Principles of MOLECULAR BIOLOGY

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Chapter 8 DNA Replication

- DNA replication is semiconservative
 - 2 parental strands separate allowing each separated strand to serve as a template
 - Each daughter molecule has one parental strand and one newly synthesized strand

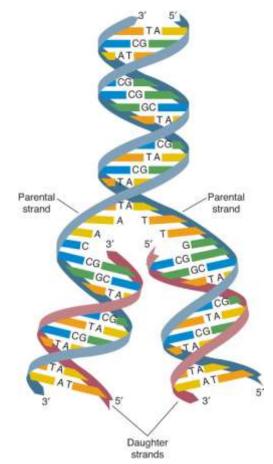


Figure 08.01: Watson-Crick model of DNA replication.

- 2 alternative models
 - Conservative replication
 - DispersiveReplication

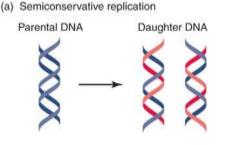


Figure 08.02A: Three models of replication. (a) Semiconservative DNA replication.

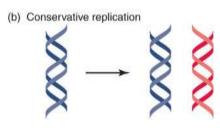


Figure 08.02B: Three models of replication. (b) Conservative DNA replication.

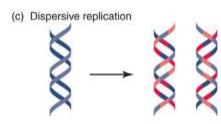


Figure 08.02C: Three models of replication. (c) Dispersive DNA replication.

- Conservative Replication
 - Parental strands unwind at replication site to allow the sequence to be read by the DNA polymerase and then rewinds
 - One of the 2 molecules contains both original strands
 - Other is made of 2 new strands

- Dispersive Replication
 - Each strand of the daughter molecules is interspersed with sections of both old and new DNA

Meselson and Stahl experiment

- Used ¹⁵N heavy nitrogen isotope to label bacterial DNA
- After uniform labeling bacteria were transferred to a "light" medium with ¹⁴N
 - Removed samples at different times
 - Extracted DNA
 - Separated molecules using CsCl equilibrium density centrifugation
- Semi-conservative replication model is the only one consistent with results

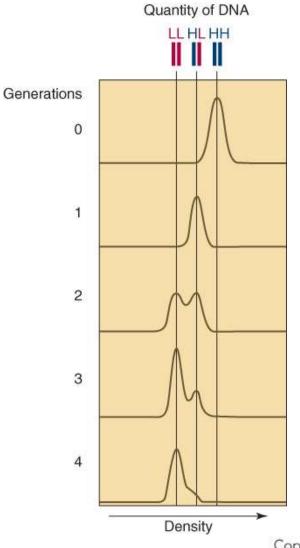
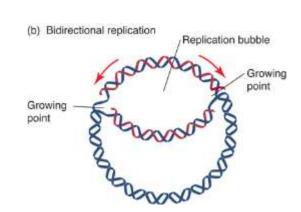


Figure 08.03: Meselson-Stahl experiment showing semiconservative DNA replication.

- Bacterial and eukaryotic DNA replication is bidirectional
 - θ-structure can be explained by unidirectional or bidirectional replication
 - Labeling expt.
 confirmed that it is bidirectional



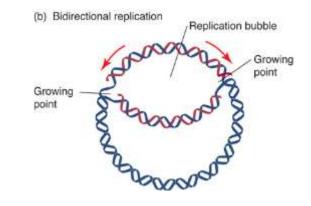


Figure 08.05A: Two alternate methods of replication. (a) In unidirectional replication a single growing point moves in the direction shown by the red arrow.

Figure 08.05B: Two alternate methods of replication. (b) In bidirectional replication two growing points move in opposite directions, as shown by the red arrows.

