

Conservation de l'information génétique: la réplication de l'ADN

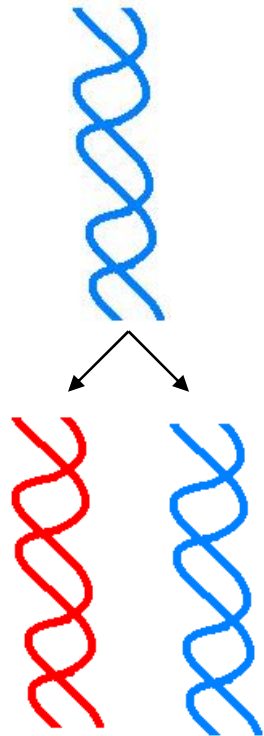
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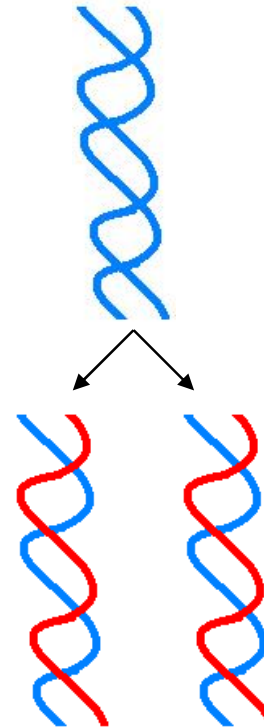
La réplication de l'ADN

Deux modèles :

