

DNA Replication

Learning objective 6.2.A Describe the mechanisms by which genetic information is copied.

Name: _____

Date: _____

Period: _____

Use the tool **Copy Both Sides**. Parts 1 and 2 use **Three models, one experiment**, Part 3 uses **At the fork** and Part 4 uses **Why the copy is accurate**. The first two parts are as much about **how an experiment discriminates between hypotheses** as about DNA. Watch which round rules out which model.

Part 1 · What each model predicts

Open **Three models, one experiment** and step the slider from 0 to 2. Record what each model predicts at each round — how many bands, and where.

Rounds	Conservative	Semiconservative	Dispersive
0			
1			
2			

1. The real result after one round was a single intermediate band. State which model this rules out, and which models survive it.

2. Explain why one round of replication could not have identified the correct model on its own.

Part 2 · The second round

Stay on the same tab. The real result after two rounds was **two bands — one intermediate and one light**. Set the slider to 2, 3 and 4 and follow the semiconservative tube.

Rounds	Molecules	In the intermediate band	In the light band	Fraction intermediate
1				
2				
3				
4				

3. Explain why the second round is what separates the semiconservative model from the dispersive one.

4. The intermediate band never disappears, however many rounds you run. Explain why, in terms of the original strands.

5. State one thing all three models predict identically at every round, and explain why that makes it useless as evidence.

Part 3 · At the fork

Switch to **At the fork**. Fragments are **200 bases** throughout. Work each row out before you read it off.

Length copied	Leading strand pieces	Okazaki fragments	Ligase joins	Primers
400 bases				
1000 bases				
2000 bases				
5000 bases				

6. One column of your table does not change as the length increases. Identify it and explain why.

7. Explain why the two strands are copied differently, given that the two templates are chemically identical.

8. Explain why the number of primers is one more than the number of Okazaki fragments.

Part 4 · Putting it together

These do not need the tool.

9. State the role of helicase, primase, DNA polymerase and ligase in replication.

10. Explain why one strand of DNA is enough to rebuild the whole molecule.

11. A lagging strand of 1200 bases is made in fragments of 200 bases. Calculate the number of Okazaki fragments and the number of ligase joins, showing your working.

12. Explain how replication achieves an error rate far lower than base pairing alone would give, and why the mechanisms multiply rather than add.

What the model simplifies

The gradient is drawn as sharp bands at exact positions. Real bands are fuzzy, and the intermediate band becomes hard to see against the light band well before it disappears — which is why the experiment was run for a small number of generations.

Density is shown as the fraction of a molecule that is heavy nitrogen, from 1.0 down to 0. The real measurement is a buoyant density in caesium chloride, which is not linear in that fraction; the ordering of the bands is right and the exact spacing is not.

The fork is drawn with one fragment size and a single fork. A real chromosome opens at many origins at once, each with two forks, and Okazaki fragments are 1000–2000 bases in bacteria and around 100–200 in eukaryotes. The tool uses 200 throughout so the arithmetic stays checkable.

The enzymes are listed in the order the course asks for. A real fork also involves single-strand binding proteins holding the templates apart, a sliding clamp keeping the polymerase attached, and a separate enzyme removing the RNA primers before ligase seals the joins.

The error rates are order-of-magnitude figures for the stages of accuracy, not measurements of a particular organism, and are used because the multiplication is the point.