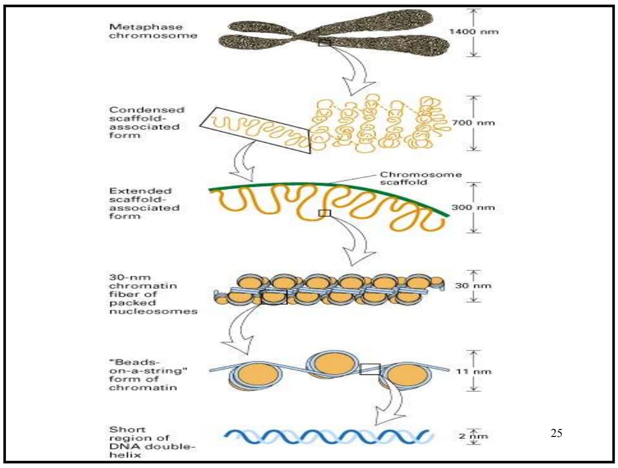


WWW.SUNHOPE.IT 24



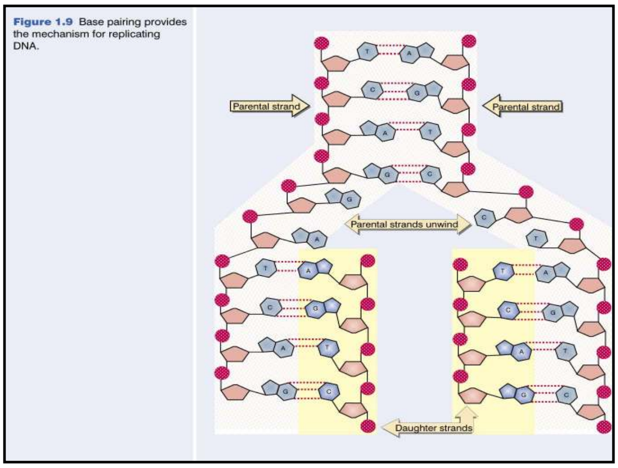


Figure 1.9 Base pairing provides the mechanism for replicating DNA.

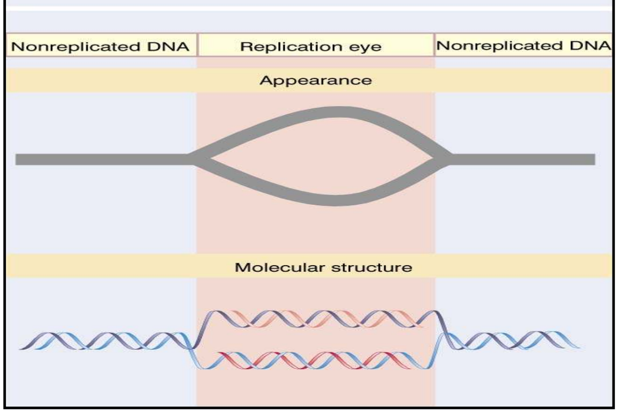


Figure 12.1 Replicated DNA is seen as a replication eye flanked by nonreplicated DNA.

