Phylogenetic Analysis of Cytochrome c Protein Sequences Across Vertebrates

Research Question

Do cytochrome c protein sequences accurately reflect the known evolutionary relationships between vertebrate species?
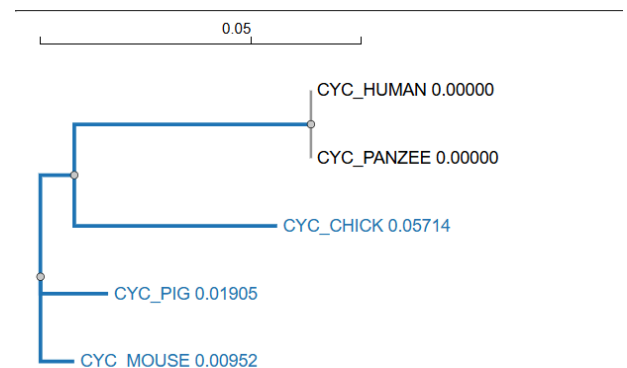
Introduction

Cytochrome c is a small hemeprotein, found in the mitochondria of eukaryotic cells. It is conserved across a wide range of species, except oxidase-negative bacteria, since they do not contain Cytochrome c oxidase. Cytochrome c is present in nearly all aerobic organisms because it plays an essential role in ATP production.It is commonly used in molecular evolution research with its ability to help compare and understand evolutionary relationships. This project analyzes the Cytochrome c protein sequences in animals and determines similarity in their evolution.

Methods

- Collected cyc-sequences for human, chimpanzee, mouse, pig, and chicken from Uniprot.
- Formatted the sequences into FASTA format and combined them into one file.
- Performed a multi sequence alignment using Clustal Omega.
- Generated a phylogenetic tree using the aligned sequences
- Interpreted the closeness and relationships of the vertebrates chosen.

Results

Phylogenetic Tree

0.05

CYC_HUMAN 0.00000
CYC_PANZEE 0.00000
CYC_CHICK 0.05714
CYC_PIG 0.01905
CYC_MOUSE 0.00952

Key Observations

- Humans and Chimpanzees are closely related in evolution. (0.000000 distance)
- Mouse and Pig are moderately close to primates but are both closely related to each other.
- Chickens are the farthest from primates.

Discussion

The phylogenetic tree accurately reflects established theories with humans and chimpanzees being close in the same taxon, clustering together with a 0.000000 distance, pigs and mice being closely related to humans, pigs in anatomy and mice in microbiology, and chickens being with birds who diverged earlier than primates. This supports the idea that cytochrome c is a reliable indicator of evolutionary patterns and has enough proof to reveal those patterns while still containing enough genetic variation to distinguish themselves from major groups.

Conclusion

This project concludes that cytochrome c can be used to interpret evolutionary relationships among ATP producing vertebrates. The resulting phylogenetic tree accurately aligns with findings in biological classifications, showing that molecular data can be used as strong evidence to support common ancestry in vertebrates.

Reflection

Completing this project showed me how useful bioinformatic tools can be used to turn raw proteins into meaningful molecular findings with phylogenetic trees. This project strengthened my interest in microbiology/molecular biology and showed me how computational methods can reveal patterns that can only be seen under these microscopes. This experience backs up my passion for biology and motivates me to continue more of these data-driven approaches.