DNA Structure

DNA is a Double Helix composed of 3 two repeating units (P – DR – P – DR – P –DR)

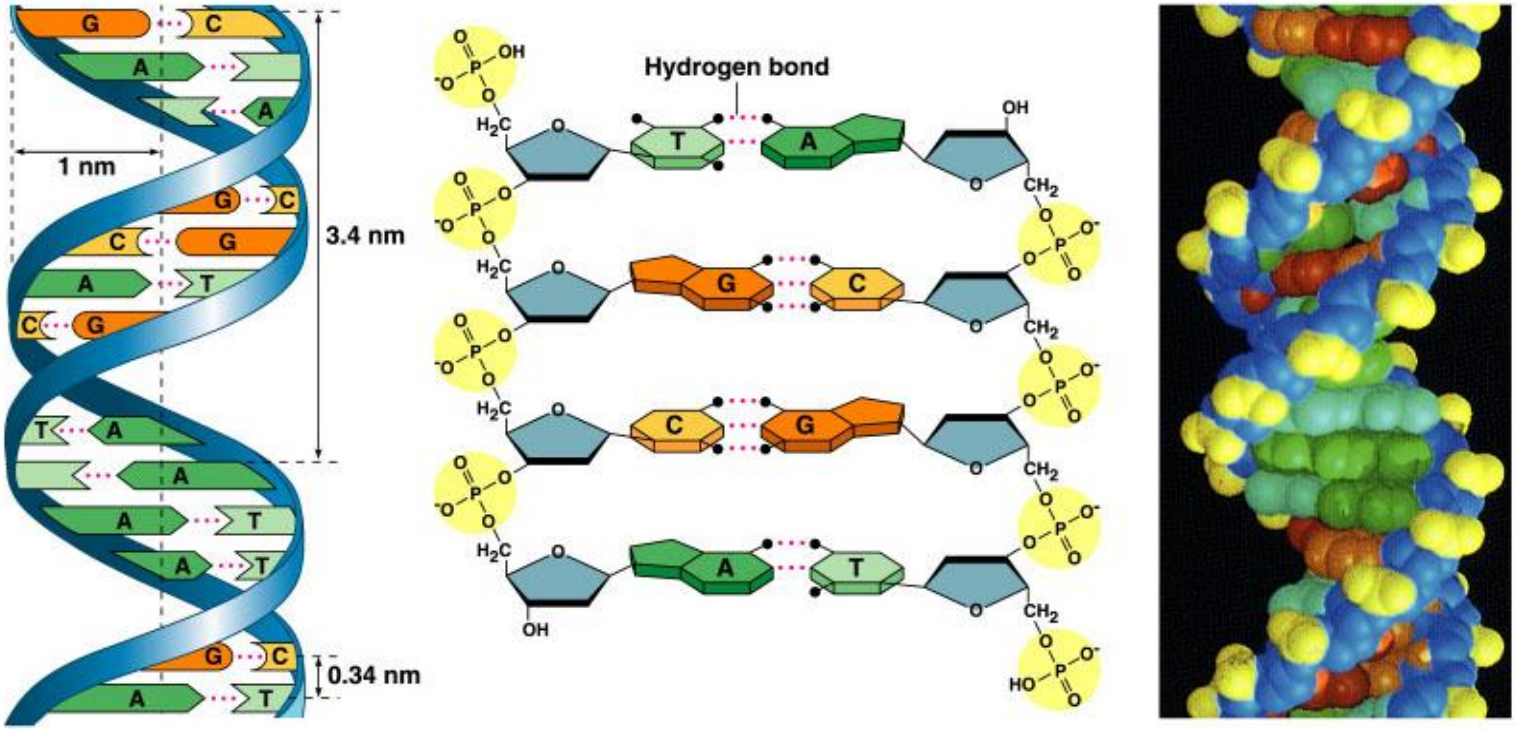
On each unit is 1 Nitrogen base (a ring structure)

- Purine: Guanine (G), Adenine (A)
- Pyrimidine Thymine (T), Cytosine C

Completes one "twist" every 10 bases

Complimentary Pairing (A – T) and (C – G)

- Strands are antiparallel (parallel but in opposite direction)
  - 3′ = OH group at end 5′ = P at end
  - DNA is always read 3′ to 5′
- Held together with H bonds between bases



