PEEBEDU

Sickle Cell Simulation

Unit 6: Gene Expression and Regulation

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.

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.

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

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 — Free Response Questions

Conceptual Analysis

Question 1 — Point Mutation and Protein Function

> *Simulation Task: Set both **Chromosome 11 copies** to **HbA Normal**. Observe the DNA template strand, mRNA codons, and amino acid sequence for codon 6 on both panels. Note the blood vessel animation on the right. Then switch **Copy 2** to **HbS Sickle** and compare the sequences. Finally, set both copies to **HbS Sickle** and observe the red blood cell shapes and blood flow.*

(A) (1 pt) **Describe** the process by which a change in a DNA nucleotide sequence results in a different amino acid in the polypeptide chain.

(B) (1 pt) **Explain** how replacing glutamic acid with valine at position 6 of the hemoglobin beta chain alters the structure and function of the protein.

(C) (1 pt) **Predict** what would happen to oxygen delivery in an individual who is homozygous for the HbS allele during intense physical activity.

(D) (1 pt) **Justify** your prediction.

EK 6.3.A.2, 6.3.A.3, 6.4.A.3, 1.7.A.3, 1.7.A.5

Analyze Model / Visual Representation

Question 2 — Heterozygote Advantage and Natural Selection

> *Simulation Task: Set one chromosome copy to **HbA Normal** and the other to **HbS Sickle** (heterozygous, HbA/HbS). Observe the blood flow and person status display. Then toggle the **Malaria Exposure** switch ON and observe how the simulation represents the interaction between sickle cell trait and the malaria parasite. Compare the stats displayed for all three genotypes with malaria active.*

(A) (1 pt) **Describe** the process by which natural selection acts on phenotypic variation within a population.

(B) (1 pt) **Explain** why the frequency of the HbS allele remains high in populations where malaria is endemic.

(C) (1 pt) **Represent** the difference between normal and sickled red blood cells at the molecular level. Draw a diagram showing how hemoglobin molecules are arranged differently in each cell type and how this affects cell shape.

Draw your diagram here.

(D) (1 pt) **Explain** how a change in the environment, such as the elimination of malaria from a region, could shift the direction of natural selection acting on the HbS allele.

EK 7.1.A.2, 7.2.A.1, 7.2.A.2, 7.2.A.3