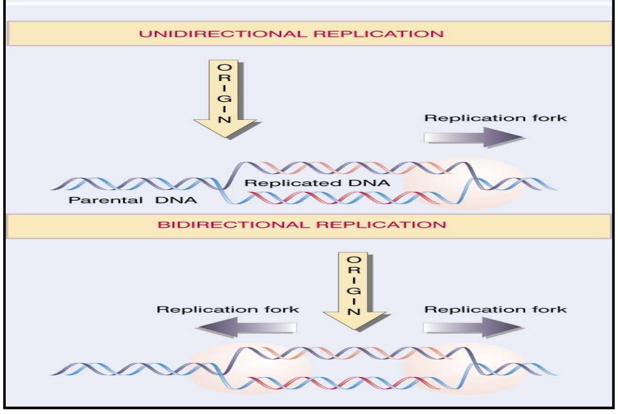
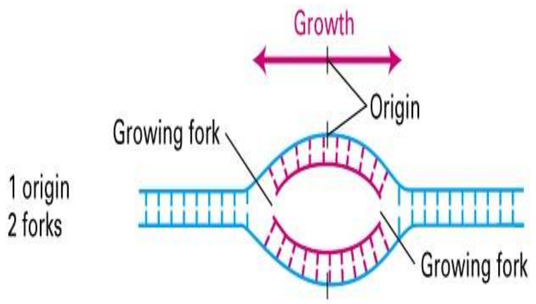
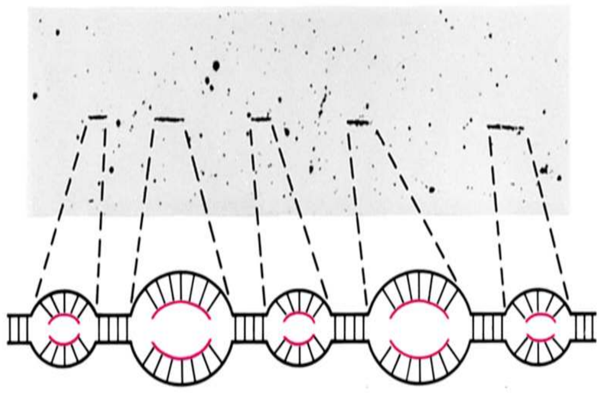


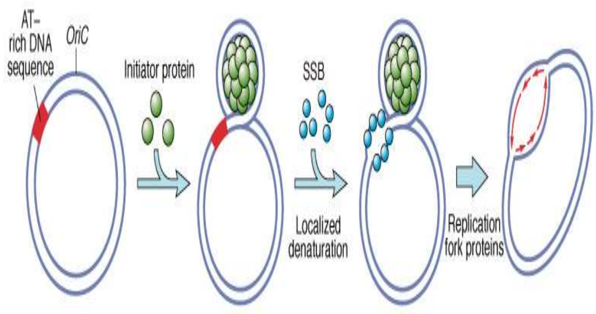
Figure 12.2 Replicons may be unidirectional or bidirectional, depending on whether one or two replication forks are formed at the origin.

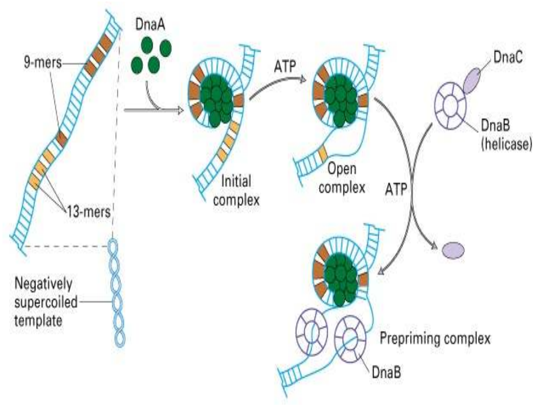
(c) Bidirectional growth of both strands from one origin

