



Biology: Phylogenetic analysis

Paper citation: Palermo MP, Elwess NL (2014). Characterization and Phylogenetic Analysis of the Cytochrome B Gene (*cytb*) in *Salvelinus fontinalis*, *Salmo trutta* and *Salvelinus fontinalis* X *Salmo trutta* within the Lake Champlain Basin. J Emerging Investigators 18: 1-9

Paper questions

In reading through the assigned papers, please answer the following questions:

1. What is phylogenetic analysis?

Phylogenetic analysis is the approach of using similarities in DNA to learn about evolutionary relationships between different species.

2. For what reasons do the authors propose that routine genetic screening of trout populations is important?
 - 1) **The NYDEC has made genetic screening of brook trout populations a priority due to their declining numbers.**
 - 2) **Brook trout populations serve as a quality indicator for coldwater habitats.**
 - 3) **When non-native fish (such as brown trout) are stocked in coldwater ecosystems, they often breed with native populations of brook trout. The resulting offspring are sterile, thus interbreeding (which can be assessed by genetic screening) can severely impair brook trout populations.**
3. Why is the cytochrome b (*cytb*) gene an attractive genetic marker for DNA analysis?

Cytochrome b is a gene in mitochondria that is often used in phylogenetic studies. Mitochondria DNA genes are attractive genetic markers due to their rapid evolutionary rates compared to that of DNA from the cell nucleus.



4. Describe the authors' experimental approach.

The authors collect trout from three locations in the Lake Champlain Basin, sequence the *cytb* gene from each fish, and align the DNA, comparing sequences through a CLUSTALW analysis. The authors then infer genetic relationship distance between samples and construct phylogenetic trees.

5. What was a secondary hypothesis of the experiment?

The authors hypothesized that would find genetic diversity in trout populations, and that the further the sample collection site, the greater the differences in their DNA would be.

The authors also hypothesized that there may be differences in DNA sequence between their samples and the sequences found within a national database (NCBI).

6. The authors find that there are codon usage differences between the genetic samples collected by the others and those in public genetic databases. What are codons? Why is it interesting that the authors found differences in codon usage?

Codons are three-nucleotide long codes with DNA that carry information regarding which amino acids to use in proteins. For example, CCA encodes for Proline, and CGA encodes for Arginine. However, CCT, CCC, and CCG can also encode for Proline. It is interesting that the authors found differences in codon usage because it suggests that while DNA mutations (critical to the process of evolution) are taking place within the populations, there is an evolutionary force constraining proteins to maintain the same amino acids. It's also indicative of genetic diversity.



7. What relationship do the authors find between distance and genetic diversity, based on their samples collect in Vermont vs. those collected in New York?

The authors find no relationship between distance and genetic diversity.

8. Propose two follow-up experiments that could be performed given the data presented in this paper.

The authors might sequence brook trout populations from a different watershed separated by land (isolated ecosystems) to ask whether there is still no relationship between genetic diversity and distance.

In addition, the authors might sequence more mtDNA genes or even genes within genomic DNA.