- Bidirectional replication means that one chain grows $5' \rightarrow 3'$ but other strand is $3' \rightarrow 5'$
- Problem: No DNA polymerase catalyzes in that direction
- The DNA strand that grows in an overall
 3'→5' direction is formed by joining short fragments

In 1968 Reiji Okazaki proposed 2 models

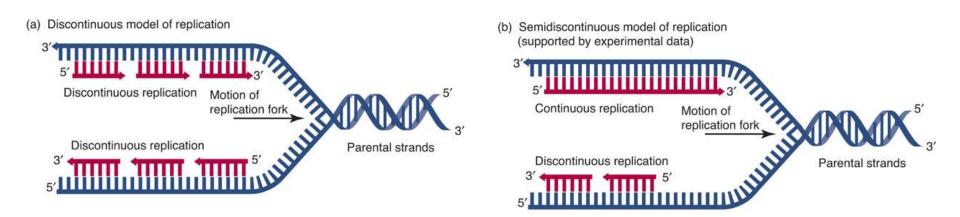


Figure 08.07: Models proposed by Reiji Okazaki to explain in vivo DNA replication. Parental strands are shown in blue and newly replicated strands are shown in red.

- Semi-discontinuous replication
 - Forms Okazaki fragments
 - Lags behind the continuously replicating strand
 - Leading strand
 - Lagging strand
- DNA ligase connects adjacent Okazaki fragments

RNA serves as a primer for Okazaki fragment synthesis

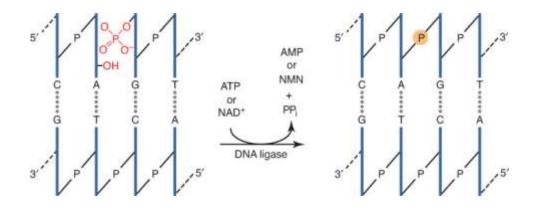
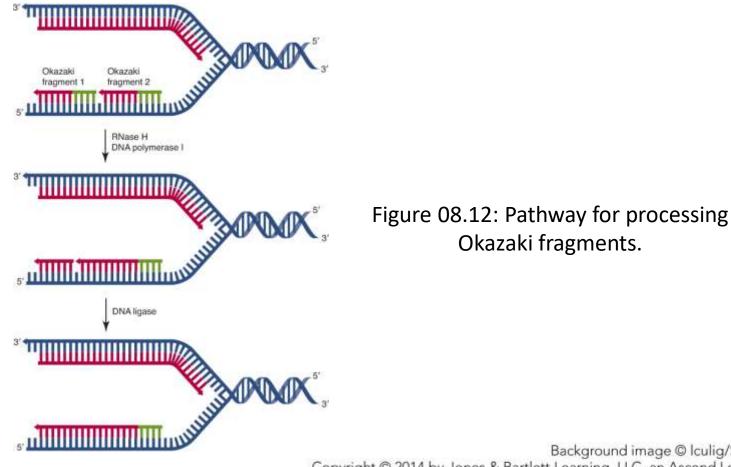


Figure 08.11: RNA primers for Okazaki fragments. The synthesis of Okazaki fragments is primed by short RNA segments.

Processing Okazaki fragments



- E. coli replication apparatus stages
 - Initiation: the assembly of the replication apparatus at a unique site
 - Elongation: leading strand is synthesized continuously. Lagging strand is synthesized discontinuously
 - Termination: the 2 replication forks meet about halfway around the bacterial chromosome

Replicon Model

- 2 specific components: initiator protein and a replicator (a specific set of DNA sequences)
- Specific site at which replication is initiated
 - Origin of replication (*ori*)
 - Eukaryotic chromosomes require many origins of replication

- E. coli chromosomal replication begins at *oriC*
 - Right side of sequence
 - Five 9bp sites (R1-R5) known as Dna A boxes
 - Left side of sequence
 - DNA unwinding element (DUE) with three 13bp AT-rich elements
 - Multiple GATC site

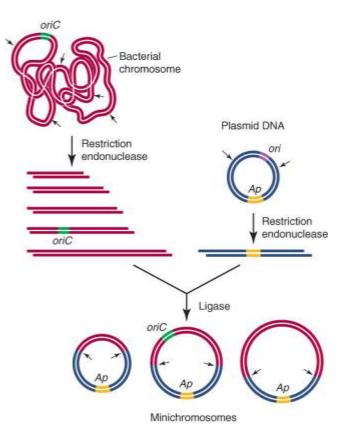


Figure 08.13: Isolation of the E. coli replication origin oriC.