Réplication
conservative

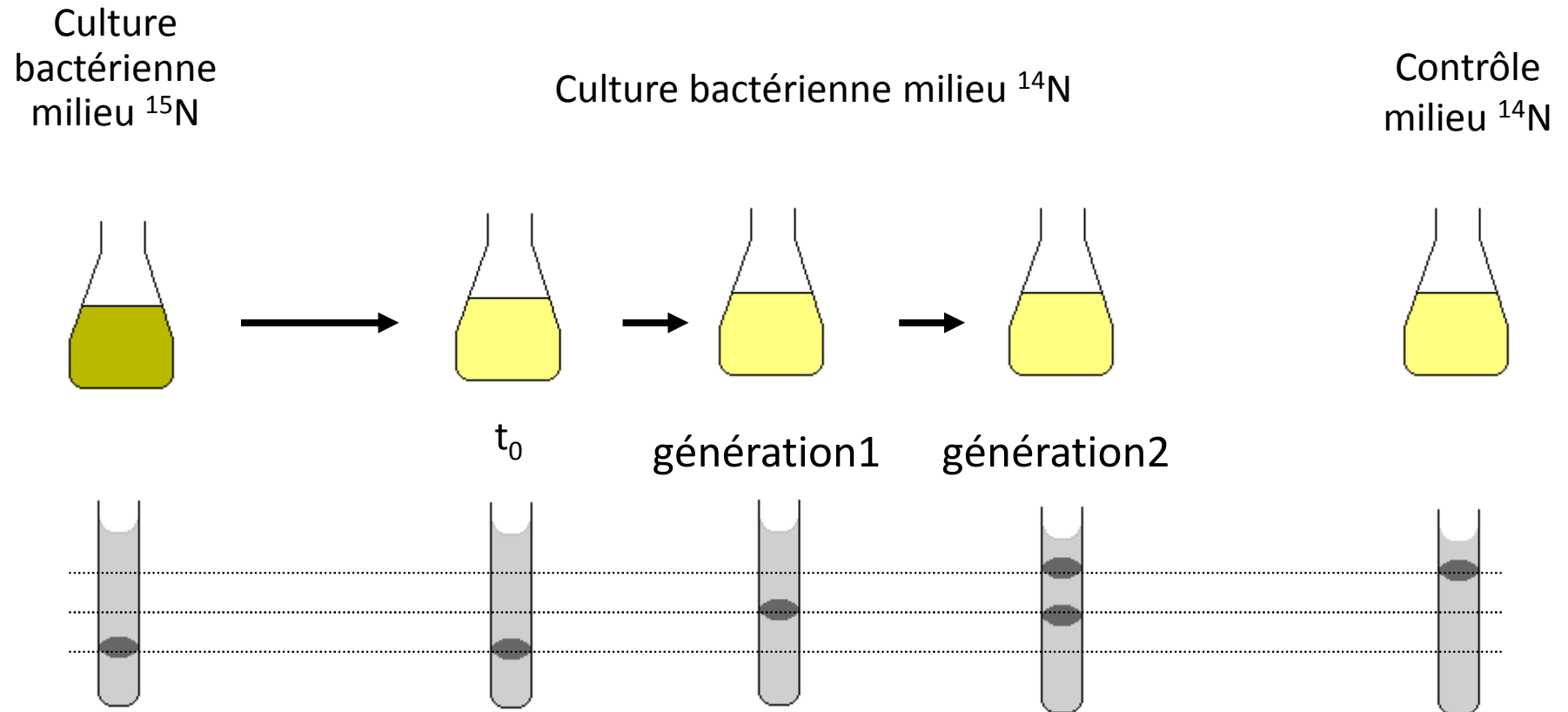


Réplication semi-
conservative



La réplication de l'ADN

- 1958, Meselson et Stahl : semi-conservative



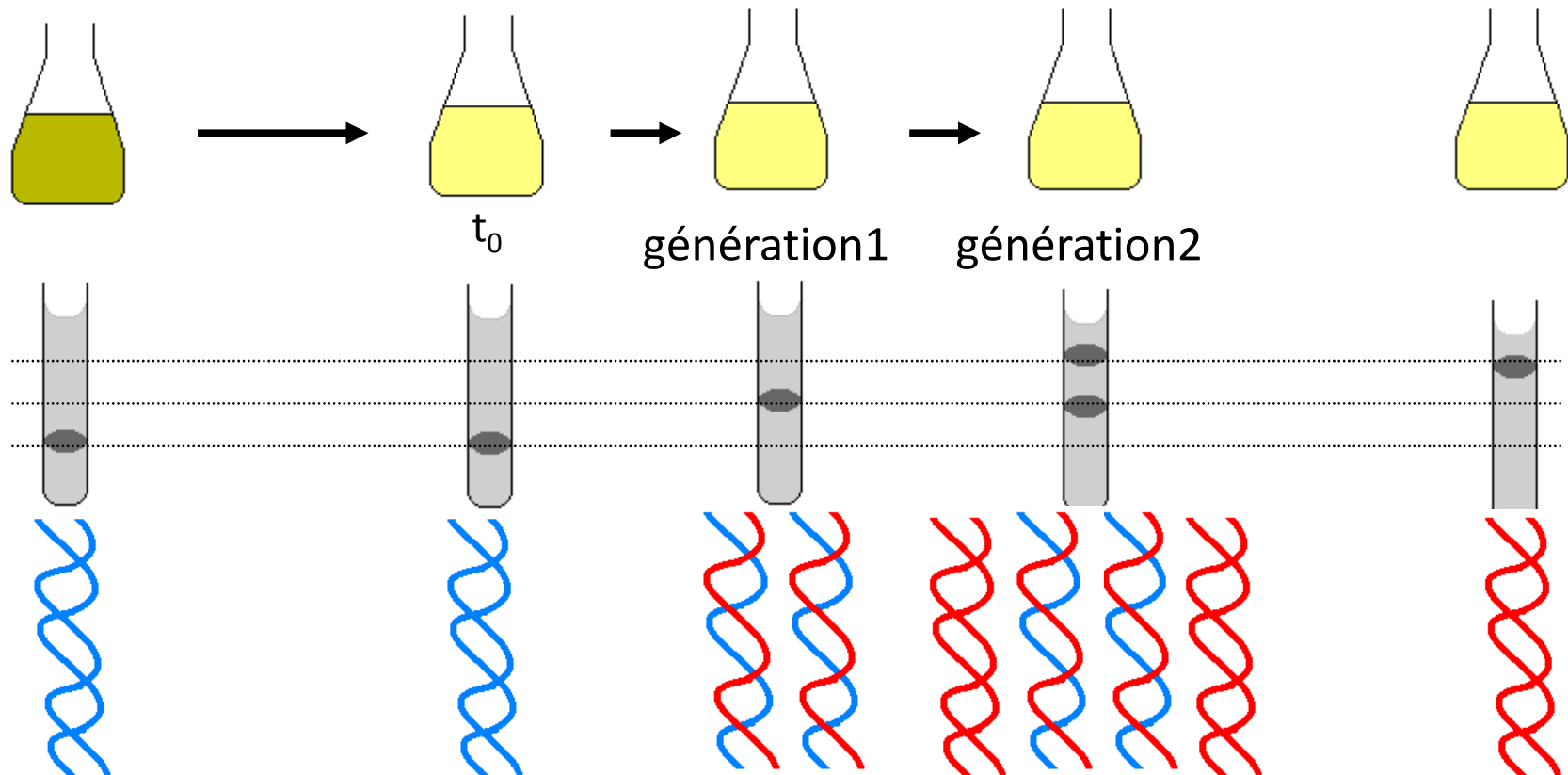
La réplication de l'ADN

- 1958, Meselson et Stahl : semi-conservative

Culture
bactérienne
milieu ^{15}N

Culture bactérienne milieu ^{14}N

Contrôle
milieu ^{14}N



La réplication de l'ADN

- 1956, Kornberg :
synthèse de l'ADN par
l'ADN polymérase
 - dNTP
 - Mg^{2+}
 - matrice ADN
 - amorce 3'OH libre
- Polymérisation dans le
sens $5' \rightarrow 3'$

Figure 13.1 Overview: DNA synthesis occurs by adding nucleotides to the 3'-OH end of the growing chain, so that the new chain is synthesized in the 5'-3' direction. The precursor for DNA synthesis is a nucleoside triphosphate, which loses the terminal two phosphate groups in the reaction.

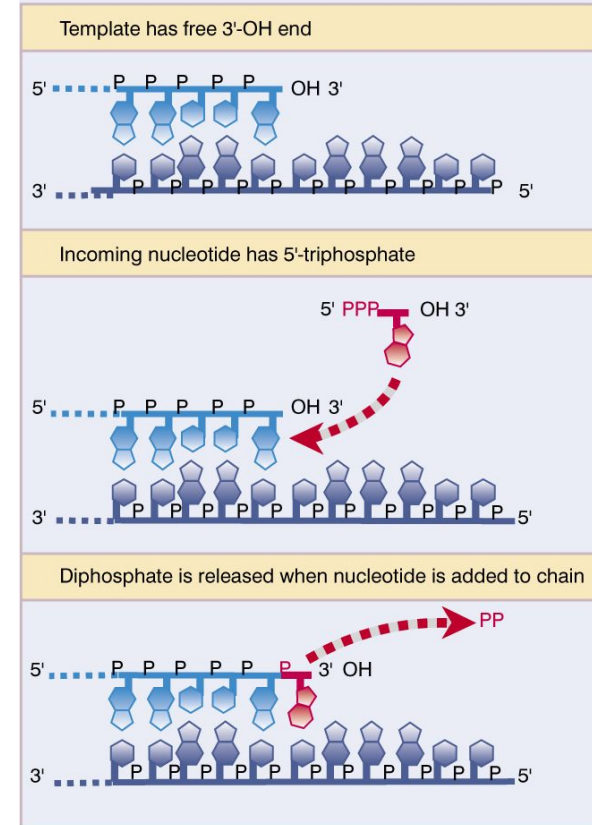


Figure 13.4 There are several methods for providing the free 3'-OH end that DNA polymerases require to initiate DNA synthesis.

