Name(s)

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Project Number

S0407

Project Title

Protein Sequences and the Testudines' Tree of Life

Abstract

Objectives/Goals

Determine if evolutionary trees for turtles, based on morphological characteristics, are as accurate as evolutionary trees made using DNA. Research the DNA similarities of squamates, mammals, birds, crocodiles, and testudines. Re-categorize these animals based on their protein sequences and determine if they share a common ancestry.

Methods/Materials

Research which animals are directly related to turtles using a morphological evolutionary tree. Select five genetic diseases afflicting humans. Identify mutated nuclear genes and chromosome locus then identify protein deficiency associated with each disease. Using taxonomy reports, identify various species of animals located on the evolutionary tree, selecting ~40. Capture related amino acid sequences using the NCBI/Genbank website. Using the BLAST program, identify the protein sequences of genetic diseases in humans, and then locate similar protein sequences in other organisms to determine if the same gene can be found. Organize/compile the amino acid sequences of the proteins from the various species in a FASTA format. Using a multiple sequencing alignment program, CLUSTAL W, line up the proteins from different sequences in a Distance Matrix. Build a dendrogram animal tree based on the specific proteins entered repeating steps for each disease.

Results

Studied five genetic diseases found throughout the animal kingdom: Thalassemia, Albinism, Sickle Cell Anemia, Myoglobinuria and Pituitary Gland disorders, from which their proteins were identified: alphaglobin, tyrosinase, betaglobin, myoglobin and prolactin, respectively. Distance matrixes were developed representing paired evaluations of species and how close they were related to each other. Some matrixes yielded very consistent data such as displayed with the betaglobin matrix. Contrary, myoglobin had extremely wide variability even within species. Resulting dendrograms were different from the ancestral dendrogram based on morphological characteristics.

Conclusions/Discussion

I successfully proved my hypothesis that a different animal tree would result from the analysis of amino acids/proteins. Combining all data from all proteins, yielded the following summary: Testudines and Birds are the closest relatives at 77% similarity by DNA; Testudines and Crocodiles have 75% in common; Testudines and Squamates have 73% in common; and Testudines and Mammals are the furthest relatives at 67% similarity by DNA.

Summary Statement

Evolutionary trees for testudines, based on morphological characteristics, are not as accurate as evolutionary trees made using DNA.

Help Received

Professor A. Islas for proving a tutorial on the use of NCBI's websites; Science Buddies on-line website for additional tutorial materials; Mrs. D. Watkins for encouragement; and finally my mother for giving me so much encouragement and assistance in understanding the websites, and focusing my research.