(Adapted from Kornberg, A., and Baker, T. A. 1991. DNA Replication (2nd ed). W. H. Freeman and Company.)

- Four proteins are critical in the DNA replication initiation process
- DnaA initiator
- DnaB helicase
- DnaC loader
- DnaG primase

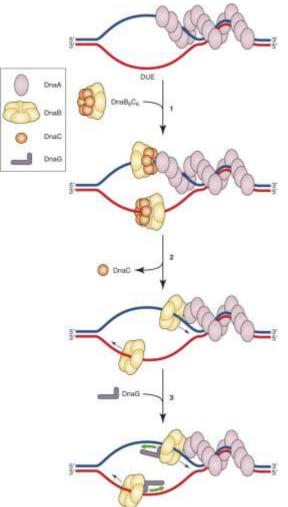


Figure 08.15: Model for loading DnaB onto single strands at DUE.

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(Adapted from Mott, M. et al. 2008. Cell 134:623-634.)

Several enzymes act together at the replication fork

- DNA polymerase I-required
- DNA polymerase II-not essential
- DNA polymerase III-required

- Purified DNA polymerase III is very slow and dissociates from its DNA frequently
 - Enzymes that remain tightly associated with their template are said to be **highly processive**

- DNA polymerase III holoenzyme has three distinct subassemblies
 - Core polymerase
 - Clamp loader
 - Sliding clamp

- The core polymerase has one subunit with 5'3" polymerase activity and another with 3'5' exonuclease activity
 - Core polymerase (previously DNA PolIII)
 - α-subunit

$$-5' \rightarrow 3'$$
 chain growth

• ε-subunit

$$-3' \rightarrow 5'$$
 exonuclease activity

• θ-subunit

-Stimulates ε-subunit but not essential

The sliding clamp forms a ring around DNA, tethering the remainder of the polymerase holoenzyme to the DNA

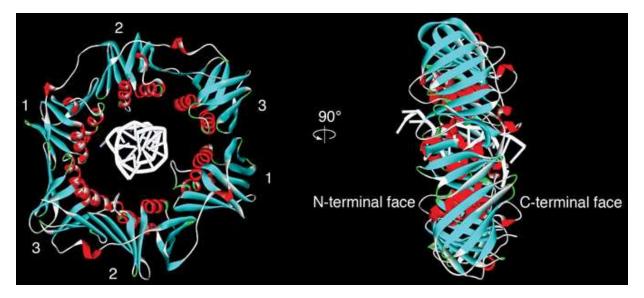


Figure 08.18: Structure of an E. coli sliding clamp on DNA. The two subunits are shown as solid ribbons. α -Helices are red, β -structures are cyan, and turns are white.

(Protein Data Bank ID: 3BEP. Georgescu, R. E., et al. 2008. Cell 132:43–54.)

The clamp loader places the sliding clamp around DNA

• Uses energy provided by ATP to load the sliding clamp onto a DNA template-primer with a 5' overhang

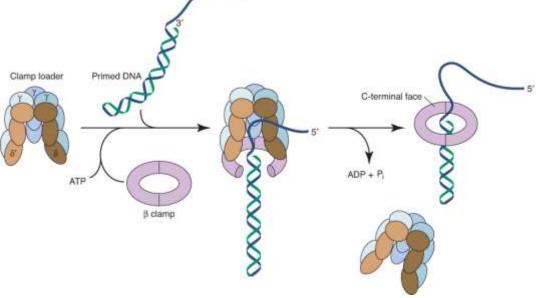


Figure 08.19: The clamp loading cycle.

(Adapted from Pomerantz, R. T., and O'Donnell, M. 2007. Trends Microbiol 15:156–164.)