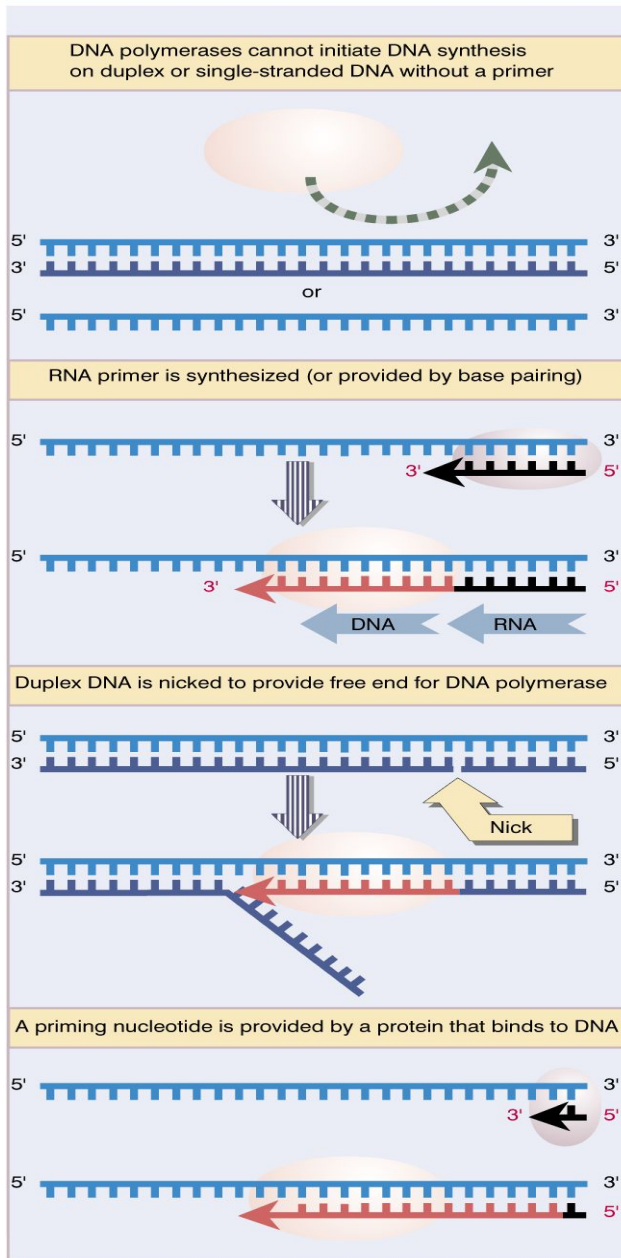
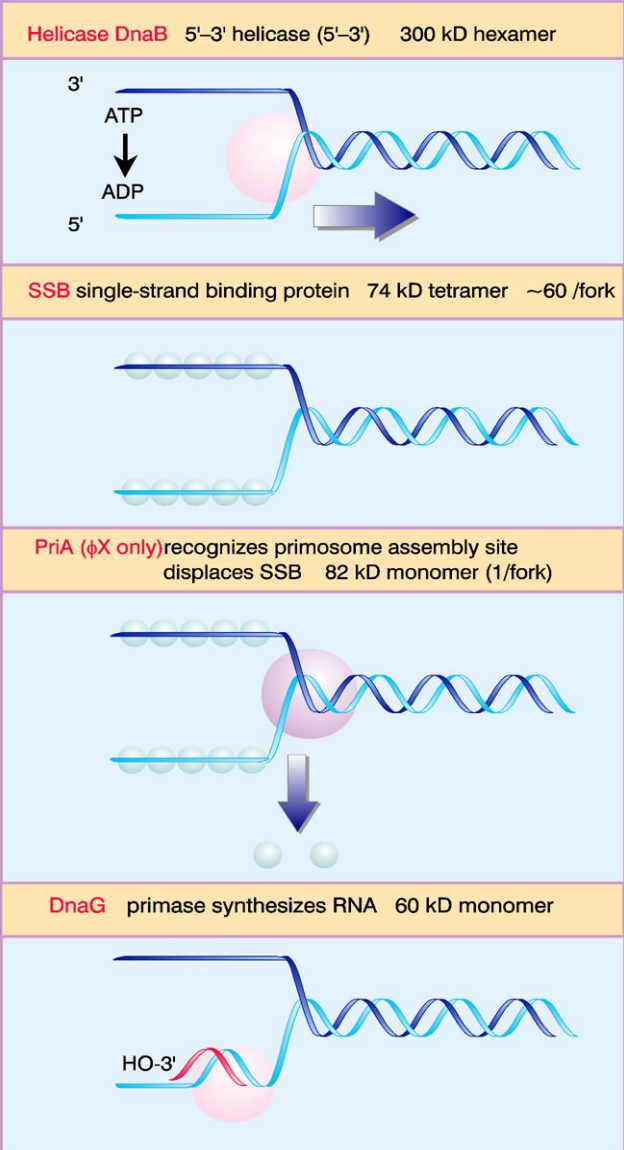


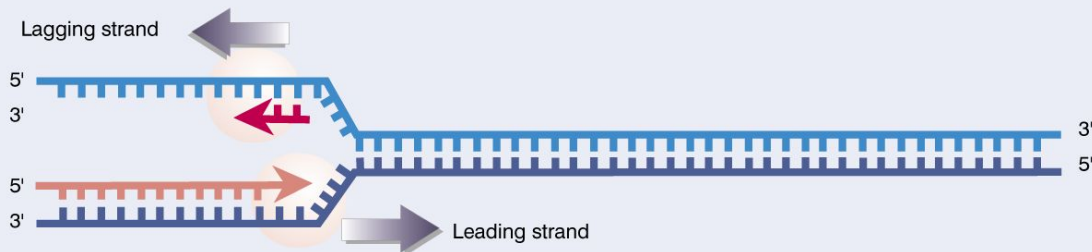
Figure 13.11 Priming requires several enzymatic activities, including helicases, single-strand binding proteins, a means of recognizing the primosome assembly sequence, and other structural proteins.



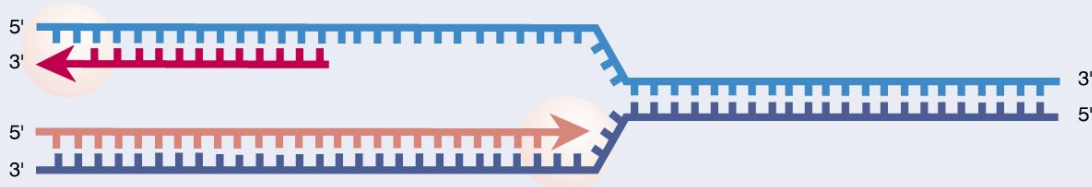
Les deux brins sont répliqués différemment

Figure 13.12 Leading and lagging strand polymerases move apart.

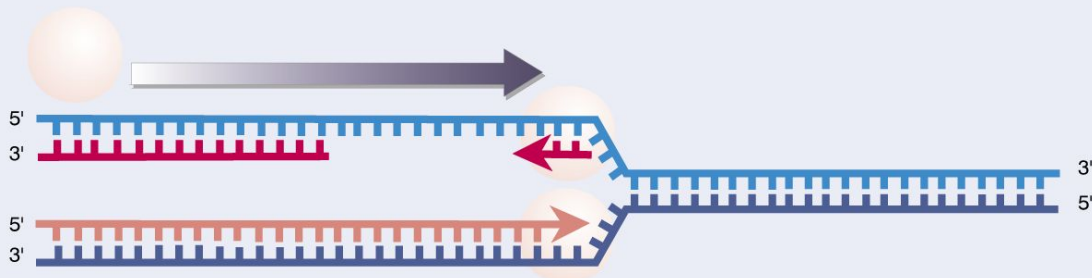
Leading and lagging enzymes start at same point on double helix



Enzymes move in opposite direction and are far apart at completion of Okazaki fragment

