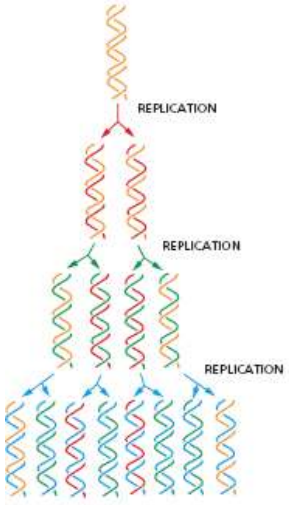
DNA Replication

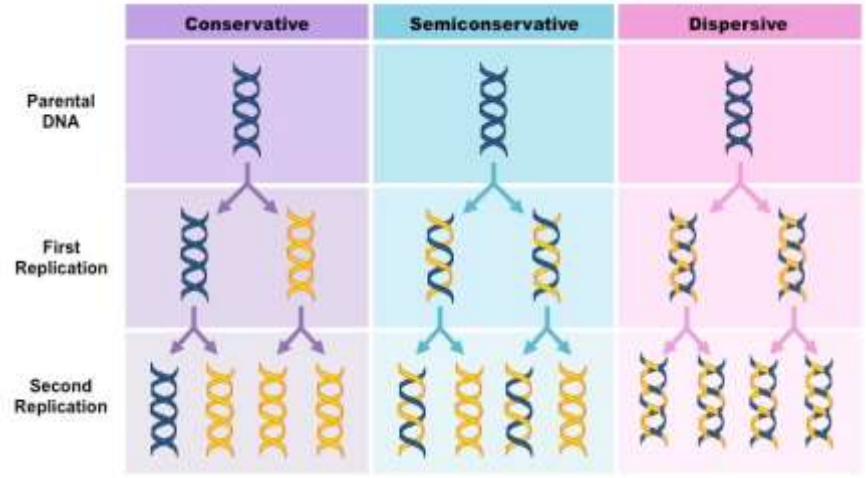
DNA replication produces two complete double helices from the original DNA molecule, with each new DNA helix being identical (except for rare copying errors) in nucleotide sequence to the original DNA double helix (see Figure 6–2). Because **each parental strand serves as the template for one new strand**, **each of the daughter DNA double helices ends up with one of the original (old) strands plus one strand that is completely new**; this style of replication is **said to be semiconservative** (Figure 6–3). In How We Know, pp. 200–202, we discuss the experiments that first demonstrated that DNA is replicated in this way. In it, they proposed that complementary bases—adenine and thymine, guanine and cytosine—pair with one another along the center of the double helix, holding together the two strands of DNA. At the very end of this succinct scientific blockbuster, they comment, almost as an aside, **"It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material**."



Although the hydrogen bonds collectively make the DNA helix very stable, **individually each hydrogen bond is weak (as discussed in Chapter 2). Separating a short length of DNA a few base pairs at a time therefore does not require a large energy input**,and the **initiator proteins can readily unzip the double helix at normal temperatures. ----Personal Note 6g impacts hydrogen release in the cells as well as dna and can see how it can Unzip the dna strands to be allowed to upload any new code**

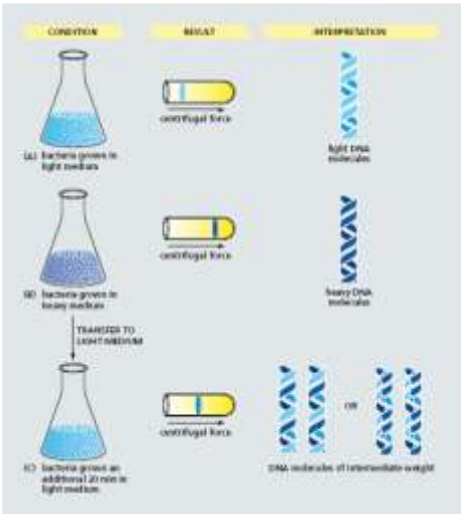
Explanation:
DNA replication is semi-conservative, **so when you get a "new strand" of DNA**, it is made of an old single strand and a new single strand.