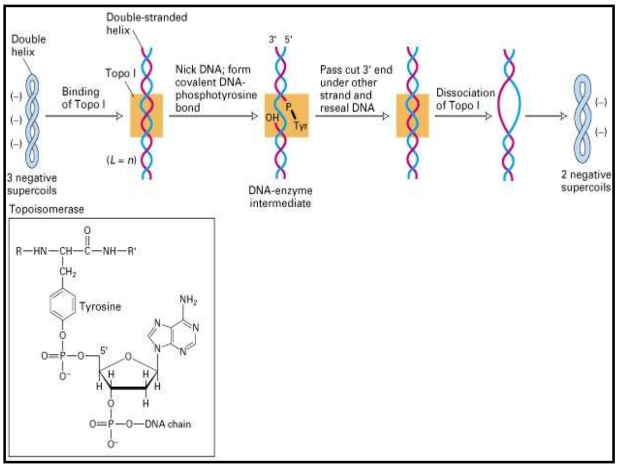


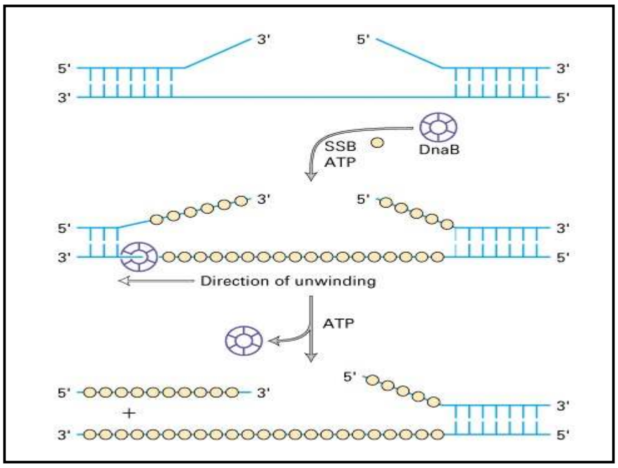


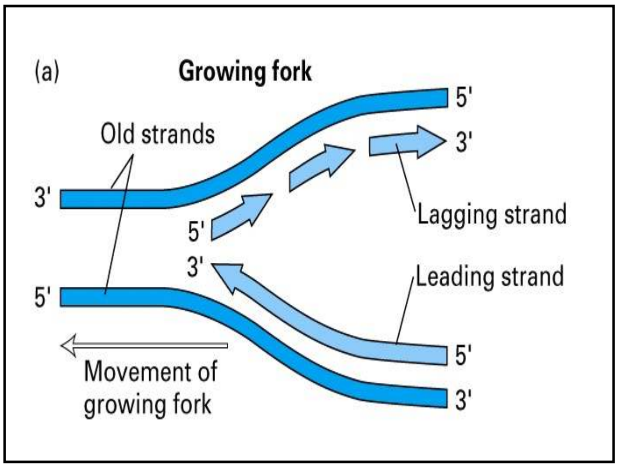
Micrograph courtesy of Joel Huberman.

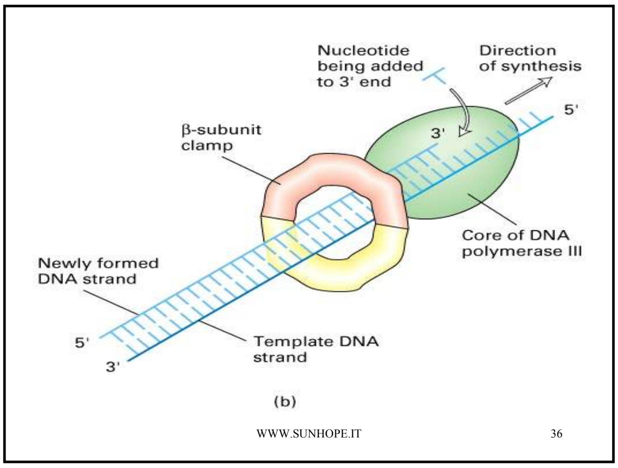





Double helix
3 negative supercoils
Binding of Topo I
Double-stranded helix
Topo I
(L = n)
Nick DNA; form covalent DNA-phosphotyrosine bond
DNA-enzyme intermediate
Pass cut 3' end under other strand and reseal DNA
Dissociation of Topo I
2 negative supercoils
Topoisomerase
Tyrosine
DNA chain


SSB
ATP
DnaB
Direction of unwinding
ATP


(a)
Growing fork
Old strands
Lagging strand
Leading strand
Movement of growing fork