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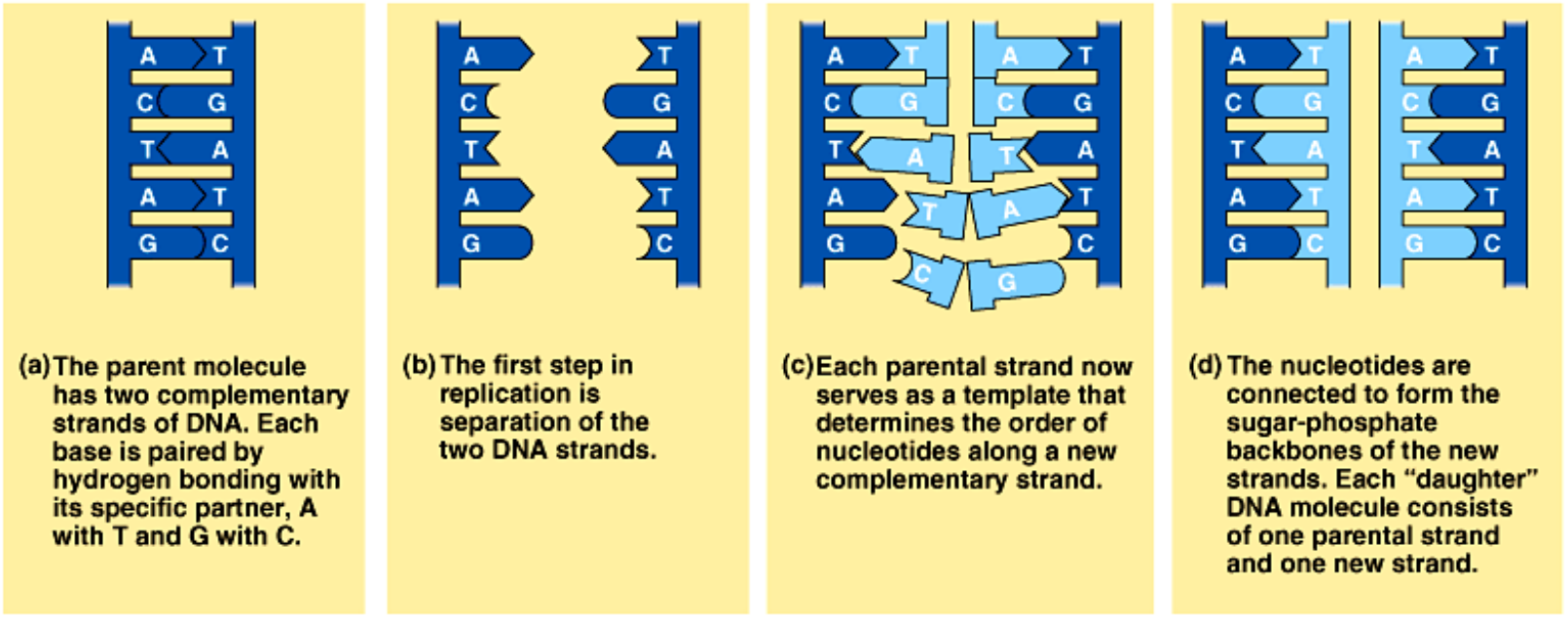
DNA Replication is Semiconservative



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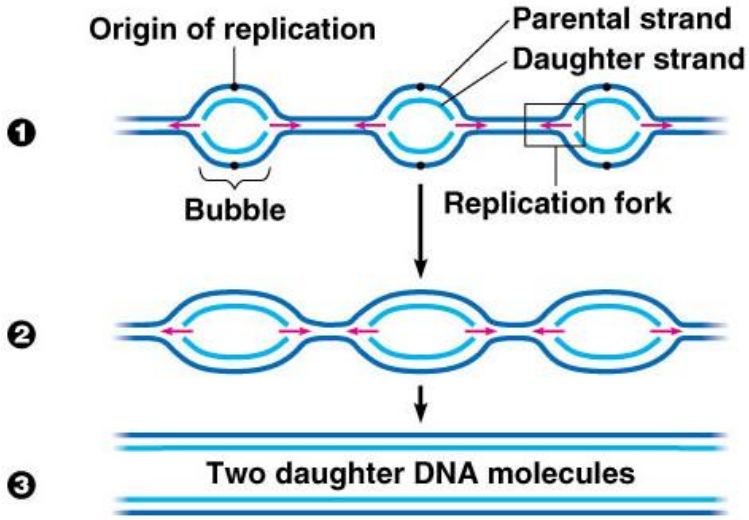
Replication Results in 2 identical strands

Semiconservative: ½ parental strand, ½ daughter strand

Begins in many places, not beginning to end (too slow)

