PEEBEDU

CFTR Channel Simulation

Name: _____ **Period:** _____ **Date:** _____

> Open **peebedu.com** and navigate to **CFTR Channel Simulation**. Read through the **Introduction** slides, which cover the CFTR protein, the central dogma, the deltaF508 mutation, membrane transport, and the cholera connection. 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 CFTR Channel Simulation as a scientific model.

M — Mode

What type of model is the CFTR Channel Simulation? Describe how this computational simulation represents the relationship between genotype, protein structure, and membrane transport.

A — Accuracy

(a) Identify two things this simulation represents accurately about how mutations affect protein function and membrane transport.

(b) Identify two things this simulation oversimplifies or leaves out about the real biological process from gene to functional protein at the cell membrane.

P — Purpose

What is the learning goal of this simulation? Explain how the CFTR Channel Simulation is designed to help you understand how a DNA mutation can alter protein structure and disrupt cellular function.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries about CFTR protein trafficking or gene therapy 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 the connection between genotype and phenotype?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the cholera toggle help you understand heterozygote advantage?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — From Gene to Protein: The Central Dogma and CFTR

> *Simulation Task: Set both the **Maternal Allele** and **Paternal Allele** to **Wild-type** and click **Run Simulation**. Observe the central dogma steps displayed on the left panel (DNA, mRNA, protein sequence) and the chloride ion movement on the membrane canvas. Then change one allele to **deltaF508** and run again. Compare the DNA sequences, mRNA codons, and protein products for both alleles.*

(A) (1 pt) **Describe** the process by which genetic information encoded in DNA is used to produce a functional protein.

(B) (1 pt) **Explain** how the deletion of three nucleotides in the deltaF508 mutation leads to a misfolded CFTR protein.

(C) (1 pt) **Predict** what would happen to chloride ion transport and mucus production in the lungs of an individual homozygous for the deltaF508 allele.

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

EK 6.3.A.2, 6.3.A.3, 6.4.A.1, 6.4.A.3, 1.7.A.3

Analyze Model / Visual Representation

Question 2 — Heterozygote Advantage and Selective Pressure

> *Simulation Task: Set one allele to **Wild-type** and the other to **deltaF508** (heterozygous). Run the simulation and observe chloride ion flow. Then activate the **Add Cholera** button and observe the change in ion movement and water flow. Compare this to the homozygous wild-type (both wild-type alleles) with cholera active.*

(A) (1 pt) **Describe** the process by which a change in amino acid sequence affects the three-dimensional structure and function of a protein.

(B) (1 pt) **Explain** why heterozygous carriers of the deltaF508 mutation have reduced vulnerability to cholera compared to homozygous wild-type individuals.

(C) (1 pt) **Represent** the structure of a cell membrane with an embedded CFTR channel protein. Label the phospholipid bilayer, the CFTR channel, and the direction of chloride ion movement under normal conditions.

Draw your diagram here.

(D) (1 pt) **Explain** how the persistence of the deltaF508 allele in human populations can be understood as a result of natural selection in environments where cholera is prevalent.

EK 1.7.A.3, 1.7.A.5, 2.3.A.1, 7.2.A.2