



CALIFORNIA STATE SCIENCE FAIR 2014 PROJECT SUMMARY

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Project Title Tree Relations: Investigating Tree Evolution Using Computer Science	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals Our project explores the evolutionary relationships between native and non-native trees using their rubisco sequence and the computer program Clustal Omega.</p> <p>Methods/Materials In this project, we explored relationships between California evergreens using their rubisco (ribulose-1,5-bisphosphate carboxylase/oxygenase) sequences, available on the GenBank database. Rubisco is a specialized protein involved in carbon fixation. We took the known sequences and used the computer program Clustal Omega to create a phylogram that displayed their evolutionary relationships and grouped them by theoretical common ancestor. Then, we identified non-native, sequenced evergreens similar to the ones we had used and hypothesized where on the phylogram they would fit based on their genera classification and physical characteristics. In order to better understand how sequences are compared on computer programs similar to Clustal Omega, we included on our board a Punnett square diagram showing the fundamentals of such an algorithm.</p> <p>Results Our post-hypothesis DNA phylogram mostly matched our hypothesis, with a few notable exceptions. Some of the trees that we expected to be together were not. Interestingly, the parts of our hypothesis that our DNA phylogram countered were shown as correct in our protein phylogram.</p> <p>Conclusions/Discussion This project led us to several interesting discoveries. When we started, we planned on only having DNA phylograms, but then realized that we needed to interrogate aligned protein phylograms as well. This is because mRNA comprises four nucleotides that are translated in groups of three into amino acids. However, each amino acid is encoded by multiple nucleotide triplets, which differ at the third position. As a result, changes can occur in the DNA sequence that may not be represented in the protein sequence. Because proteins perform the work inside the cell, only changes in the protein sequence affect function and potentially represent a significant difference between species. Our hypotheses were based on the genus classification Linnaeus created 300 years ago. While our post-hypotheses phylograms mostly supported Linnaeus classification, they differed in some notable ways. These differences may represent new information about the relatedness of tree species based on genomic similarities rather than physical characteristics.</p>	
Summary Statement We investigated the relationships between native and non-native trees using the computer program Clustal Omega.	
Help Received	