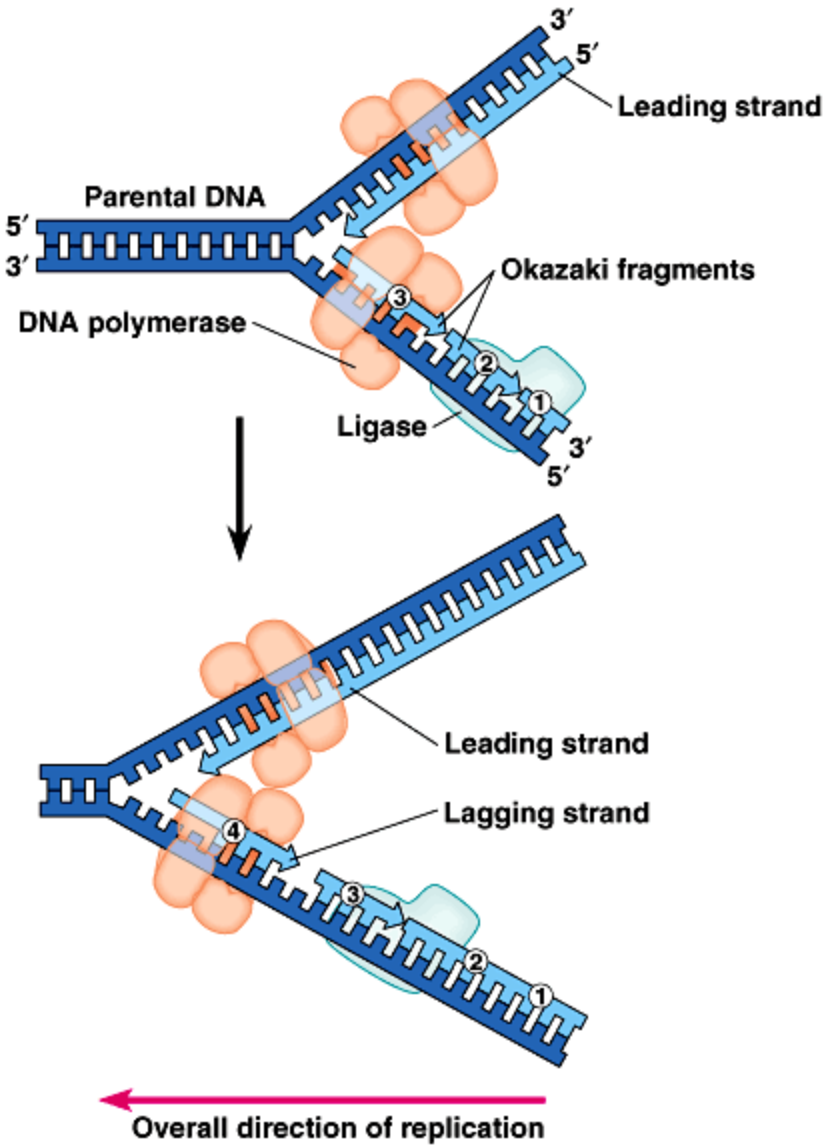
- Like reading a book by starting on page 1 of every chapter simultaneously.
- Each region where replication is happening is called a replication bubble.
- The point where the bubble unzips the DNA is the replication fork



(a) In eukaryotes, DNA replication begins at many sites along the giant DNA molecule of each chromosome.

Method of replications

1. Unzip DNA using Helicase (breaks the helix)
2. Primase adds 10 base RNA Primer (starter) at 3′ end
3. DNA polymerase begins adding complimentary base pairs starting at the primer and working in 5′ direction (Like any written language, it only makes sense when read in one direction (Eng L to R / Hebrew R to L)
    a. Leading strand – read continuously **3′ to 5′**
    b. Lagging strand is read in short segments (Okazaki Fragments) as the strand is exposed. Still 3′ to 5′. (like uncovering text in backwards order)
4. DNA polymerase then replaces RNA bases of Primer with permanent DNA bases.
    a. Leading Strand – replication is complete
    b. Lagging Strand – Ligase joins the individual Okazaki Fragments into one long chain. Replication complete.