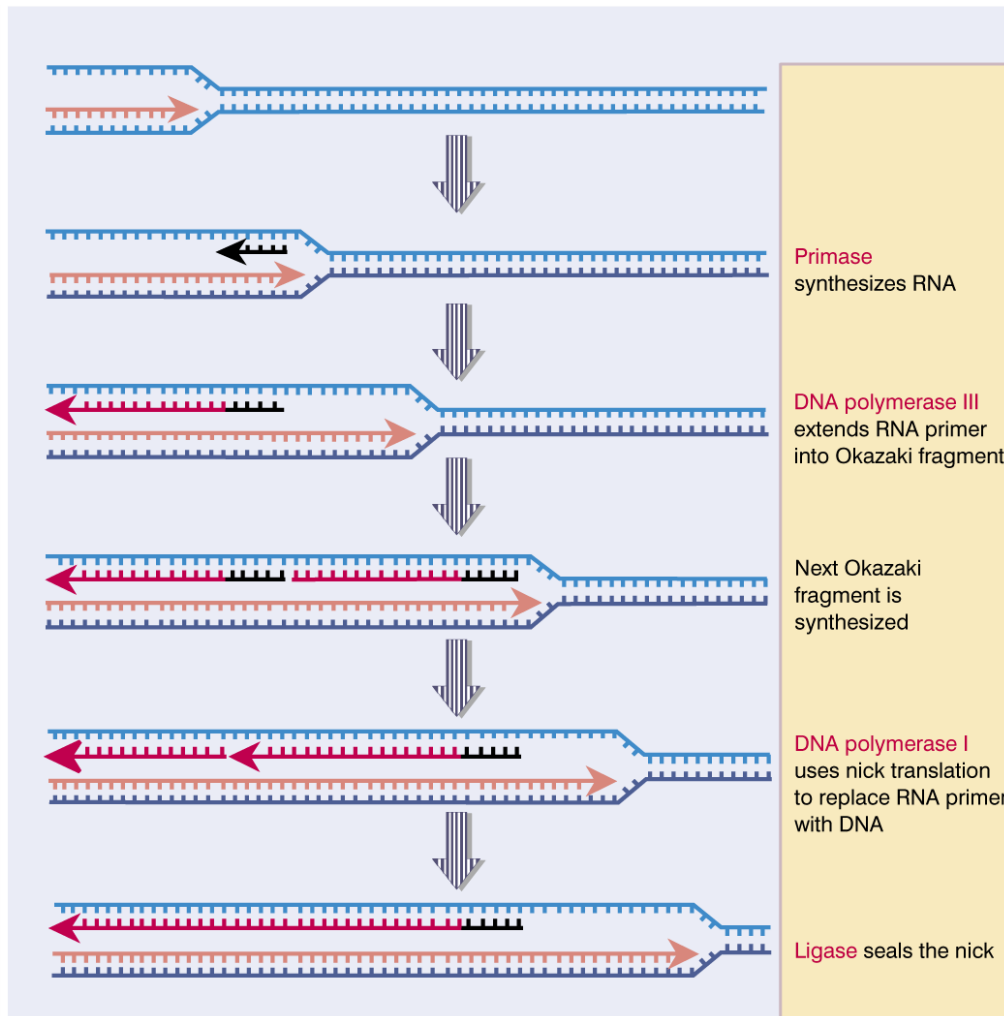


Lagging enzyme must translocate to new position to start another Okazaki fragment



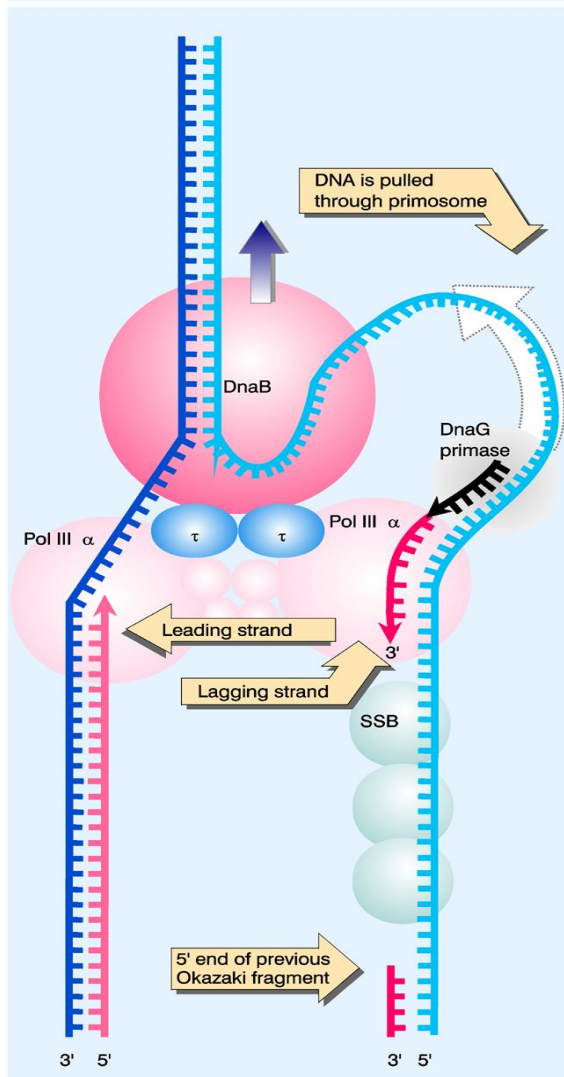
Les deux brins sont répliqués différemment

Figure 13.8 Synthesis of Okazaki fragments requires priming, extension, removal of RNA, gap filling, and nick ligation.



Le complexe de réplication

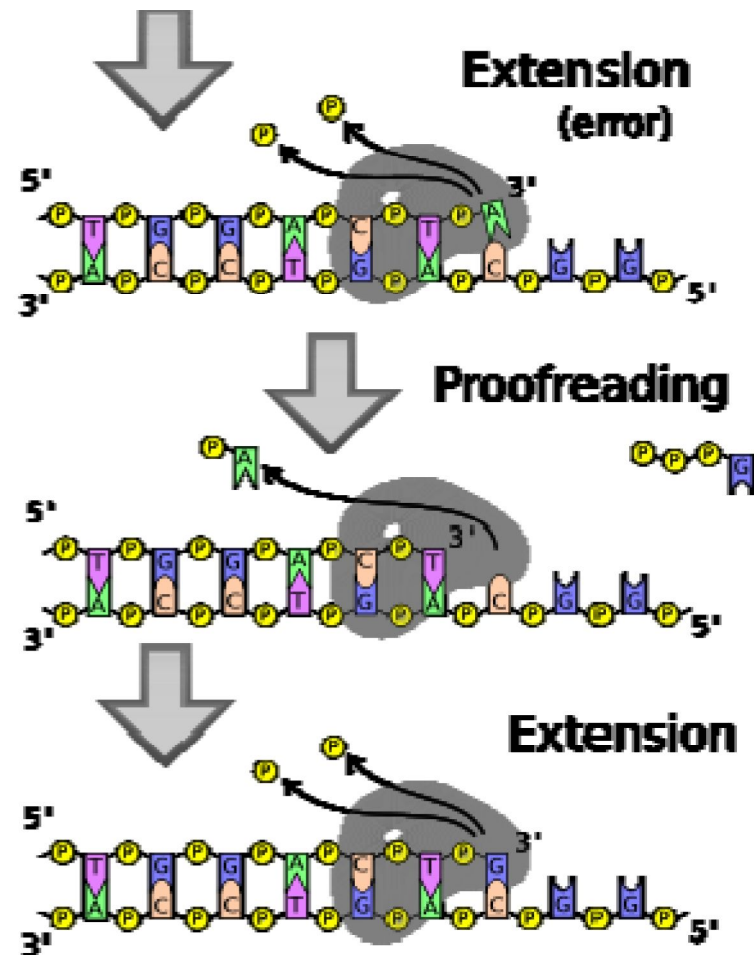
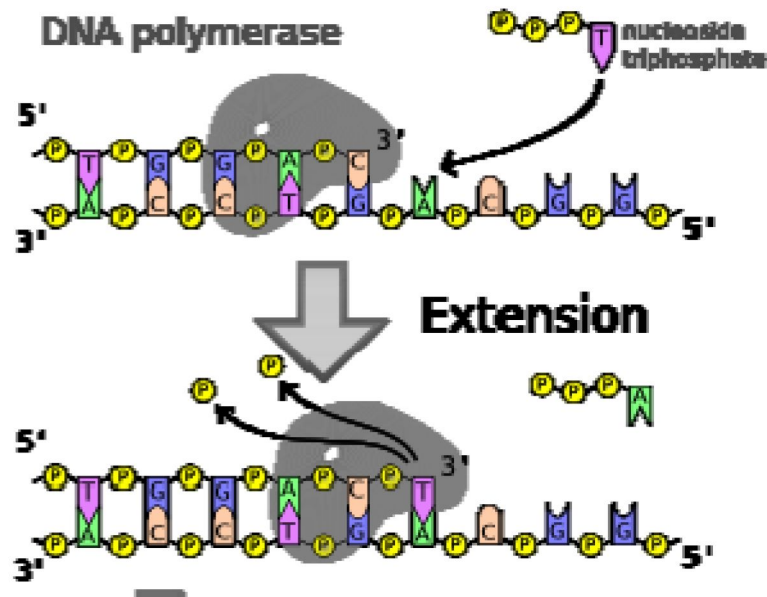
Figure 13.15 Each catalytic core of Pol III synthesizes a daughter strand. DnaB is responsible for forward movement at the replication fork. The primosome pulls a DNA template strand through.



