

In brief: Name and describe the genes used in phylogenetic analysis and “bar-coding” of plants, and discuss the advantages and disadvantages of each gene for these purposes (250-300 words). **Due Tues Oct 28. Value: 5%**

Efforts to determine evolutionary history and relationships of organisms, or phylogenetic analysis, are increasingly based on sequence analysis of selected genes or regions of DNA sequence. There is a lot of DNA to choose from, and different genes or regions vary to differing degrees, with different levels of faithfulness to the evolutionary record. A “conserved” gene evolves slowly, and may be excellent for resolving the relationships of groups of organisms that diverged long ago, but would show no resolution in a phylogeny of closely related (recently evolved) taxa. Sometimes, we just want to know what something is – what is its name? For this, we want a region of DNA that is relatively invariant across members of a species, but clearly distinct from other species. The algorithm for identification might be based on simple matching, not phylogenetic analysis; indeed, a phylogeny based on this variable gene might not accurately portray deep evolutionary branches. This piece of DNA would be described as moderately to highly variable; too highly variable and it would be great for distinguishing individuals, but no longer any help at distinguishing species. For some organisms (which?), the Barcode of Life group based in Guelph <see <http://www.barcodinglife.org/views/login.php>> has selected the mitochondrial CoI gene (and what does that mean?) as a piece of DNA that acts as a species barcode. Unfortunately (but not surprisingly), no single gene works for all groups of organisms, and the bar-coders of fungi and plants are left looking for more suitable genes to act as barcodes for their groups of organisms.

In your review, which will amount to about one page of text (250-300 words, counting just the text - not the title, your name, or your references), summarize the primary genes (name and location – i.e., nuclear, mitochondrial or chloroplast) used for phylogenetic analysis and bar-coding of plants, and discuss the advantages and disadvantages of each gene (or group of genes) for these purpose. You will need to look for recent papers (perhaps also websites) reporting results of phylogenetic analyses and bar-coding, and papers that actively discuss the advantages or problems of particular genes for these purposes.

Be sure to use the scientific writing style, and try to make effective points (i.e., clearly convey facts) in as few words as possible so that your paper has real substance despite its brevity. Avoid fluff.

The format of your paper should be exactly:

Title

Your name, SN

Body of text (several paragraphs, with logical organization including a beginning, middle, and a concluding statement at the end), of 250-300 words

References (use the format of American Journal of Botany – i.e., Keeling 2004 or Palmer et al. 2004)

Save your file as a Word file (.doc, **not .docx**) or pdf, and submit it on OwlWebCT

<<https://owl.uwo.ca/webct/logon/419321598051>> by 5 pm **Tues Oct 28**.

Grading:

1. Suitable articles/websites chosen (the number required will depend on their content): **(+1)**
2. Clear, concise summary of the issues, the genes or gene regions, advantages/disadvantages, and a sense of where we are now and might be going next: **(+4)**
3. Incorrect grammar or spelling: **(-1)**
4. Incorrect reference citation or reference formatting: **(-1)**
5. Plagiarism (copying any part of your paper from a classmate or from the web, etc.): **(-5, and will be reported to the Dean for possible academic sanction)**