(the Middle)



Once an initiator protein binds to DNA at a replication origin **and locally opens up the double helix, it attracts a group of proteins that carry out DNA replication.** These **proteins form a replication machine, in which each protein carries out a specific function.--- suggesting how DNA might be duplicated. In this paper, they proposed that the two strands of the double helix unwind, and that each strand serves as a template for the synthesis of a complementary daughter** strand. In their model, dubbed **semiconservative replication**, each **new DNA molecule consists of one strand derived from the original parent molecule and one newly synthesized strand**

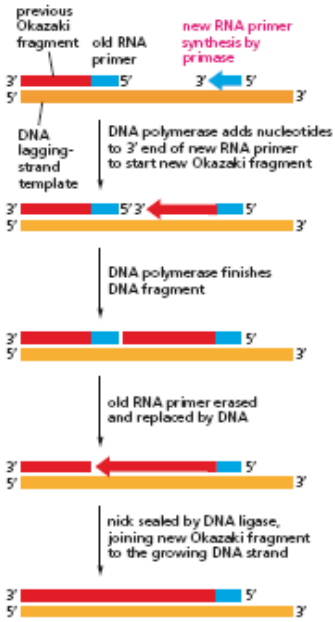
Delbrück proposed that **DNA replication proceeds through a series of breaks and reunions**, in which the DNA backbone is **broken and the strands copied in short segments—perhaps only 10 nucleotides at a time—before being rejoined. In this model, which was later dubbed dispersive**, the resulting copies would be patchwork collections of old and new DNA, **each strand containing a mixture of both** After one generation of growth, the researchers **found that the parental, heavy DNA molecules—those made of two strands containing 15N—had disappeared** and **were replaced by a new species of DNA that banded at a density halfway between those of 15N-DNA and 14N-DNA (Figure 6–7). These newly synthesized daughter** helices, Meselson and Stahl reasoned, **must be a hybrid—containing both heavy and light isotopes**

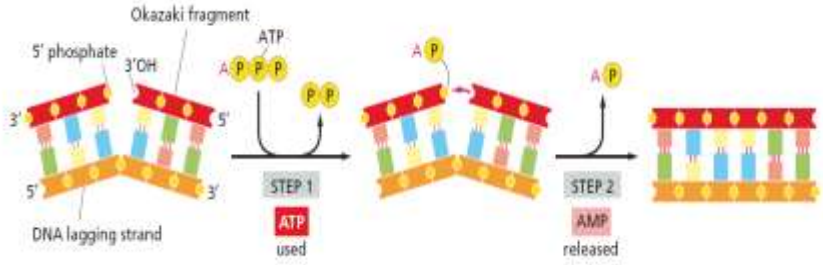


Personal Note – if this was done by inserting just 2 strands of DNA and the one became predominant causing a metamorphis and a mutation or hybrid what happens when you add 10E50power of nucleotides and nanoparticles into a person directly programming the nanobio to access the dna with a new code

The DNA strand that appears to grow in the incorrect 3'-to-5' direction is actually **made *discontinuously*, in successive, separate, small pieces,** with the DNA polymerase moving backward with respect to the direction of replication-fork movement, as each new piece is made in the correct 5'-to-3' direction. **The resulting small DNA pieces—called Okazaki fragments after the biochemist who discovered them—are later joined together to form a continuous new strand**. The DNA strand that is made discontinuously in this way is called the lagging strand, because the backstitching imparts a slight delay to its synthesis; the other strand, which is synthesized continuously, is called the leading strand (Figure 6–13).

Figure 6–17 Multiple enzymes are required to synthesize Okazaki fragments on the lagging DNA strand. In eukaryotes, **RNA primers are made at intervals of about 200 nucleotides on the lagging strand, and each RNA primer is approximately 10 nucleotides long**. **Primers are removed by nucleases that recognize an RNA strand in an RNA/ DNA helix and degrade it; this leaves gaps** that are filled in by a DNA repair polymerase that can proofread as it fills in the gaps. The completed fragments are **finally joined together by an enzyme called DNA ligase, which catalyzes the formation of a phosphodiester bond between the 3'-OH end of one fragment and the 5'-phosphate end of the next, thus linking up the sugar–phosphate backbones**. This nicksealing reaction requires an input of energy in the form of ATP (not shown; see Figure 5–18)




Okazaki fragment
5' phosphate
3'OH
ATP
3'
5'
5'
3'
DNA lagging strand
STEP 1
ATP
used
STEP 2
AMP
released