La réplication de l'ADN

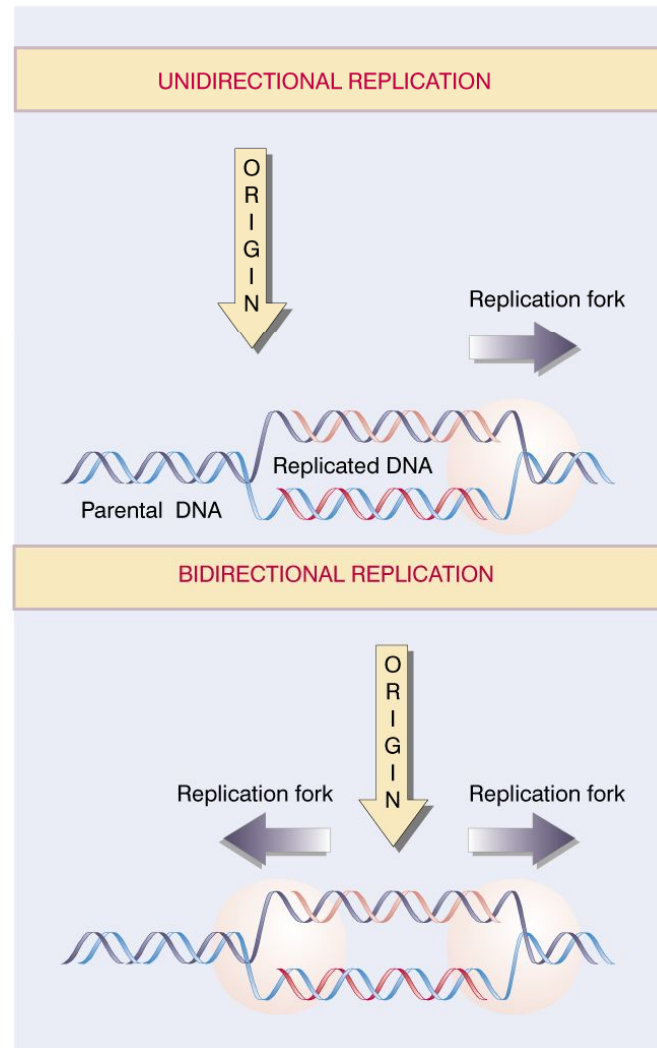
Réplication très fidèle grâce à l'activité 3'→5'
exonucléase de l'ADN polymérase

(="proofreading")



