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 polyemrease move along the 3' to 5' DNA to create a copy 5' to 3'. Meaning, the polymerize is able to add nucleotide onto the 3' end of the DNA.

- Open the DNA at an arbuiturary 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 rushes 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 helicate 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 ogazaki fragment

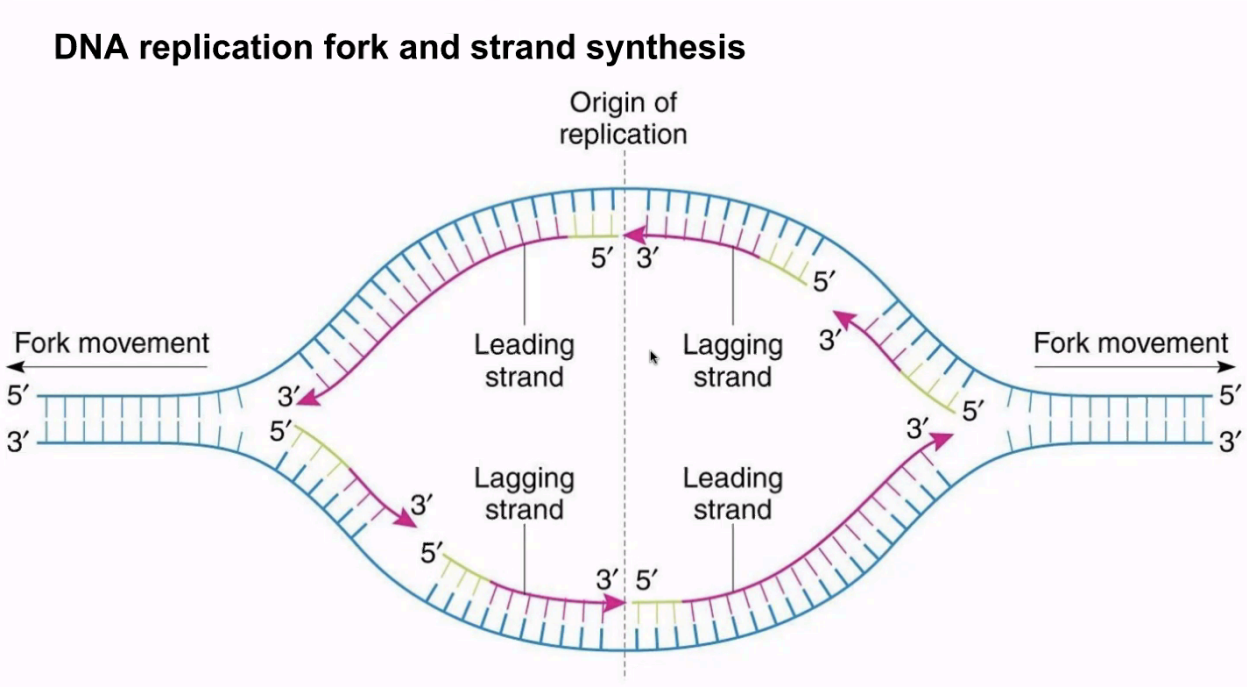

Figure 1: leadinglagging.png

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

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