Nucleotide being added to 3' end
Direction of synthesis
β-subunit clamp
Core of DNA polymerase III
Newly formed DNA strand
Template DNA strand
(b)
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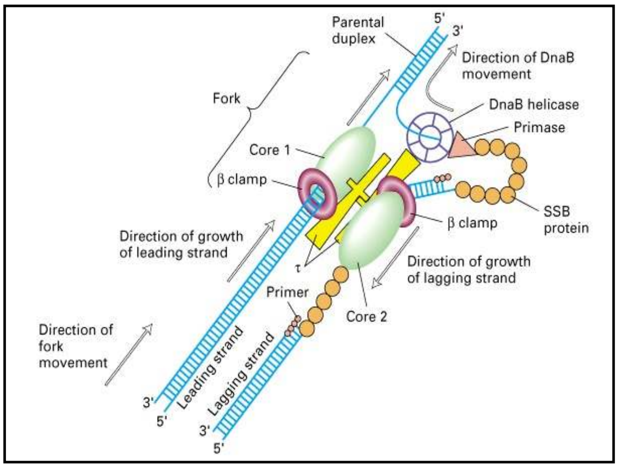
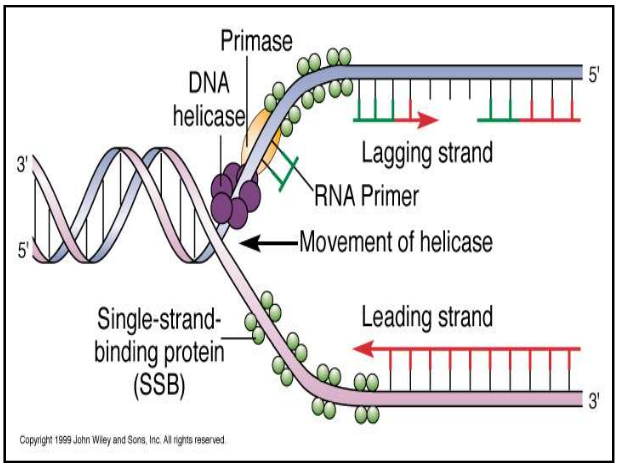
36


Parental duplex
5'
3'
Direction of DnaB movement
Fork
DnaB helicase
Primase
Core 1
β clamp
β clamp
SSB protein
Direction of growth of leading strand
τ
Direction of growth of lagging strand
Primer
Core 2
Direction of fork movement
Leading strand
Lagging strand
3'
5'
3'
5'


Primase
DNA helicase
5'
Lagging strand
3'
RNA Primer
5'
Movement of helicase
Single-strand-binding protein (SSB)
Leading strand
3'
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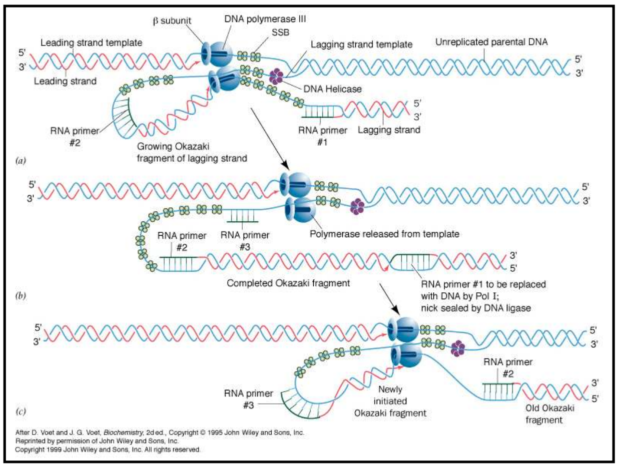
β subunit
DNA polymerase III
SSB
Leading strand template
Lagging strand template
Unreplicated parental DNA
Leading strand
DNA Helicase
RNA primer #2
Growing Okazaki fragment of lagging strand
RNA primer #1
Lagging strand
(a)
RNA primer #2
RNA primer #3
Polymerase released from template
Completed Okazaki fragment
RNA primer #1 to be replaced with DNA by Pol I; nick sealed by DNA ligase
(b)
RNA primer #2
RNA primer #3
Newly initiated Okazaki fragment
Old Okazaki fragment
(c)
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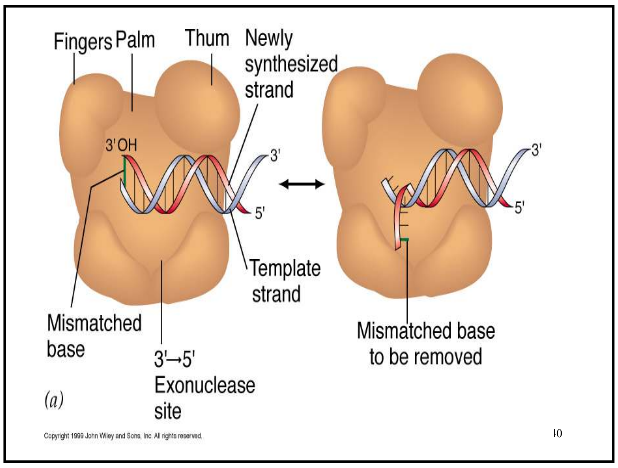
Fingers
Palm
Thum
Newly synthesized strand
3'OH
3'
5'
3'
5'
Template strand
Mismatched base
3'→5' Exonuclease site
Mismatched base to be removed
(a)
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10