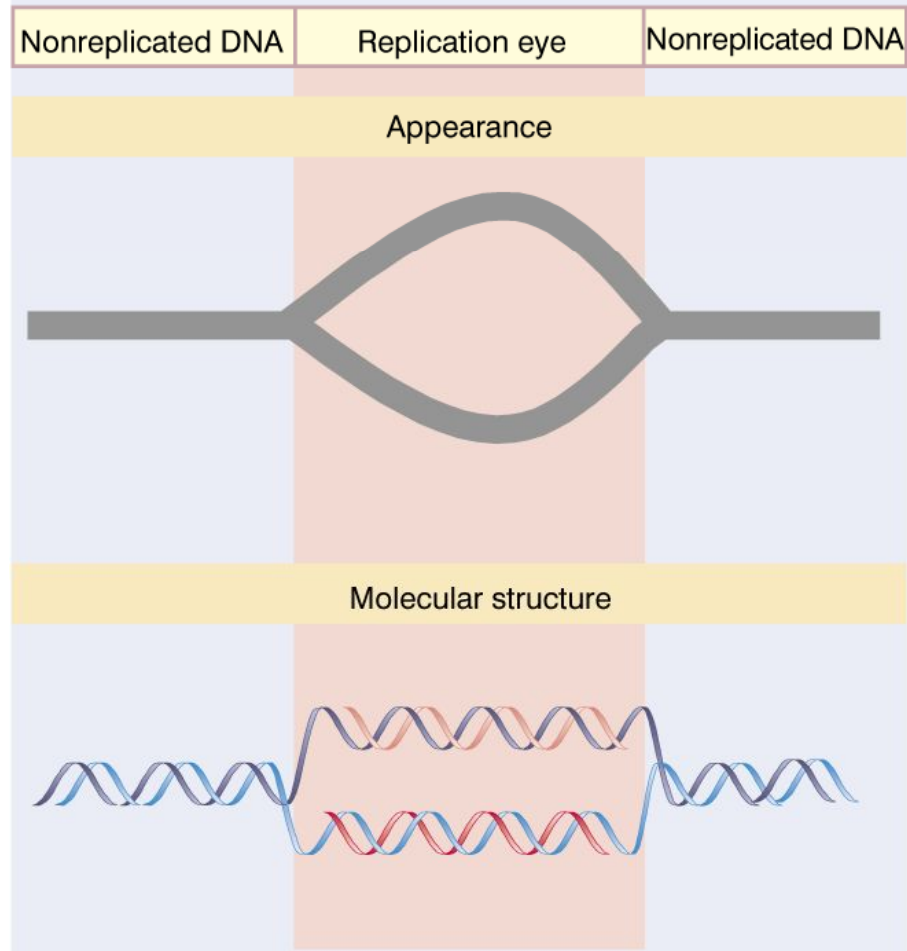
Directionnalité de la réplication

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

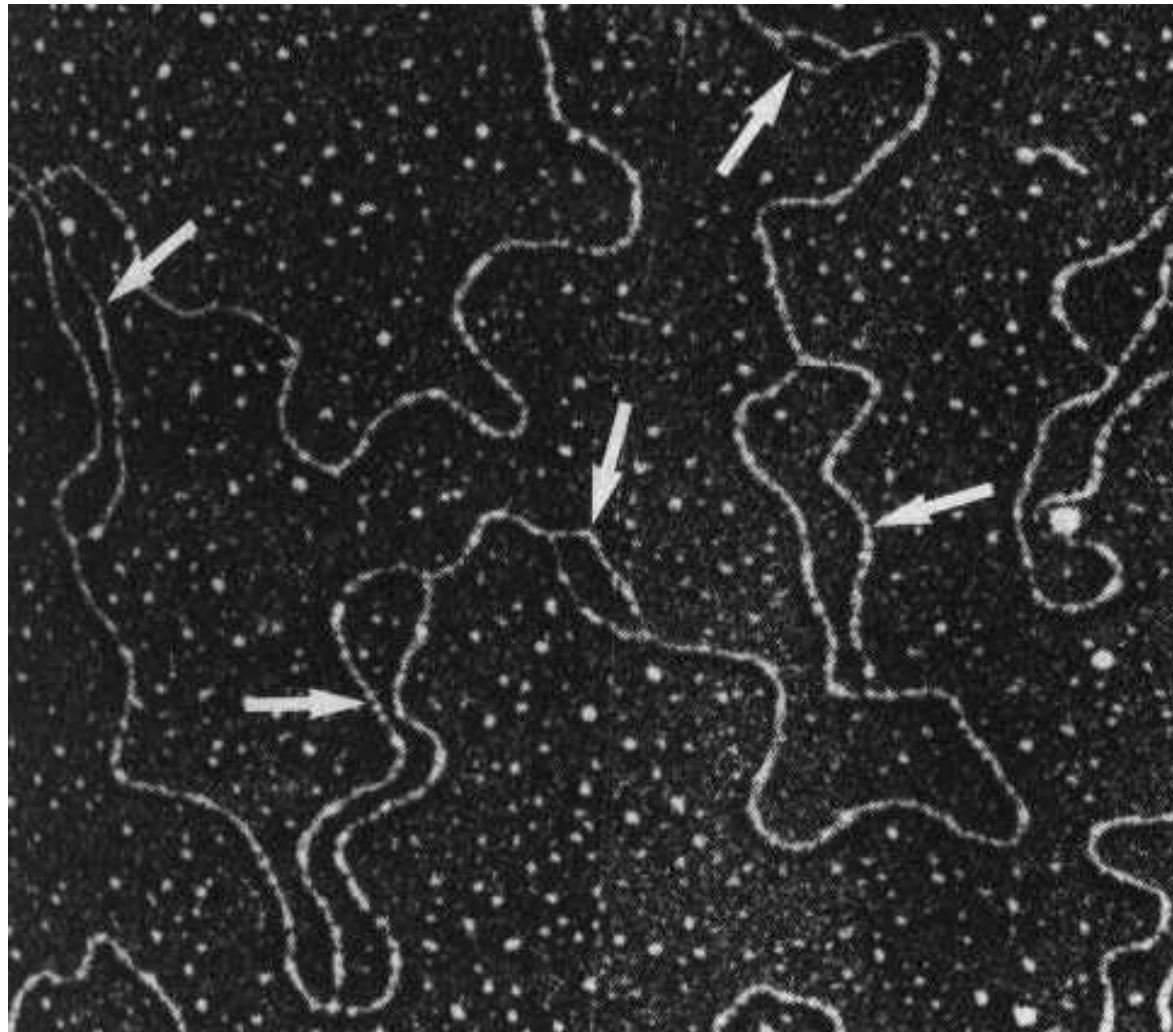


Oeil de répliation

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



Oeil de répliation



Les biais de composition liés à la réplication

- Les fragments du brin « lagging » (antisens) sont exposés plus longtemps au milieu environnant que ceux de l'autre brin
- Ils subissent préférentiellement des mutations comme les désaminations de cytosine C → T (140 fois plus rapide sur un brin « nu » que sur un double brin)
- Ceci a des conséquences sur le contenu global du génome

Retour au code génétique

		Second letter				
		U	C	A	G	
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA Stop UAG Stop	UGU } Cys UGC } UGA Stop UGG Trp	U C A G
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G
	A	AUU } AUC } Ile AUA } AUG Met	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G

Figure 1.10 Replication of DNA is semiconservative.

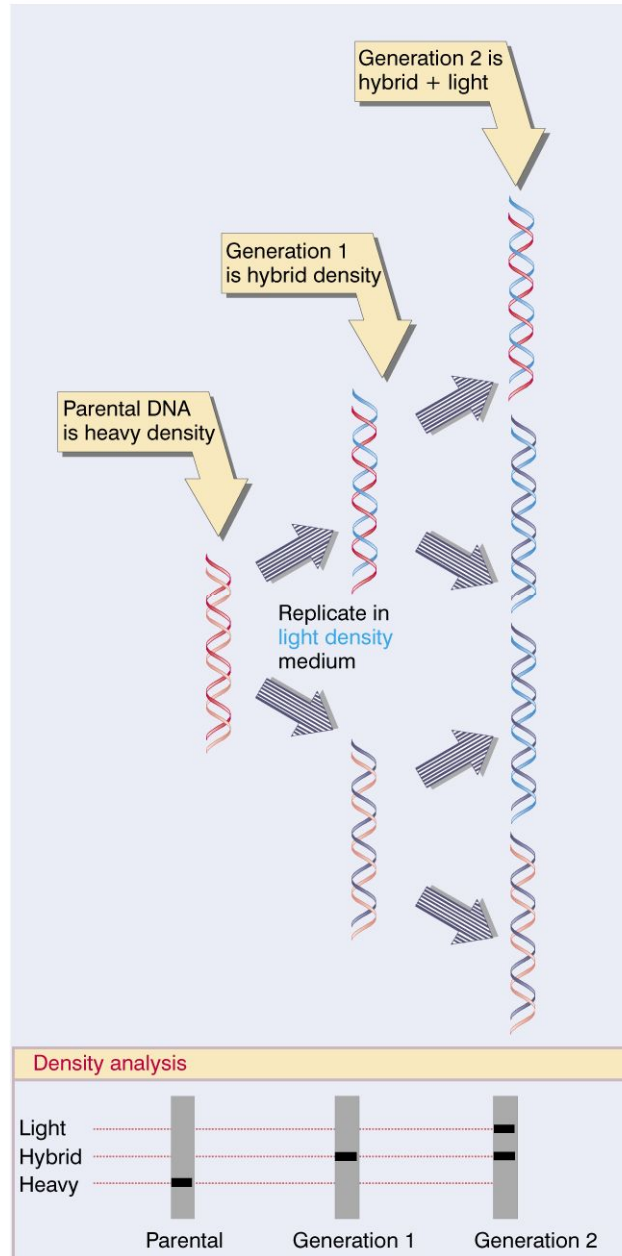
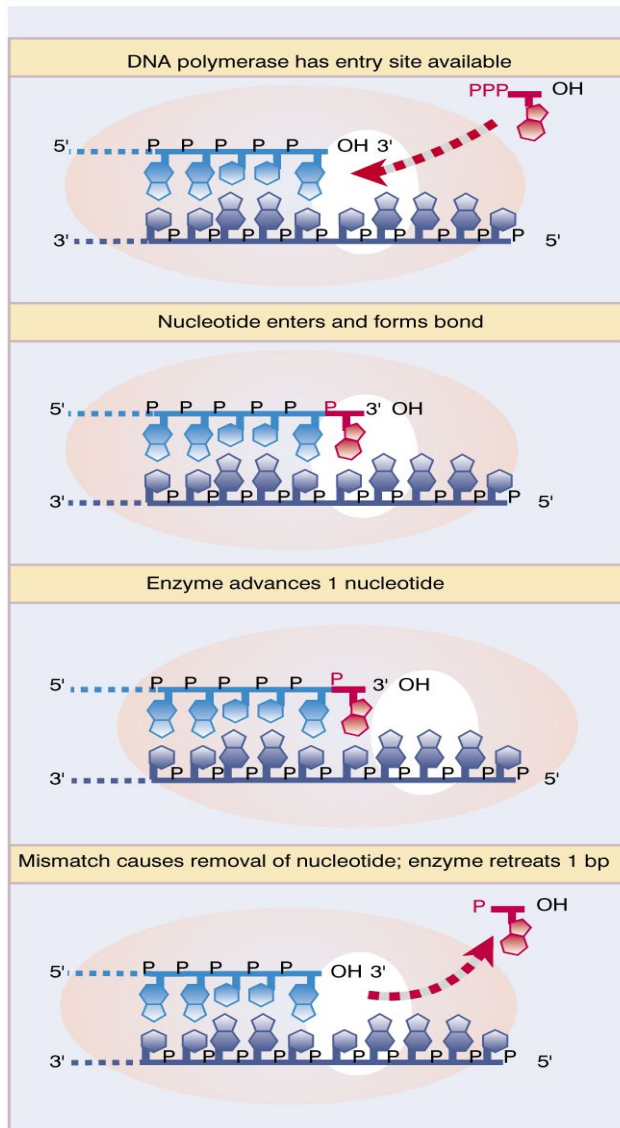


