PEEBEDU

Operail (Operon Regulation)

Unit 6: Gene Expression and Regulation

Name: ______________________ **Period:** ________ **Date:** ______________

> Open **peebedu.com** and navigate to **Operail**. Click the **Introduction** button and read the popup, which explains how an operon functions using a train analogy: the promoter is a station, RNA polymerase is a locomotive, the operator is a signal switch, and the repressor is a crossing gate. Then explore the simulation by toggling components and clicking **All Aboard!** to run transcription.

Part 1 — Model Evaluation (MAPP Framework)

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

M — Mode

What type of model is Operail? Describe how this computational simulation represents operon regulation in prokaryotes. In your answer, identify at least three specific simulation elements and explain what each one is designed to show about gene regulation.

A — Accuracy

(a) Identify two things this simulation represents **accurately** about operon regulation. For each, name the specific simulation feature and explain what aspect of gene regulation it demonstrates.

(b) Identify two things this simulation **oversimplifies or leaves out** about operon regulation. Consider what you cannot observe in the simulation that would be important for a complete molecular-level understanding of how operons function in living cells.

P — Purpose

What is the learning goal of this simulation? Explain how Operail is designed to help you understand how regulatory sequences, repressors, and transcription factors control gene expression in prokaryotes. In your answer, connect at least one specific simulation feature to a biological scenario where operon regulation is important for a prokaryotic cell.

P — Permanency

Could this model change with new scientific evidence? Describe one way that new discoveries might change or improve a simulation like Operail. Explain why scientific models, including computational simulations, are revised as new evidence becomes available.

Small-Group Discussion

With your group, discuss the following:

- What are the strengths of this simulation as a model for operon regulation?
- What are its limitations?
- If you could add one feature to improve this simulation, what would it be and why?
- How does the train analogy help (or hinder) your understanding of the molecular mechanisms of gene regulation?

Part 2 — Free Response Questions

Conceptual Analysis

Question 1 — Repressor Regulation and Gene Expression

> *Simulation Task: Toggle all genes (A, B, C) and the promoter ON, and toggle the repressor OFF. Click "All Aboard!" and observe the Event Log as RNA polymerase transcribes the genes and mRNA is delivered to the ribosome. Then click "Reset," toggle the repressor ON, and click "All Aboard!" again. Compare the two outcomes.*

(A) (1 pt) **Describe** how negative regulatory molecules, such as repressor proteins, inhibit gene expression by binding to DNA and blocking transcription in a prokaryotic operon.

(B) (1 pt) **Explain** how the presence or absence of the repressor at the operator determines whether RNA polymerase can transcribe the structural genes in the operon, and how this leads to differential gene expression that influences cell products and functions.

(C) (1 pt) **Predict** what would happen to gene expression in a bacterial cell if a mutation in the operator prevented the repressor from ever binding, even when the repressor protein is present and functional.

(D) (1 pt) **Justify** your prediction by explaining how the inability of the repressor to bind to a mutated operator disrupts normal gene regulation and results in a specific pattern of gene expression.

EK 6.6.A.2, 6.6.B.1

Analyze Model / Visual Representation

Question 2 — Operon Structure and Transcription Factor Function

> *Simulation Task: Toggle all genes (A, B, C), the promoter, and the transcription factor ON. Toggle the repressor OFF. Click "All Aboard!" and observe how the transcription factor affects transcription in the Event Log. Then click "Reset," toggle the transcription factor OFF (keeping everything else the same), click "All Aboard!" again, and compare.*

(A) (1 pt) **Describe** how RNA polymerase and transcription factors bind to promoter sequences to initiate and regulate the rate of transcription in prokaryotic operons.

(B) (1 pt) **Explain** how the coordinated regulation of multiple genes within a prokaryotic operon allows a bacterial cell to efficiently control the production of related proteins in response to environmental signals.

(C) (1 pt) **Represent** the structure of a prokaryotic operon and its regulatory elements.

Draw your labeled diagram here.

(D) (1 pt) **Explain** how a mutation in the promoter region of an operon that prevents RNA polymerase binding could affect the phenotype of a bacterial population over many generations.

EK 6.5.B.1, 6.6.A.1

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