Branches in DNA

Use NCBI sequences to test a plant family tree

BOT.2.5 "Enrichment: Referencing the National Center for Biotechnology Information's gene/protein databases, propose and design a scientifically supportable cladogram or phylogenetic tree that illustrates the evolutionary modifications of the plant..."

NAME _____ DATE _____

1 READ AND MARK

Read it twice

YOUR JOB Underline each NCBI record named in the passage, circle the gene to compare, and number the two proposed branches in order from older to more recent. These marks will help you trace how sequence evidence supports a tree.

Testing a Plant Family Tree

1. A pine and a flowering plant both make seeds, but how can DNA help show where they belong on a plant family tree? Compare the same gene in each plant. The chloroplast gene *rbcL* is useful because it occurs in many photosynthetic plants. NCBI stores chloroplast genome records for the moss *Physcomitrium patens* (NC_005087), the fern *Adiantum capillus-veneris* (NC_004766), the pine *Pinus thunbergii* (NC_001631), and the flowering plant *Arabidopsis thaliana* (NC_000932). Each genome record contains an *rbcL* sequence that can be retrieved for comparison.

2. First, find *rbcL* in each NCBI record and align the four DNA sequences. An alignment places corresponding positions in the same column, even if a sequence needs a gap. Compare matching positions across all four plants, not pieces taken from different genes. The expected tree groups pine and *Arabidopsis* as seed plants. The fern joins that pair on an older branch, and the moss joins farther back. Check whether the aligned sequences support those branches. A single shared letter is weak evidence because it could arise by chance; a pattern across many positions is stronger.

3. Add traits to the tree only after its branches are clear. Moss lacks the vascular tissue found in ferns and seed plants. The pine and *Arabidopsis* share seeds, while flowers belong on the *Arabidopsis* branch, not the pine branch. These traits describe evolutionary changes, but they do not replace the sequence comparison. You could expand the test with the liverwort *Marchantia polymorpha* (NC_001319). Retrieve its *rbcL* sequence and add it to the same alignment. If the new sequence changes the proposed branches, report that result rather than forcing the DNA to fit the first tree.

2 ANSWER WITH EVIDENCE

Use the passage

1. Which two NCBI records would you compare to test the proposed seed-plant pair? Name the gene you would align.

2. In the proposed four-plant tree, where does the fern branch relative to the pine and *Arabidopsis*? What sequence comparison would test that placement?

3. Why would matching letters at just one aligned *rbcL* position be weak support for a branch?

4. If aligned sequences instead place the moss next to the fern, what should you do with the proposed tree and its trait labels?

3 YOUR TURN

Your own words

Use NCBI to retrieve and align *rbcL* from the five records named in the passage. In the box, draw a proposed five-plant tree, label its tips with the record accessions, mark where vascular tissue, seeds, and flowers arose, and write which pair your alignment supports most clearly.

Branches in DNA

PART 1 · READ AND MARK

Underline each NCBI record named in the passage, circle the gene to compare, and number the two proposed branches in order from older to more recent. These marks will help you trace how sequence evidence supports a tree. Accept any marking that follows this job and points at the right text.

PART 2 · ANSWERS

#	QUESTION	ANSWER
1	Which two NCBI records would you compare to test the proposed seed-plant pair? Name the gene you would align.	**Compare *Pinus thunbergii* (NC_001631) and *Arabidopsis thaliana* (NC_000932) using their *rbcL* sequences.**
2	In the proposed four-plant tree, where does the fern branch relative to the pine and *Arabidopsis*? What sequence comparison would test that placement?	**The fern branches before the pine and *Arabidopsis* split. Compare aligned *rbcL* positions to see whether pine and *Arabidopsis* share a stronger sequence pattern with each other than either shares with the fern.**
3	Why would matching letters at just one aligned *rbcL* position be weak support for a branch?	**One match could occur by chance. A pattern across many corresponding positions provides stronger support.**
4	If aligned sequences instead place the moss next to the fern, what should you do with the proposed tree and its trait labels?	**Report and examine the different sequence result rather than forcing the proposed tree. Reconsider the branch placement, then place trait labels on the tree being evaluated.**

PART 3 · YOUR TURN (SAMPLE ANSWER)

Sample tree: ((Marchantia NC_001319, Physcomitrium NC_005087), (Adiantum NC_004766, (Pinus NC_001631, Arabidopsis NC_000932))). Mark vascular tissue on the branch leading to the fern and seed plants, seeds on the branch leading to pine and Arabidopsis, and flowers on the Arabidopsis branch. The aligned *rbcL* sequences support the pine and Arabidopsis pair most clearly.

Accept a different five-plant branching pattern if the student explains how the retrieved, aligned NCBI sequences support it. Trait labels should identify inferred changes on branches, not serve as a substitute for sequence evidence.