Figure 13.2 Bacterial DNA polymerases scrutinize the base pair at the end of the growing chain and excise the nucleotide added in the case of a misfit.



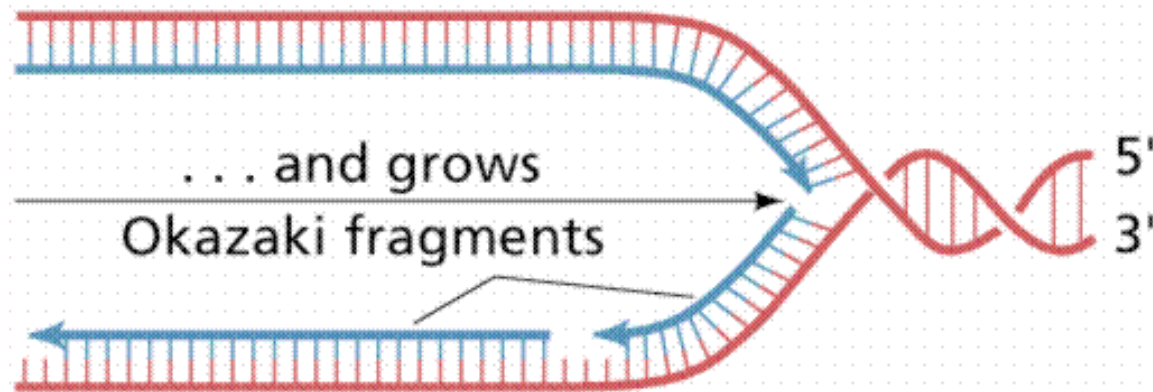
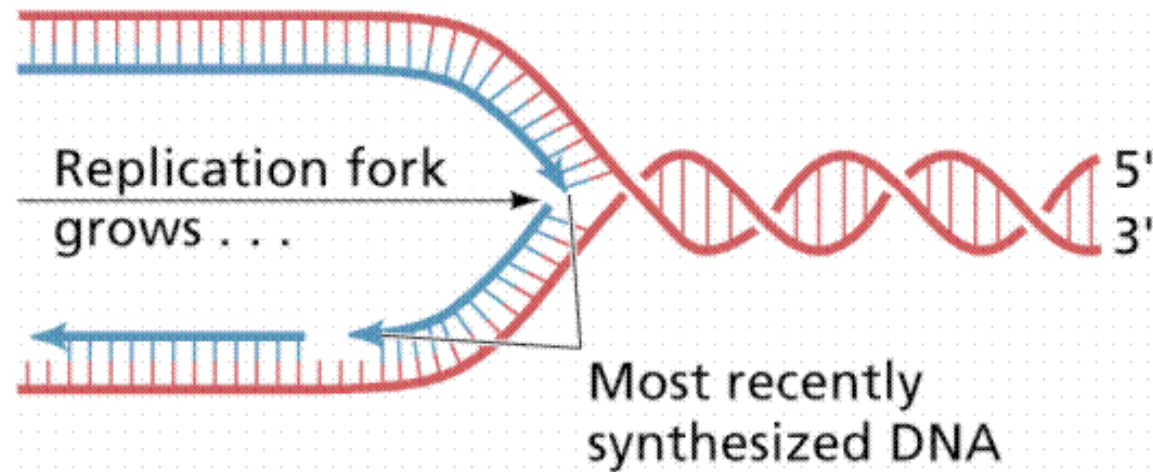
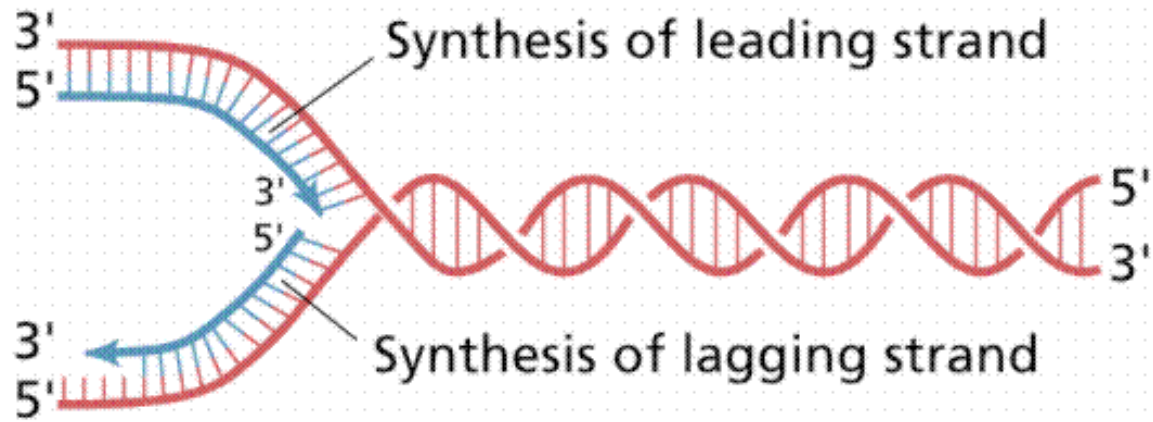


Figure 13.9 DNA ligase seals nicks between adjacent nucleotides by employing an enzyme-AMP intermediate.

