

Source: [KBBIO101CentralDogma](#)

1 | DNA Replication

DNA replication is known to be “semi-conservative” — meaning that it is a process that pairs a synthesized half of the DNA with an original half of the DNA (i.e. takes the ORIGINAL template strand + makes the NEW coding strand & takes the ORIGINAL coding strand + makes the NEW template strand.)

Because **polymerases copy uni-directionally** => DNA polymerase move along the 3' to 5' DNA to create a copy 5' to 3'. Meaning, the polymerase is able to add nucleotide onto the 3' end of the DNA.

- Open the DNA at an arbitrary point using the Helicase
 - Uses two helicase => one open rightward, and one leftward. The movement of the helicase opening the DNA is called the “fork movement”
 - DNA polymerase could only add nucleotides 5' to 3'
 - As helicase open a little bit of the DNA, polymerases rush to copy the area that opened
 - In the **leading** strand (3' to 5'), polymerase will run alongside the helicase for they are opening and replicating on the same direction
 - In the **lagging** strand (5' to 3'), polymerase will wait until the helicase opens a little segment, and rushes forward and move backwards
 - NOTE: the lagging strand... 1) takes longer to transcribe 2) is done in small chunks (each “rush forward”). Each chunk is called an okazaki fragment

DNA replication fork and strand synthesis

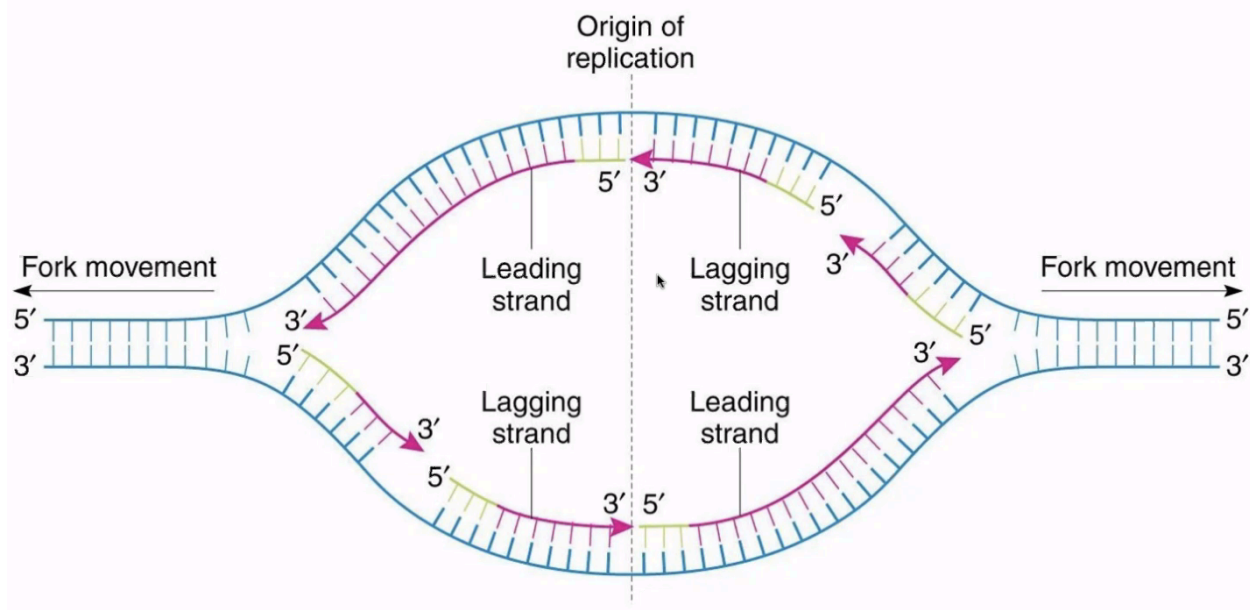


Figure 1: leadinglagging.png

- DNA polymerase will REQUIRE a double-stranded area to begin work from, so Primase synthesizes already double-stranded RNA primers that DNA polymerase could bootstrap to the single-stranded DNA to begin the replication process (think: create-react-app)

- DNA polymerase will detect unfitting bonds and remove leftover RNA primer bootstrap units to repair them in a process called “proofreading.” DNA polymerase is assisted with “glue” ligase to help the DNA polymerase pick out and replace problematic/unneeded nucleotides and perhaps their neighbors. This is where the Okazaki fragments get joined.

Stage of DNA Replication Main purpose of this step Key enzymes and structures involved Outcome of this process DNA is unzipped at the origin of replication The parent DNA strand serves as a template for the new strand; when it is unzipped, the nucleotides are exposed for complementary base pairing Helicase is the enzyme that unzips the DNA molecule, breaking the hydrogen bonds between nucleotides The nucleotides of the DNA molecule are exposed for complementary base pairing Unwinded DNA is primed

The unwinded DNA is primed to help DNA polymerase's replication process Primase is responsible for priming the DNA strand for replication. Working in conjunction in the rejoining step below, a DNA molecule will be ready to be transcribed. Unwinded DNA is broken and rejoined The unwinded DNA is broken and rejoined in order to reduce strain caused by unzipping. Topoisomerase is responsible for relieving unwinding-induced strain.

The resulting DNA is ready to be read from the 3' to 5' end in order to synthesize a new strand 5' to 3'. Actually replicating

The DNA is replicated via fitting the pairing nucleotides against the primed DNA DNA polymerase, in addition to the primer RNAs aforementioned, perform this process. Two new sets of DNA ready to be checked and later utilized. Proofreading

Replicated DNA is checked for any irregularities + patched as needed in order to prevent error DNA polymerase and “mismatch repair enzymes” #ask? A DNA ready to be utilized