PEEBEDU   Sickle Cell Simulation

Name: _____   Period: _____   Date: _____

Open **peebedu.com** and navigate to **Sickle Cell Simulation**. Read through the **Introduction** slides, which cover red blood cells and hemoglobin, the sickle cell mutation, genotypes and their effects, and the connection between sickle cell trait and malaria resistance. Click **Get Started** to begin.

Part 1 — Model Evaluation (MAPP Framework)

Scientific models are simplified representations of complex biological phenomena. Use the MAPP framework below to evaluate the Sickle Cell Simulation as a scientific model.

M — Mode

What type of model is the Sickle Cell Simulation? Describe how this computational simulation represents the connection between a DNA mutation, protein structure, and red blood cell shape.

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A — Accuracy

(a) Identify two things this simulation represents accurately about how a point mutation in the HBB gene affects hemoglobin and red blood cell function.

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_____

(b) Identify two things this simulation oversimplifies or leaves out about how sickle cell disease affects the human body.

_____

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_____

P — Purpose

What is the learning goal of this simulation? Explain how the Sickle Cell Simulation is designed to help you understand how a single nucleotide change can alter protein function and produce a disease phenotype.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries about gene therapy or hemoglobin biology might change or improve a simulation like this one.

Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for understanding how genotype determines phenotype?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the malaria toggle help you understand why the sickle cell allele persists in certain populations?

Part 2 — NGSS Questions

1.

Simulation Task: Set both Chromosome 11 copies to HbA Normal. Observe the DNA template strand, mRNA codons, and amino acid sequence displayed for codon 6 on both panels. Note the round red blood cells flowing smoothly through the blood vessel animation on the right.

Describe the process by which the DNA sequence of the HBB gene is used to produce the hemoglobin beta chain protein.

HS-LS1-1

2.

Simulation Task: Switch Copy 2 to HbS Sickle. Compare the DNA template strand, mRNA codon, and amino acid at position 6 between the two panels. Note how the single nucleotide change produces a different amino acid.

Explain how a single nucleotide substitution in the HBB gene results in a different amino acid being incorporated into the hemoglobin protein.

HS-LS3-1

3.

Simulation Task: Set both copies to HbS Sickle (homozygous HbS/HbS). Observe the red blood cell shapes in the blood vessel animation and note the change in blood flow compared to the normal genotype.

Describe the process by which replacing glutamic acid with valine at position 6 causes hemoglobin molecules to aggregate and red blood cells to change shape.

HS-LS3-1

4.

Explain why individuals who are heterozygous for the sickle cell allele generally have normal blood flow under most conditions.

HS-LS3-2

5.

Explain why the frequency of the HbS allele remains high in populations where malaria is endemic, even though homozygous HbS individuals have severe disease.
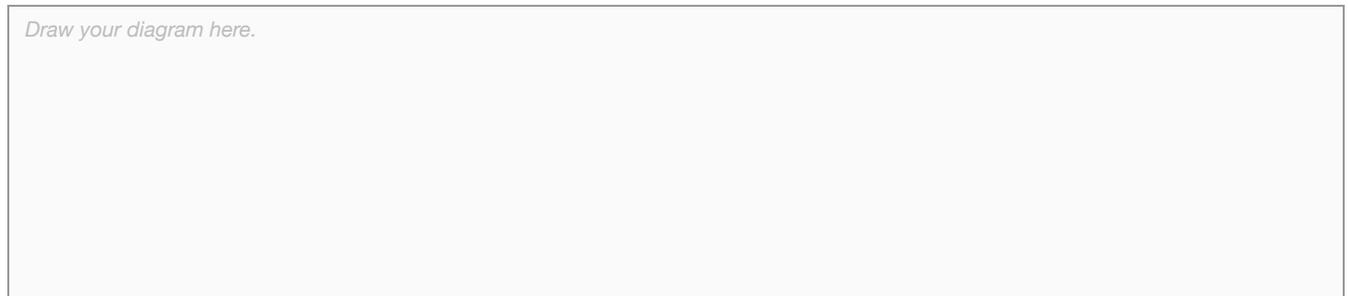
HS-LS4-2

6.

In the box below, draw a diagram comparing normal and sickled red blood cells. Show the arrangement of hemoglobin molecules inside each cell type and how cell shape affects blood flow through a narrow vessel.

Draw your diagram here.

HS-LS1-1

7.

Simulation Task: Consider your observations across all three genotypes with and without malaria exposure. Think about what would happen to the frequency of the HbS allele if malaria were eliminated from a region.

Predict how the frequency of the HbS allele in a population would change over many generations if malaria were completely eliminated from that region, and explain why the change in environment would alter the direction of natural selection.

HS-LS4-3