- The replisome catalyzes coordinated leading and lagging strand DNA synthesis
- The trombone model of replication
- Lagging strand loops out
 - Allows the pair of core polymerases to coordinate leading and lagging strand synthesis
- Requires
 - DNA Pol III holoenzyme
 - Helicase
 - Primase
 - Single-stranded DNA binding protein
- This is the **replisome**

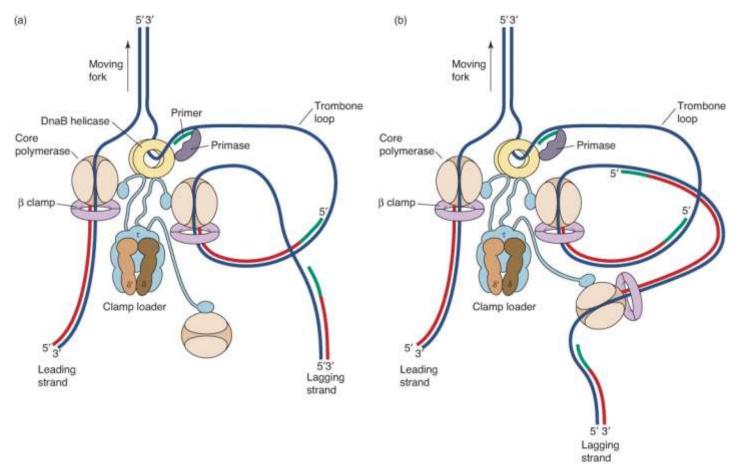


Figure 08.20: DNA replisome with three core polymerases.

(Adapted from McInerney, P. et al. 2007. Mol Cell 27:527–538.)

There are 3 steps for lagging strand synthesis

- 1. Core polymerase extends the Okazaki fragment and clamp loader loads on a new sliding clamp
- 2. Core polymerase dissociates upon reaching an adjacent double-stranded duplex
- 3. Core polymerase binds to the new sliding clamp and synthesizes DNA
- The trombone loop is reset after each Okazaki fragment has been completed

- E. coli DNA replication terminates when the two growing forks meet in the terminus region
- Terminus utilization substance (Tus) binds to the termination site (Ter site)

 Arrests the progress of the replication fork
 Topisomerase IV and recombinase separate newly formed sister chromosomes

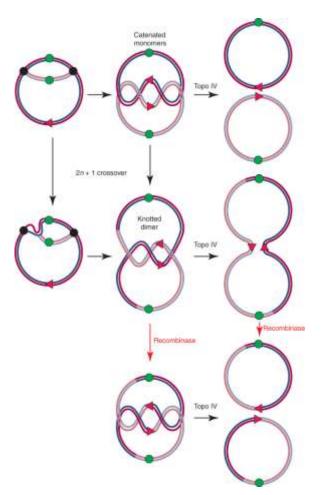


Figure 08.24: Links between replication, recombination, and chromosome segregation.

(Adapted from Sherratt, D.J., Lau, I.F., and Barre, F.X. 2001. Curr Opin Microbiol 4:653–659.)

- The SV40 DNA replication system is a good model for *in vitro* eukaryotic DNA replication
- 6 large T antigen molecules form a helicase that interacts with the origin of replication
 - Recruits DNA polymerase α -primase (Pol α)
 - Forms RNA primers 8-12 nucleotides long then incorporates 15-25 deoxyribonucleotides before dissociating
 - Pol α generates an RNA primer joined to a short DNA segment (initiator DNA)

Additional proteins required for replication:

- 1. DNA Pol δ
 - Catalyzes leading and lagging strand synthesis
- PCNA (proliferating cell nuclear antigen) 2.
 - The eukaryotic sliding clamp
- **Replication Factor C** 3.
 - Eukaryotic clamp loader
- Flap endonuclease (FEN1) 4.
 - Acts during Okazaki fragment maturation
- 5. DNA ligase
 - seals the nick between adjacent Okazaki Background image © Iculig/ShutterStock, Inc. fragments Copyright © 2014 by Jones & Bartlett Learning, LLC, an Ascend Learning Company

