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Precision Microbiome Engineering
NSF Engineering Research Center

This lesson plan was created by a teacher participating in the Research Experiences for Teachers (RET) program from the Precision Microbiome Engineering Research Center. Are you interested in spending part of your summer in a lab getting paid to do microbiome research and create lesson plans?

Learn more here: https://premier-microbiome.org/for-teachers-ret/

Lesson Plan created by April Hester

Title:

Who Made Them Sicker? Analyzing Hospital-Acquired Infections with Bioinformatics

Overview:

In this investigation-based biology lesson, 10th-grade students will act as medical detectives. They will analyze patient case studies and use DNA sequences to identify hospital-acquired pathogens using the NCBI BLAST tool. Students will apply knowledge of microbial biology, DNA structure, and bioinformatics to classify pathogens and propose interventions to prevent future infections.

Vocabulary:

- Hospital-acquired infections (Nosocomial infections)
- Pathogen
- DNA sequence
- BLAST (Basic Local Alignment Search Tool)
- Antimicrobial resistance
- Bacterial vs viral infection
- Hospital-acquired infection (HAI)
- Bioinformatics
- Septicemia, UTI, COVID-19, Pneumonia

Learning Objective:

1. Students will analyze and interpret DNA sequence data to identify microbial pathogens using BLAST
2. Students will evaluate case study symptoms and clinical context to infer disease origin
3. Students will classify the pathogens by domain and type (bacterial, viral, fungal)
4. Students will apply knowledge of genetics, microbiology, and epidemiology to real-world healthcare challenges

Curriculum Standards:

NC Standard Course of Study:

LS. Bio.5.2 Engage in argument from evidence to evaluate various solutions to reduce the impact of human activities on biodiversity and ecosystem health.

LS. Bio.8.2 Obtain and communicate information that summarizes the impact of biotechnology applications on the individual, society, and the environment, including agriculture and medicine.

Science Practices: Analyzing and interpreting data, engaging in argument from evidence, using computational tools

Class Time Required:

2 class periods (52 minutes)

- 30 min: Introduction to DNA Sequencing (16s ribosomal subunit), Hospital-acquired infections and pathogen types, BLAST
- 40 min: Case study analysis and DNA comparison
- 30 min: Answer Critical thinking questions

Choice: Extended activity will take 1 class period (52 minutes) to complete

Materials and Technology:

6 patient case studies with original condition + symptoms developed post-admission
DNA sequence files (FASTA format or printed sequences)
Computers with internet access (for BLAST: https://blast.ncbi.nlm.nih.gov/)
Graphic organizer worksheets

Safety:

Ensure students are using online tools responsibly
Review digital citizenship before online research
No lab-based hazards present

Teacher Preparation for Activity:

Curate 6 detailed patient scenarios with accurate symptom progressions
Generate or select realistic DNA sequences for common nosocomial pathogens (e.g., E. coli, Pseudomonas aeruginosa, Klebsiella pneumoniae, MRSA, C. difficile, Norovirus)
Test DNA sequences in BLAST and pre-download matches as backup

Student Preparation of Activity (*optional*):

Pre-lesson reading on:

DNA and genetic sequencing
Pathogen types (bacterial, viral, fungal)
How to read BLAST output (basic overview)

Introduction:

Amoeba Sisters video: Bacteria (With a comprehensive handout)
Khan Academy: DNA and RNA Structure
Virtual lab: HHMI Biointeractive: “Bacterial Identification Using DNA Sequences”

Procedure:

Engage (15 min)

- Spark curiosity and connect with real-world healthcare challenges
- Pose the question: “Why do some patients get sicker in hospitals?”
- Brief presentation on hospital-acquired infections (HAIs), types of pathogens, preventative practices to decrease HAIs
- Quick review: Bacteria vs. viruses, and basics of DNA sequencing

Explore (15 min)

- Introduce BLAST as a tool to compare DNA sequences to known organisms
- Provide tutorial/demo on how to input DNA sequences and interpret results

Explain (30 min)

- Gallery Walk: students rove around the class and read cases
- Fill out the provided graphic organizer with findings and analysis
- Two scenarios describe patients that have acquired a hospital infection
- DNA sequences are provided for BLAST search to assist in matching the DNA sequence with the pathogen causing the HAI
- Students use **BLAST** to match the DNA to a known organism.
- Research the pathogen’s characteristics (transmission, symptoms, antibiotic resistance)
- Fill in Hospital-Acquired Infection Case Study chart and BLAST graphic organizer

Elaborate (20 min)

- Discuss the case studies, identify pathogen and classification
- Groups discuss and create what measures could have prevented the infection (e.g., hygiene protocols, antibiotic stewardship, tools, apps, machines)
- Complete Design Challenge Worksheet

Evaluate (10 min)

- Class discussion: How does identifying pathogens through DNA help control outbreaks?
- Students complete reflection questions (attached to the graphic organizers)

Differentiation:

Support: Provide guided BLAST instruction with screenshots; offer structured case notes with hints
Extension: Encourage advanced students to research antibiotic resistance genes or propose epidemiological tracking strategies

Assessment/Check for Understanding:

Completed graphic organizer with:

- BLAST match
- Pathogen classification
- Evidence from case study and DNA

Exit Ticket: Describe one advantage of using DNA to identify infections.

Required resources:

NCBI BLAST

Supplemental Resources *(optional)*:

Hospital Acquired Infection exercise