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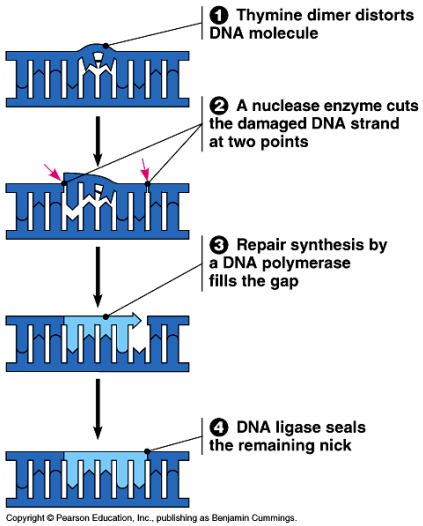

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Proofreading (Nucleotide Excision Repair): mis-paired bases won't H bond. They are cut out by Ligase and replaced with correct base. These are some of the anti-cancer spellcheckers we mentioned.

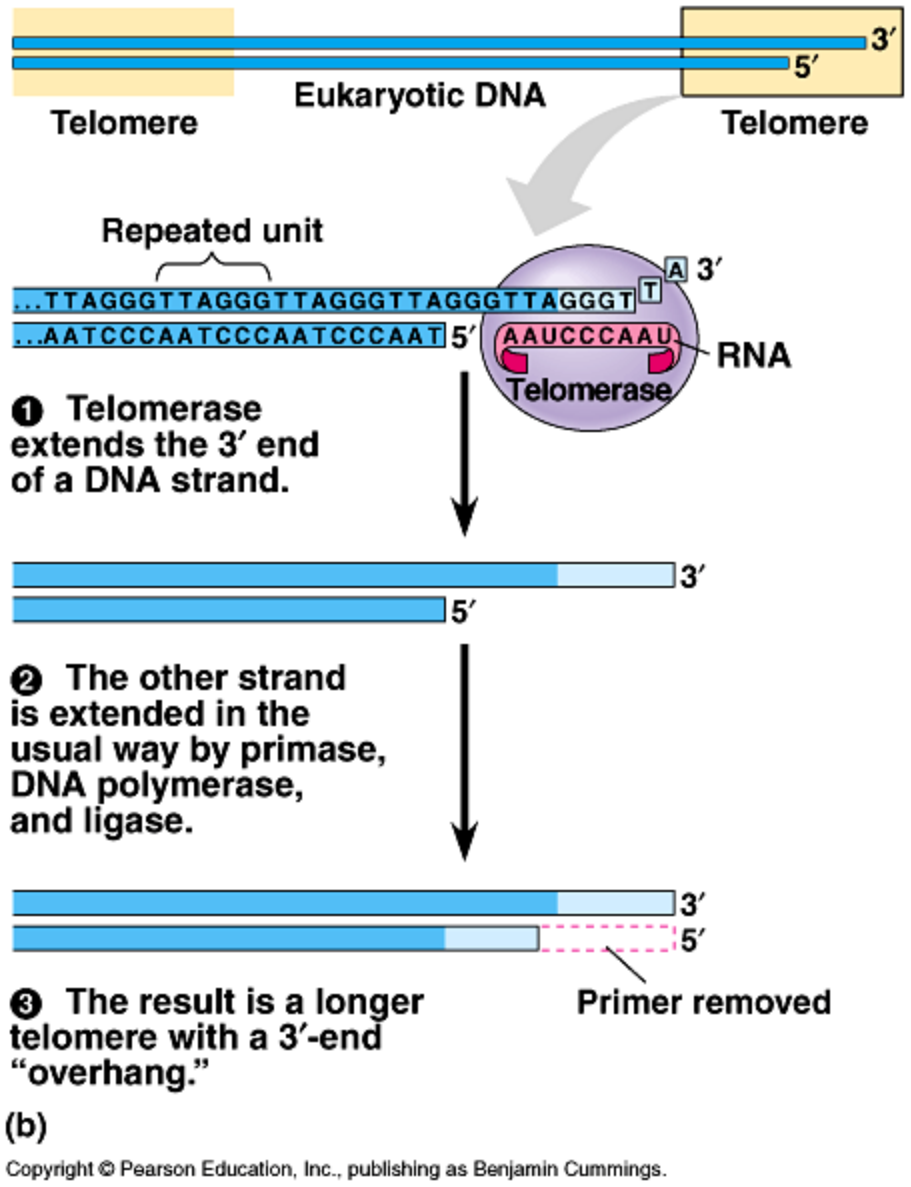
Telomeres:

Because DNA can only be copied from 3′ to 5′, and can only begin AFTER a primer, there is no way to convert the Primer to regular bases on the Lagging strand.

The Primer is just removed, making the DNA strand shorter.

This region has no info. It is a repeating base pattern, but it is only so long. Eventually enough will be lost through repeated replications that it will be gone. At that point, the DNA cannot be replicated again without losing coding data.

Decreasing length may potentially the key to aging.



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