



# CALIFORNIA SCIENCE & ENGINEERING FAIR 2019 PROJECT SUMMARY

<b>Name(s)</b> <b>Tristan Pflieger</b>	<b>Project Number</b> <b>J0515</b>
<b>Project Title</b> <b>Are Minke Whales or Mice More Closely Related to Humans?</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives</b> Abstract</p> <p>Scientists use different sources of genetic material to determine the evolutionary relationship between species. They utilize RNA transcripts from the nucleus or mitochondria which act as code for important proteins in living organisms. In my research of understanding how many sources of RNA are required to generate phylogenetic trees that agree on lineage for the same sets of species, I've used three cytochrome c oxidase subunits from the mitochondria and four nuclear transcription factor y subunits, both from a Minke whale. Using the BLAST search tool and GenBank from the National Center for Biotechnology Information (NCBI) website, I created phylogenetic trees to determine how closely related minke whales are to other mammals (specifically rodents and humans). I included comparisons for zebrafish and plants for reference. All changeable options were set to default, with the exception of the Max Target Sequence, which was set to fifty rather than one hundred. Performed using the blastp algorithm.</p> <p>I've found that in both the nuclear and the cytochrome c oxidase subunits from the minke whale, five out of the seven trees show that rodents and humans are more closely related than Minke whales and humans. The other two trees show that the Minke whale and rodents are closer related, which is untrue. More of the trees are in agreement that rodents are more closely related to humans, which I believe to be correct. This proves that rodents and humans are more closely related than humans and Minke Whales are.</p> <p><b>Methods</b> Materials: A Computer-To use GenBank and BLAST search tool. Procedures: Open GenBank. Search Minke Whale under genomes. Click "proteins" and find the seven (cytochrome c 1-3, nuclear trans factor y 1-4). Take accession number and input into BLAST, keep all parameters default but change Max Sequence to 50. Click SMARTBLAST and from there select all additional and best hits, then click view full multiple alignment. Click view phylogenetic trees.</p> <p><b>Results</b> The results of my experiment are that mice are more closely related to humans. I derived this answer from consulting the seven phylogenetic trees I procured. Out of the seven, five agreed that mice were more closely related to humans. One stated that mice and Minke whales were closer, and the other said humans</p>	
<b>Summary Statement</b> I have found that mice are more closely related to humans than Minke Whales through observance of phylogenetic trees.	
<b>Help Received</b> Giacomo Bernadi, Professor of Ecology and Evolutionary Biology at UC Santa Cruz. Helped me understand BLAST and GenBank. My science teacher also helped me understand these sites as well as molecular biology.	