Cornell Guided Notes

Genetics of Disease (Medical Interventions) | 2026-09-10

Name	Period	Date	Lesson
		2026-09-10	

Lesson focus

Pathogen-ID report submission

Key words and questions	Prepared details and student notes
Essential question **What is today's target?**	Submit a complete pathogen-identification report defending your BLAST result with evidence. Big idea: How does a scientist turn computational evidence into a defensible scientific claim? **My notes, examples, and questions**
Key words **What vocabulary unlocks the lesson?**	- DNA sequence - PCR - Sanger sequencing - BLAST - E-value - query coverage - control **My notes, examples, and questions**

Cornell Notes - Continued

Key words and questions	Prepared details and student notes
Must-know ideas **What should I understand by the end?**	- A credible identification report cites percent identity, E-value, and query coverage together, not just one number. - A control run proves the tool worked correctly; without it, the result cannot be trusted. - Sequence-based identification has limits: databases are incomplete, and contamination or sequencing errors can produce false matches. **My notes, examples, and questions**
Process notes **What happens during class?**	- 0-10 min: Assemble materials: hit-table screenshot, top hit data, control run result, and comparison table from Thursday - 10-25 min: Draft the Claim: one sentence naming the pathogen with full organism name - 25-45 min: Write the Reasoning paragraph: cite E-value, query coverage, and percent identity; explain why each supports the claim - 45-58 min: Add the control explanation: how the control run validates the workflow - 58-70 min: Write the limitation sentence; proofread the full report for accuracy and completeness - 70-80 min: Submit in the course shell; confirm it shows as turned in **My notes, examples, and questions**

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Cornell Notes - Continued

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Steps and evidence **What do I do and turn in?**	- Assemble your hit-table screenshot, top organism name, E-value, and query coverage. - Write a Claim naming the pathogen and a Reasoning paragraph using your match-quality numbers. - Explain how your control run shows the workflow was reliable. - Add one sentence on a limitation of identifying a pathogen by sequence alone. - Submit the report in the PLTW course shell. - Confirm it is turned in and note what you would test to confirm in a real lab. Evidence: Lab report - Pathogen-ID report: claim naming organism, reasoning paragraph citing E-value/query coverage/percent identity, control validation explanation, and one limitation sentence. **My notes, examples, and questions**
Checks for understanding **How do I know I got it?**	- You will be able to defend a pathogen ID with BLAST evidence. - You will be able to cite E-value and coverage to justify a match. - You will be able to state a limitation of sequence-based identification. **My notes, examples, and questions**

Cornell Notes - Continued

Key words and questions

Prepared details and student notes

Lab or safety notes What must I handle carefully?

Supplies:
- Lab computers with internet access
- NCBI BLAST nucleotide tool
- Unknown pathogen DNA sequence file
- Known control sequence file
- Shared results spreadsheet
- Screenshot tool

My notes, examples, and questions

Summary

Today's lesson focused on Pathogen-ID report submission. The main target was: Submit a complete pathogen-identification report defending your BLAST result with evidence. The evidence of learning is Lab report: Pathogen-ID report: claim naming organism, reasoning paragraph citing E-value/query coverage/percent identity, control validation explanation, and one limitation sentence.. In my own words, the most important idea from today is:

My summary

My final question or connection