AP BIOLOGY · UNIT 6 · TOPIC 6.2

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**. Parts 1 and 2 are as much about **how an experiment discriminates between hypotheses** as about DNA. Notice which round rules out each model.

Part 1 · What each model predicts

Open **Three models, one experiment** and move the Rounds of replication slider from 0 to 2. At each round, record the number of bands each model predicts and where each band sits.

Rounds	Conservative	Semiconservative	Dispersive
0			
1			
2			

1. The real result after one round of replication was a single band of intermediate density.
(a) Identify the model that this result rules out.

(b) Identify the models that are consistent with this result.

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 1, 2, 3 and 4 in turn. At each round, record the total number of molecules in the semiconservative tube and the number in each band, then calculate the fraction of the molecules that are in the intermediate band.

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

3. Explain how the result after the second round distinguishes between the semiconservative model and the dispersive model.

4. In the semiconservative model, the intermediate band is present after every round of replication. Explain why, in terms of the two original strands.

5. (a) Identify one prediction that all three models make identically at every round.

(b) Explain why this prediction cannot be used as evidence to distinguish between the models.

Part 3 · At the fork

Switch to **At the fork**. Okazaki fragments are **200 bases** long throughout. Calculate each row first, then drag the Length of the region copied slider to that length to check it.

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

6. (a) Identify the column of the Part 3 table that does not change as the length increases.

(b) Explain why this column does not change.

7. The two template strands at a replication fork are chemically identical. Explain why one new strand is made continuously and the other is made in fragments.

8. In every row of the Part 3 table, the number of primers is one more than the number of Okazaki fragments. Explain why.

Part 4 · Putting it together

Read the Why the copy is accurate tab, then answer questions 9 to 12.

9. Describe the role in DNA replication of each of these enzymes: helicase, primase, DNA polymerase and ligase.

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. Show your work for each part.
(a) Calculate the number of Okazaki fragments.

(b) Calculate the number of ligase joins needed to join the fragments.

12. (a) Explain how replication achieves an error rate far lower than base pairing alone would give.

(b) Explain why the error rates of the three 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 cesium 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.