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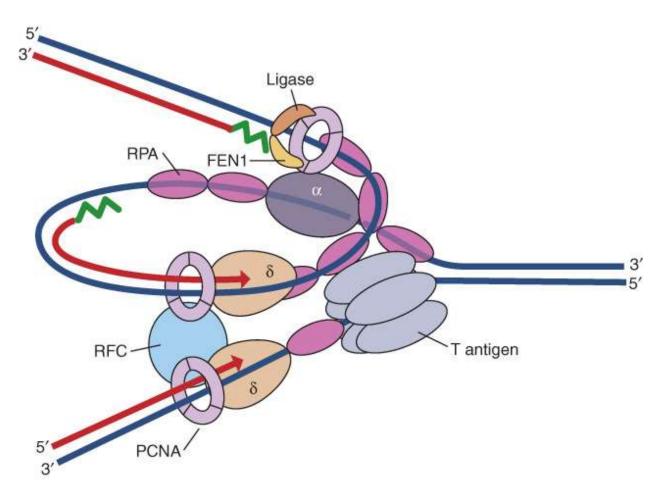


Figure 08.27: Model for the organization of proteins and enzymes at SV40 replication fork.

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(Adapted from Stillman, B. 2008. Mol Cell 30:259–260.)

Eukaryotic replication machinery must replicate long linear duplexes with multiple origins of replication

- Requires multiple origins of replication
- Requires 3 different DNA polymerases
- Linear eukaryotic chromosomes require telomerase to form their ends

Eukaryotic DNA replication initiates at multiple sites

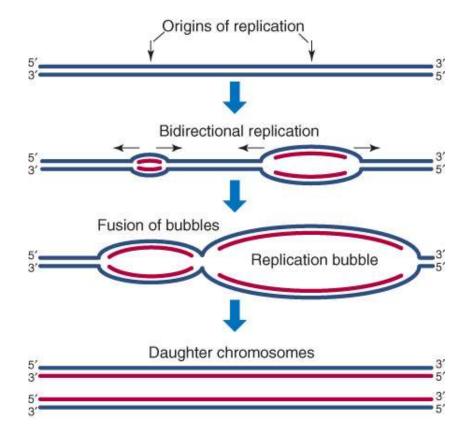


Figure 08.29: Schematic showing the fusion of a pair of replication bubbles.

Eukaryotic cells must ensure that each origin fires once and only once in each cell cycle

- Origin Recognition Complex (ORC)

- 6 protein subunits
- When bound to DNA recruits Cdc6 which is degraded once initiation is completed

- Three DNA polymerases are necessary for eukaryotic replication
- 1. Pol α
 - Responsible for forming RNA primer and initiator DNA
- 2. Pol δ
 - Responsible for lagging strand synthesis
- 3. Pol ε
 - Responsible for leading strand synthesis

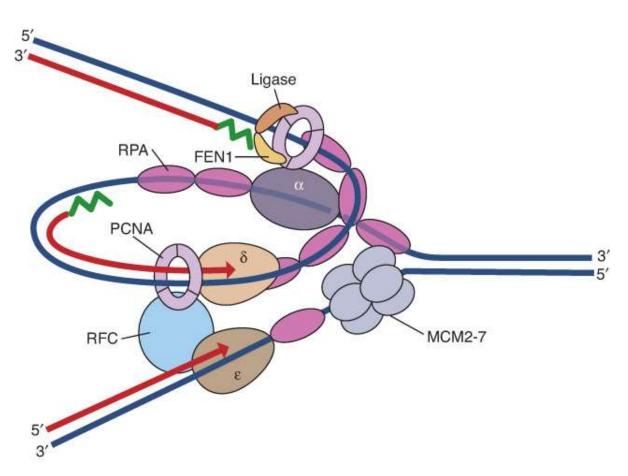


Figure 08.33: Simplified model for the organization of proteins and enzymes at the eukaryotic replication fork.

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(Adapted from Stillman, B. 2008. Mol Cell 30:259–260.)

