**INTRODUCTION**

The objective of this research was to study regenerative ability of certain organisms through the analysis of evolutionary relationships. Relation of the organisms was determined through taking the 28s and 18s genes and constructing phylogenetic trees from their genetic sequence. The trees were created through Phylogeny.fr, FigTree and MEGA.

**METHODS**

Research methods used 25 in-groups and one out-group taxa.

-For our data set we used the 18S and 28S ribosomal DNA sequences for phylogenetic analysis

-Sequences were aligned in muscle using Phylogeny.fr and FigTree was used to edit tree visualizations.

-Note: Sequences which were deemed unconserved were cut out using MEGA software.

**DISCUSSION**

As we analyzed our tree to look at the evolutionary relationships between organisms we saw some unexpected developments. We first noted that the first few organisms to evolve from our outgroup were the ctenophora (comb jellies), the two cnidaria (Hydractiniidae and Hydridae), and the Porifera (sponges). Between the 18S and 28S trees there was agreement that these are the first few organisms to evolve, but the exact order does not have 100 percent confidence between the two trees. It also stood out as interesting that the organisms which developed the most recently are all in echinodermata (Star fish, brittle stars, etc)

**FUTURE RESEARCH**

-Need to study different genes which are more conserved between the chosen taxa.

-Further research is needed into regenerative ability and the genes that correlate to organisms which have this ability.

-Could do future studies on different types of regenerative ability in marine life.

**CITATIONS**