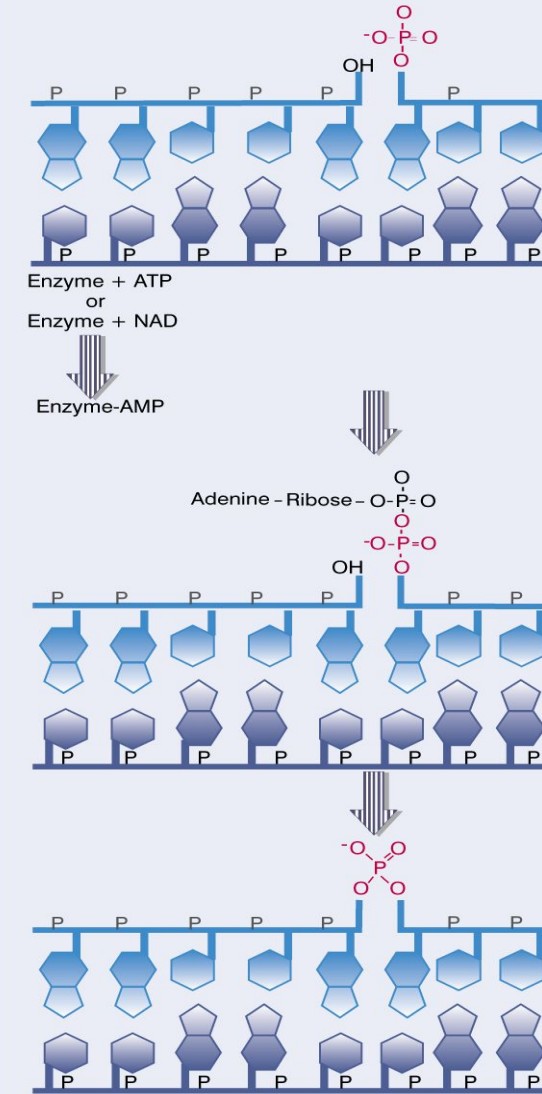


Figure 12.8

Measuring the size of the replicon requires a stretch of DNA in which adjacent replicons are active.

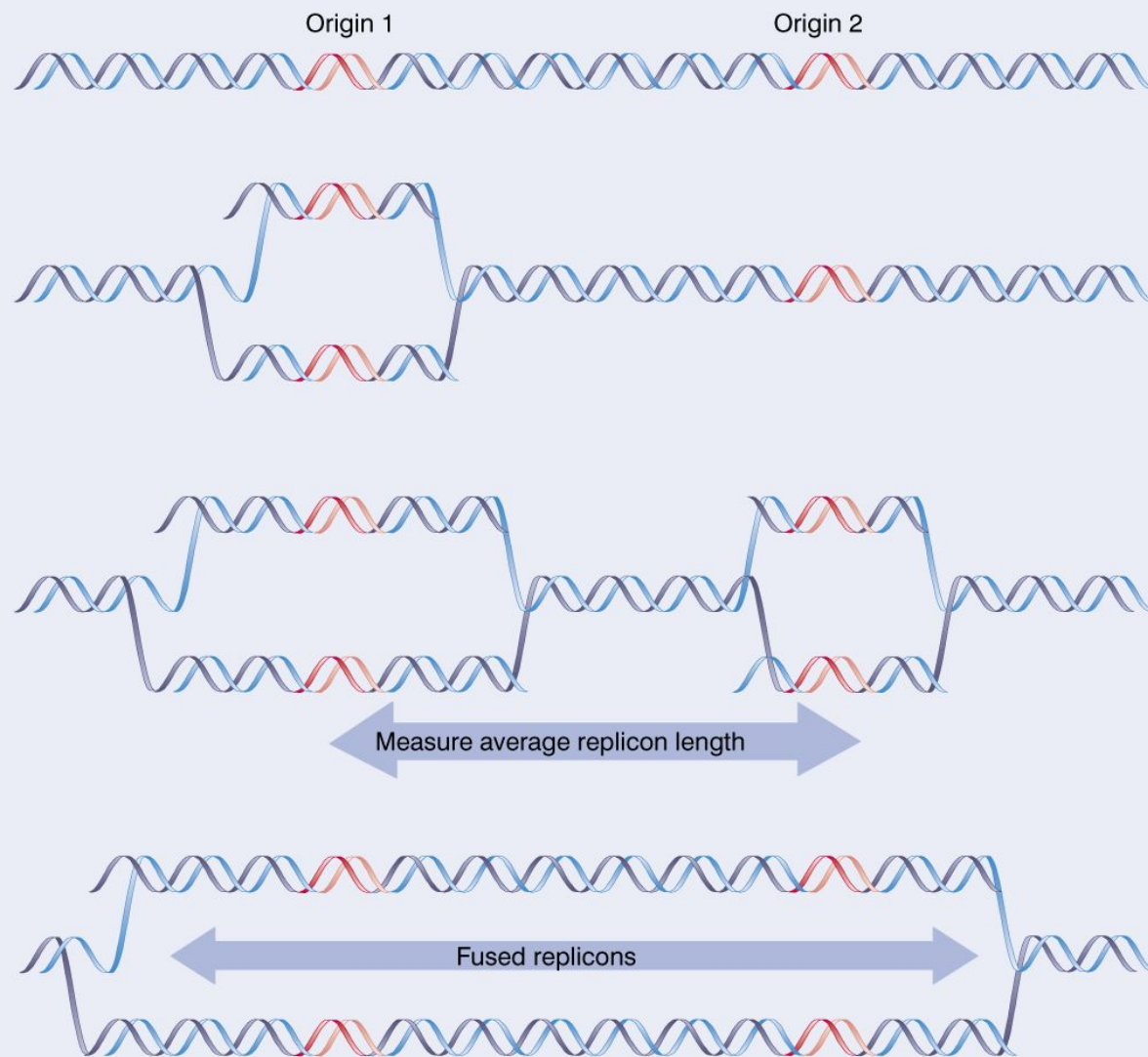


Figure 13.20 Prepriming involves formation of a complex by sequential association of proteins, leading to the separation of DNA strands.

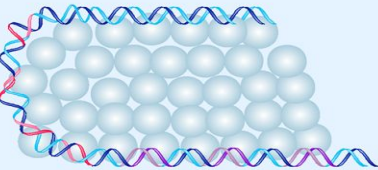
The origin has 3×13 bp repeats and 4×9 bp repeats



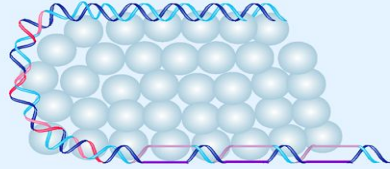
DnaA monomers bind at 9 bp repeats



20–40 DnaA monomers form large aggregate



DNA strands separate at 13 bp repeats



DnaB/DnaC joins complex, forming replication forks

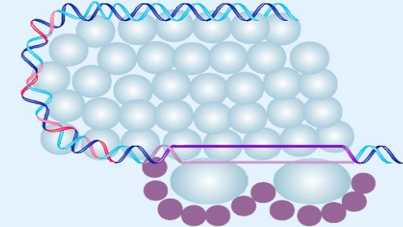


Figure 13.7 The leading strand is synthesized continuously while the lagging strand is synthesized discontinuously.

