

# The *COX1* gene sequence of human is more similar to *Oryzias latipes* than *Caenorhabditis elegans*



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## Summary

- Our goal is to determine whether *Caenorhabditis elegans* (roundworms) or *Oryzias latipes* (medaka) is more genetically similar to humans.
- We compared *COX1* sequences from all three species and created a phylogenetic tree
- We found that *O. latipes* are more genetically similar to humans than *C. elegans*

## Abstract

Two common model organisms are the roundworm, *C. elegans*, and the medaka, *O. latipes*: both can be easily raised in a lab and possess remarkable genetic similarity to humans. Animal models such as these two species can be used to test new medicine or analyze the effects of various diseases. Our goal is to determine which of the two is more genetically similar to humans, which would thus allow for more accurate and helpful results from such lab tests when compared to humans. We analyzed the *COX1* gene from human, roundworm, and medaka and produced phylogenetic trees to compare the three and found greater genetic similarity between medaka and humans.

## Introduction

**Hypothesis.** *Oryzias latipes* (medaka fish) are more genetically similar to humans than *Caenorhabditis elegans*.

**Animal Models.** Animal models are an incredibly useful tool in the field of medicine.<sup>[1]</sup>

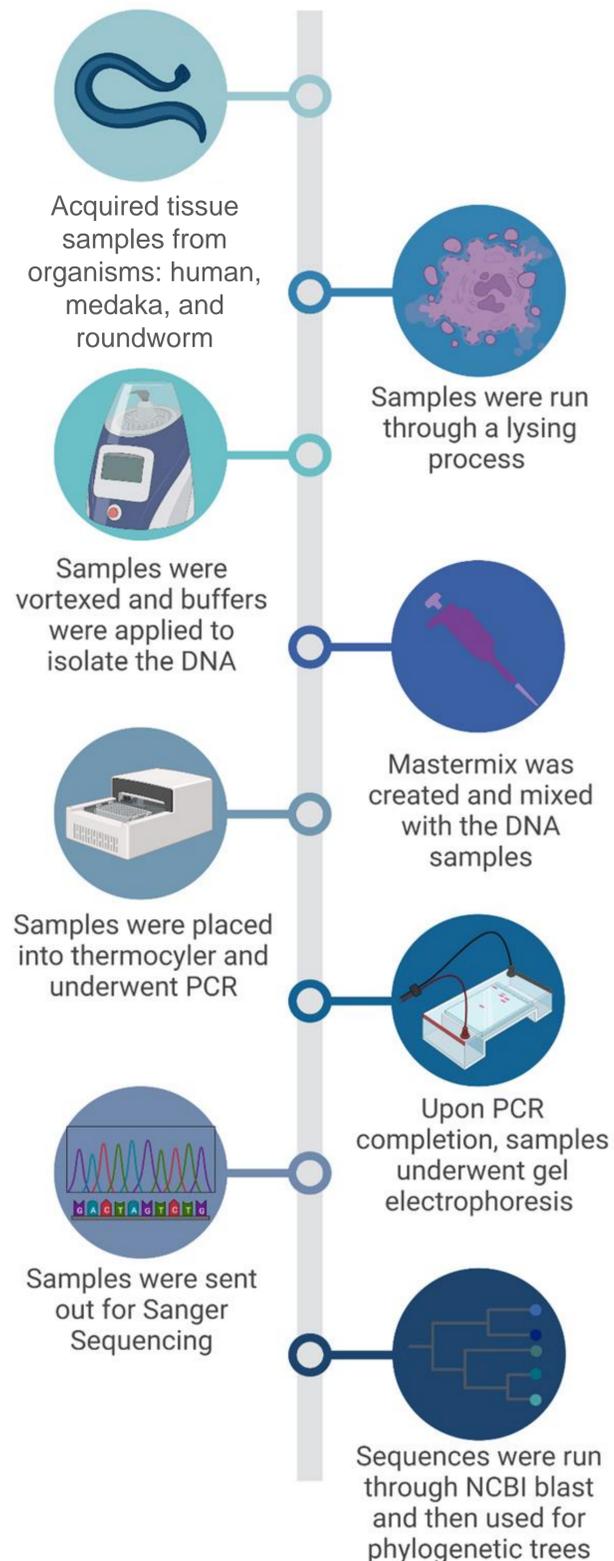
**Chosen Subjects.** Both of the species researched by this experiment have been used as model organisms for environmental and toxicological studies.