- A terminal transferase-like enzyme is required for telomere formation
- Eukaryotic DNA polymerases work by extending a preformed primer and therefore cannot copy the very end of a linear duplex

- Telomerase uses an RNA template to add nucleotide repeats to chromosome ends
- Contains an RNA that acts as a template for telomeric DNA synthesis.
 - Acts as an RNA dependent DNA polymerase that supplies its own template RNA

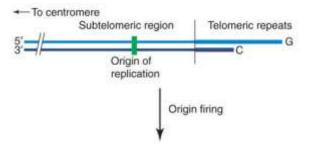


Figure 08.37A: Leading strand problem. (a) The telomere G-rich strand ends in a 3'-single strand that overhangs the C-rich strand.

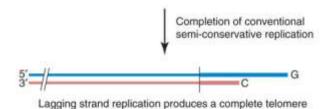


Figure 08.37C: Leading strand problem. (c) Synthesis of lagging strands does not necessarily present a problem for the replication machinery.

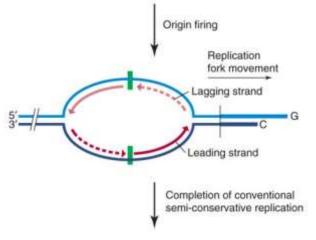


Figure 08.37B: Leading strand problem.(b) Semiconservative replication initiates at origins internal to the telomeric repeats.



Leading strand replication produces a blunt end that is missing sequences in the 3' overhang

Figure 08.37D: Leading strand problem. (d) Synthesis of leading strands introduces a problem because replication stops at the 5'end of the C-rich template.

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(Adapted from Chakhparonian, M., and Wellinger, R.J. 2003. Trends Genet 19:439–446.)

Telomerase plays an important role in solving the end-replication problem

- Leading strand replication presents a serious problem
 - Leading strand replication produces a blunt end with a loss of sequence information

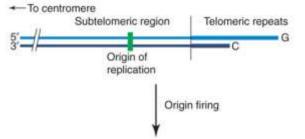


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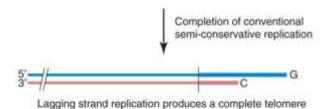


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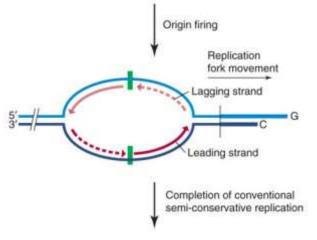


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Telomerase function

- 1. A strand specific DNA 5' \rightarrow 3' exonuclease removes nucleotides to generate an overhang
- 2. Telomerase extends the 3' overhang
- Newly synthesized region serves as a template for standard replication, restoring the 5' end 0

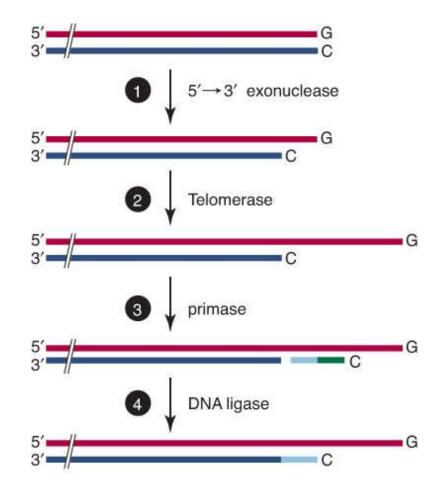


Figure 08.38: Hypothesis for solving the leading strand problem.

Replication Coupled Chromatin Synthesis

- Chromatin disassembly and reassembly are tightly coupled to DNA replication
- The nucleosome blocks direct contact between the DNA synthesis machinery and its DNA substrate
- ≈300bp of nucleosome-free (naked) DNA is present just before the replication fork
- ≈250bp of naked DNA is present just after the replication fork

Replication Coupled Chromatin Synthesis

- Histone chaperones permit ordered chromatin disassembly or assembly
- Chromatin modifiers also participate by adding acetyl, methyl, phosphate or other groups to histones or removing them from modified histones