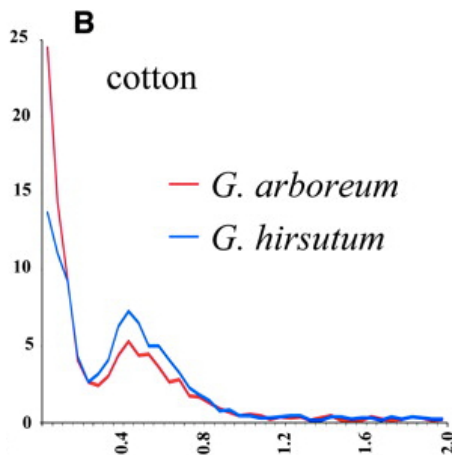


Name:

BIOL415 Quiz #6:



1. Figure 2B from Blanc and Wolfe 2004 shows the percent of gene duplication events (y-axis) as a function of substitutions per synonymous site (K_s , x-axis) for two species of cotton. Here, a K_s of 1.0 equals approx. 30 million years.

Based on these data, was an ancestor of these two species likely polyploid? Explain why/why not, including not only the graphical evidence but also the biological processes underlying it. 2–3 sentences, 2 pts.

An ancestor of these two species ($K_s = 0.3\text{--}0.6$) was likely (paleo)polyploid (0.5 pts). This can be seen by the secondary peak of gene duplication events around this time (0.5 pts) that corresponds to a large-scale gene duplication event (0.5 pts), likely a polyploid event. Individual gene duplication is otherwise expected to occur at some background rate followed by a steady rate of duplicate gene loss, which should result in an exponential decay of duplicate pairs over time in the absence of a large-scale duplication event (0.5 pts for this or something similar).

NOTE: K_s is NOT increased by polyploidy, and that is NOT what this figure shows. The figure shows an increase in the **number of duplicate genes** of a particular age (estimated by their K_s). K_s , because it only encapsulates synonymous substitutions, is not likely to pick up the signal of relaxed selection on duplicate pairs.

2. Agree or disagree with the following statement, including two pieces of evidence that support your stance: “Plants with bigger genomes are more advanced or complex than plants with smaller genomes”. 2-3 sentences, 2 pts.

This statement is not correct. There are several pieces of evidence you could use to refute it (but other reasonable points were also accepted):

- C value paradox suggests that complexity is not correlated with genome size.
- Large genome sizes in plants are largely from repetitive elements which contribute minimally to complexity.
- Large genome sizes can be a product of polyploidy which generally does not increase complexity.
- Ferns, a basal lineage, have some of the largest genome sizes.
- Small genome size is often found in plants with nitrogen limitation, not low complexity

1 pt for each piece of evidence.

3. Many original organelle genes have been lost or transferred to the host cell nucleus over time. Describe one hypothesis to explain the maintenance of the reduced organelle genomes that remain. 1 sentence, 1 pts.

Any one of the following described clearly:

- It is beneficial for the organelle to retain genes coding for hydrophobic proteins, as these are difficult to import into the organelle.
- There is potentially a fitness advantage to the co-localization of coding sequence and regulatory elements.
- Structural proteins that maintain redox balance in membranes must be synthesized when/where they are needed.
- Plastid genomes are also involved in the production of pigments and in fatty acid biosynthesis, which could explain their retention even in non-photosynthetic plants (must mention non-photosynthetic plants for full point).