**Potential Application.** Examining genetic similarities between humans and other species could eventually result in the discovery of an ideal animal model for medical research.

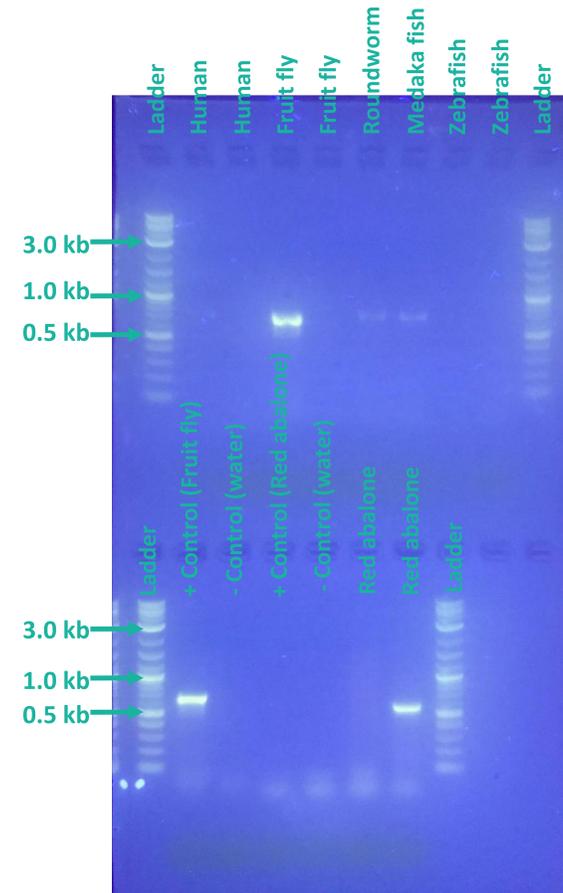
**Targeted Gene.** Targeted the *COX1* gene, located within the mitochondria.

**Reasoning.** *COX1* was chosen due to its role in the electron transport chain; it is present in most species with sequence variations, which can act as indicators for genetic similarity.<sup>[5]</sup>

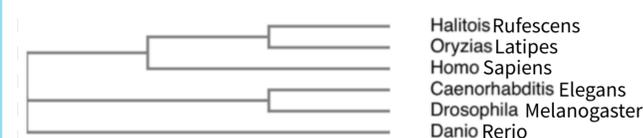
## Methodology



## Results



**Fig 1: Agarose Gel Electrophoresis of PCR Products.** Visualized PCR results on an agarose gel. A positive control with confirmed PCR amplification was used as denoted. Labels on the side indicate band sizes on the ladder. Samples are titled above the well for their respective organism.



**Fig 2: Phylogenetic Tree using *COX1* Sequences of in-lab samples** Phylogenetic tree created using the in-lab samples. Clustal omega was the tool used to create the phylogenetic tree using neighbor-joining method.



**Fig 3: Phylogenetic Tree using *COX1* sequences of database sequences.** Phylogenetic tree created using *COX1* database sequences using same methods as in-lab samples tree.

## Conclusion/Discussion

- Our results support our hypothesis:
- Despite the role *C. elegans* has played in science as an animal model<sup>[4]</sup>, *O. latipes* has notable traits/phenotypes that would indicate greater genetic similarity to human, such as bones and an epidermal layer.
  - Notably, *O. latipes* has similarities on a genetic level with *Danio rerio*<sup>[6]</sup>, which has been found to hold a great deal of similarities with humans as well<sup>[7]</sup> (Fig 2).

Although literature that investigated similar questions were relatively rare, medaka and roundworms are commonly used models for humans in terms of medical and scientific application<sup>[4][8][9][10]</sup>.

- Considerations should be taken when applying animal study conclusions to humans.

In summary, we found that between the two species, medaka is more genetically similar to humans in the *COX1* gene, thus making them a relatively better model for medical research.

## Study Limitations

- One major limiting factor on this experiment was the sample size. We only used one sample sequence for each species. The sequence might not be representative of species diversity.
- In addition to this, we saw that our in-lab samples differed from the database sequences. This variation could cause differences in trees.
- We are only looking at one region of the *COX1* Gene, not the entire gene itself (like the database sequences).

## Future Directions

- Looking at more species and determining which are more closely related to humans.
- Use multiple genetic barcodes.
- From this information, organisms that are most similar while also proper for being a research model could serve as a better way to investigate environmental stresses.

## References

