Gene Match Detective

Compare plant genome records using sequence matches and gene order.

BOT.6.2 "Compare and contrast genomes using plant genetic databases (e.g., BLAST or plant GDB)."

NAME _____ DATE _____

1 READ AND MARK

Read it twice

YOUR JOB Underline the two BLAST match measures, circle the sentence that limits claims about whole genomes, and write 1 beside sequence evidence and 2 beside neighboring-gene evidence.

Which Grass Genome Matches?

1. A seed lab wants to compare a rice starch-related gene with sequences in other grasses. Researchers copy its 600-base DNA sequence from a plant genome database and search maize, sorghum, and barley genomes with BLAST. The search reports local alignments, not whole-genome similarity. The classroom results below are simulated, but they use the kinds of evidence databases provide.

2. In the table, identity means the percentage of matching bases within the aligned stretch. These results have no gaps, so aligned bases shows how much of the rice query is covered. A high percentage across a short stretch can be misleading. Researchers also inspect neighboring genes in each genome record to compare the arrangement around the matched gene.

SIMULATED PLANT GENOME DATABASE RESULTS

Plant genome	Identity (%)	Aligned bases	Nearby gene order
Rice (query)	100	600	M, S, N
Maize	92	590	M, S, N
Sorghum	96	580	M, S, N
Barley	99	120	N, S, M

3. The letters M and N name two genes beside the starch-related gene, labeled S. Reading left to right gives their order in each genome record. Matching order supports a shared local arrangement, while a different order calls for further checks. Neither a strong BLAST hit nor matching neighbors proves that two entire genomes are nearly identical.

2 ANSWER WITH EVIDENCE

Use the passage

1. Compare the maize and sorghum matches to rice. Which has higher identity, which covers more bases, and how does their nearby gene order compare?

2. Barley has higher identity than sorghum. Why does the table give stronger evidence for a similar rice gene region in sorghum?

3. Compare the maize and barley records. Which shares rice's nearby gene order, and why would identity percentage alone give an incomplete comparison?

4. What does the rice and sorghum comparison suggest about one gene region, and what can it not establish about their entire genomes?

3 YOUR TURN

Your own words

A second rice gene is 500 bases long. BLAST finds a 94% match across 490 bases in maize and a 98% match across 80 bases in barley; both records show the same nearby gene order as rice. In three or four sentences, compare the evidence, choose the more convincing match for this gene region, and state one conclusion you cannot draw about the entire genomes.

ANSWER KEY

Gene Match Detective

PART 1 · READ AND MARK

Underline the two BLAST match measures, circle the sentence that limits claims about whole genomes, and write 1 beside sequence evidence and 2 beside neighboring-gene evidence. Accept any marking that follows this job and points at the right text.

PART 2 · ANSWERS

#	QUESTION	ANSWER
1	Compare the maize and sorghum matches to rice. Which has higher identity, which covers more bases, and how does their nearby gene order compare?	**Sorghum has higher identity (96% versus 92%). Maize covers more bases (590 versus 580). Both have the same nearby gene order as rice.**
2	Barley has higher identity than sorghum. Why does the table give stronger evidence for a similar rice gene region in sorghum?	**Sorghum matches across 580 bases and has rice's nearby gene order. Barley matches across only 120 bases and has a different nearby gene order.**
3	Compare the maize and barley records. Which shares rice's nearby gene order, and why would identity percentage alone give an incomplete comparison?	**Maize shares rice's nearby gene order. Barley has higher identity, but its match covers only 120 bases, compared with 590 for maize.**
4	What does the rice and sorghum comparison suggest about one gene region, and what can it not establish about their entire genomes?	**The matched region has 96% identity across 580 bases and the same nearby gene order. This does not establish that the entire genomes are nearly identical.**

PART 3 · YOUR TURN (SAMPLE ANSWER)

Barley has higher identity than maize, but its match covers only 80 of the rice gene's 500 bases. The maize match covers 490 bases at 94% identity. Both records have the same nearby gene order as rice, so that evidence does not separate them. Maize provides the more convincing match for this gene region, but these results cannot show that the entire maize genome is more similar to rice's genome.

Accept answers that weigh both identity and aligned length rather than ranking matches by identity alone. Gene order supports comparisons of local regions, not claims about whole-genome similarity.