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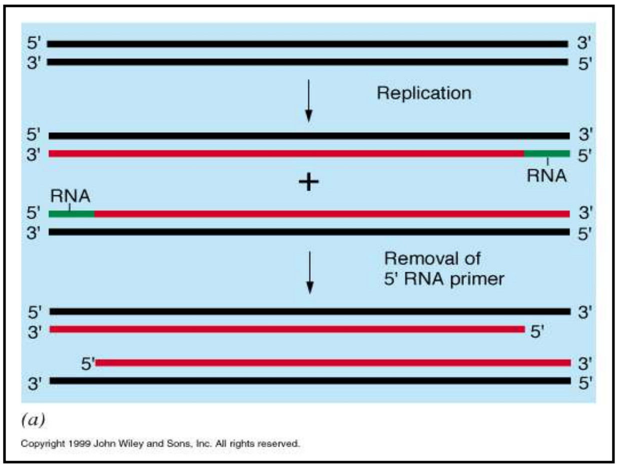
5'
3'
Replication
RNA
+
Removal of
5' RNA primer
(a)
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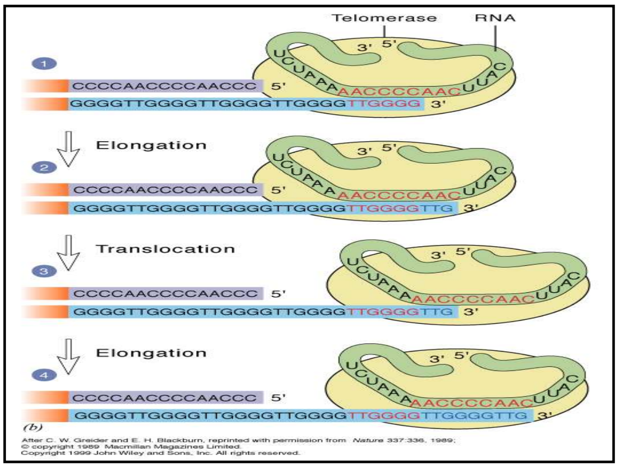
Telomerase
RNA
1
CCCCAACCCCAACCC 5'
GGGGTTGGGGTTGGGGTTGGGGTTGGGG 3'
Elongation
2
Translocation
3
Elongation
4
GGGGTTGGGGTTGGGGTTGGGGTTGGGGTTGGGGTTG 3'
(b)
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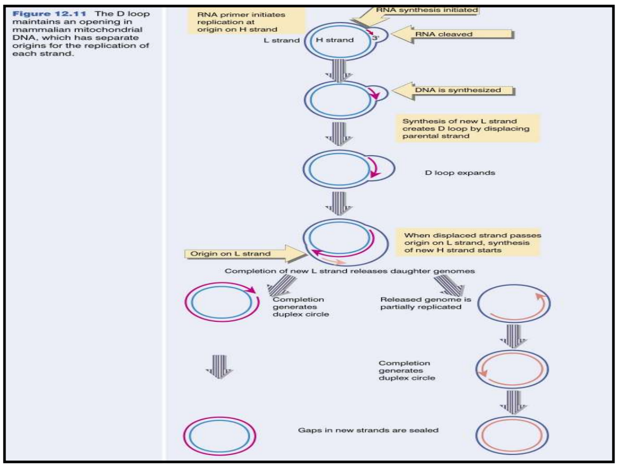
Figure 12.11 The D loop maintains an opening in mammalian mitochondrial DNA, which has separate origins for the replication of each strand.
RNA primer initiates replication at origin on H strand
RNA synthesis initiated
L strand
H strand
RNA cleaved
DNA is synthesized
Synthesis of new L strand creates D loop by displacing parental strand
D loop expands
When displaced strand passes origin on L strand, synthesis of new H strand starts
Origin on L strand
Completion of new L strand releases daughter genomes
Completion generates duplex circle
Released genome is partially replicated
Completion generates duplex circle
Gaps in new strands are sealed