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EEOB 563

Project Outline

**Research Question:** Can I provide a new way of looking at the Ecdysozoa theory correct using a developmental gene (possibly Hox) through phylogenetics?

**Introduction:** There has been some difficulty classifying Drosophila phylogenetically. It’s classification is important because researchers want to figure out how closely it is related to humans as it is used as a model for some human diseases. There was a tension between the tradition hypothesis of Coelomata and the new, alternative hypothesis of Ecdysozoa. In the traditional view, fruit flies and humans were more closely related than either and nematodes. In the new theory, fruit flies and nematodes were more closely related than either and humans. In the 2002 article from Penn State, it is mentioned that for some reason the traditional view was quickly thrown out without the typically scientific scrutiny a new theory typically receives. That is what this lab aimed to do and in fact, based on 100 genes, proved the traditional Coelomata tree. The second webpage I found was a Powerpoint from Oxford, although I am unclear on the date published. This Powerpoint is from the Zoology department and sets out to prove the opposite through multiple characteristics like homology of limbs and segmentation. This is especially important when it comes to Hox genes which aid in development.

**Methods:** Obtain a sequence of a Hox gene common to Drosophila and humans and compare through Maximum Likelihood (RAxML) and Maximum parsimony (PAUP).

**References:**

http://science.psu.edu/news-and-events/2002-news/Hedges4-2002.htm

<http://www.stats.ox.ac.uk/~hein/fly1.pdf>

-amino acid/ conservative functional group