

INVESTIGATING A DEEP SEA MYSTERY

For centuries, ichthyologists, scientists who study fishes, have been fascinated by what lives in the deep ocean. The fishes that live in this environment, where the pressure is high and sunlight does not reach, have some unusual shapes and interesting (even bizarre) adaptations. We still know very little about many of them, because they are so difficult to collect and essentially impossible to observe in their habitat. Even fundamental questions about how the fishes are related and how they should be classified are a source of ongoing investigations.

A team of scientists* from the United States, Japan, and Australia undertook an investigation into one such question. What they discovered was amazing indeed!

Your goal: Follow in the footsteps of these ichthyologists and investigate a set of deep sea fishes to generate and test hypotheses about their relationships.

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PART I - INTRODUCTION - WHAT IS A FISH?

What is a fish?

Draw a picture of a fish. Be sure to include and label the features you think all fishes have and can be used to identify something as a fish. Make a list of other important behaviors or traits that all fishes have.

Fish Checklist

After reading *What is a fish?*, create a checklist you could use to determine if something is a fish.

_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____

What are some exceptions to the general fish characteristics you listed?

PART I - INTRODUCTION - WHAT IS A FISH?

What is a Fish Notes:

PART II - CLASSIFYING SOME UNUSUAL FISHES

Notes: Deep Sea Fish Classification

What did you learn about the deep-sea fishes that you classified?

PART III - LOOKING FOR PATTERNS IN COLLECTION DATA

Fish Collection Data Table

Number of specimens collected	Cetomimidae Whalefishes	Megalomycteridae Bignose fishes	Mirapinnidae Tapetails
Total	600	65	120
Adults	600	65	0
Immature	0	0	120
Females	600	0	?
Males	0	65	?
Size (mm)	26-408	34-68	5-56
Depth caught (m)	Below 1000	Below 1000	Above 200 1 caught below 200

The table above is a summary of data from members of the three clades that has been collected by scientists over many years. Take a close look at the data. What patterns do you observe?

How does this data impact the Three Clade Hypothesis?

What is an alternative explanation or hypothesis to explain the patterns in the data?

PART III - LOOKING FOR PATTERNS IN COLLECTION DATA

Two Hypotheses to Test

1. *Three Clade Hypothesis*

2. *Single Clade Hypothesis*

What types of data would you like to collect to help you test the hypotheses?

PART IV - TESTING HYPOTHESES – USING MORPHOLOGY

Testing Hypotheses Using Morphology

Testing hypotheses involves using different types of data to evaluate each explanation. You will use three different types of morphological data to test the two hypotheses that explain the classification and relatedness of the deep sea fish specimens: gut, muscle, and gill.

Gut Morphology

Use the Gut Morphology Card to make observations about each fish group's internal anatomy associated with feeding. In the table below, use a checkmark "✓" to indicate which fishes have a normal presence of the feature. If a fish does not have a feature, leave it blank. If the feature is an unusual size or shape make a note in the table.

Feature	Whalefishes	Bignose fishes	Tapetails
Stomach			
Esophagus			
Liver			
Intestine			
Other observations			

What inference might you make about the feeding habits of each fish?

What do these data suggest about the accuracy of each hypothesis?

Muscle Morphology

Use the Muscle Morphology Card to make observations about the relative proportion of red muscle tissue visible in each type of fish. Use a checkmark “✓” to record your observations.

Visible Red Muscle	Whalefishes	Bignose fishes	Tapetails
Proportionally high			
Proportionally low			

What inference could you make about the swimming capabilities of each group of fish?

What do these data suggest about the accuracy of each hypothesis?

Gill Arch Morphology – Looking for transitional specimens

Use the Gill Arch Morphology Cards to make observations about the structures and locations of specific features in the gill arches of these fishes. In the table below, record whether each specimen has a **tongue** or no tongue; the **orientation of the bone** (horizontal, vertical, or the angle from horizontal); and the **shape of the gill rakers** (e.g. thick or thin, forked or conical, smooth or toothed).

Feature	Specimen 1 Whalefish	Specimen 2 Tapetail	Specimen 3 Young Whalefish	Specimen 4 Young Whalefish
Tongue				
Bone 1				
Gill Rakers			<i>cannot determine</i>	

Is it possible to order the specimens in a way that shows a transition from a larval form to adult (e.g. Tapetail to Whalefish)? If so, list the specimens in the order you suspect represents how they would develop.

What do these data suggest about the accuracy of each hypothesis?

External Morphology Revisited

Summary of Observations

What inferences can you make about how the fishes are related? What do these data suggest about the accuracy of each hypothesis?

What other lines of morphological evidence would you seek in order to further test the two hypotheses?

What new questions should be explored?

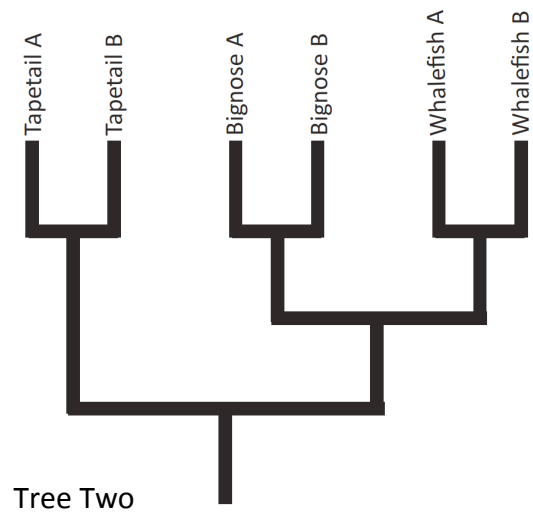
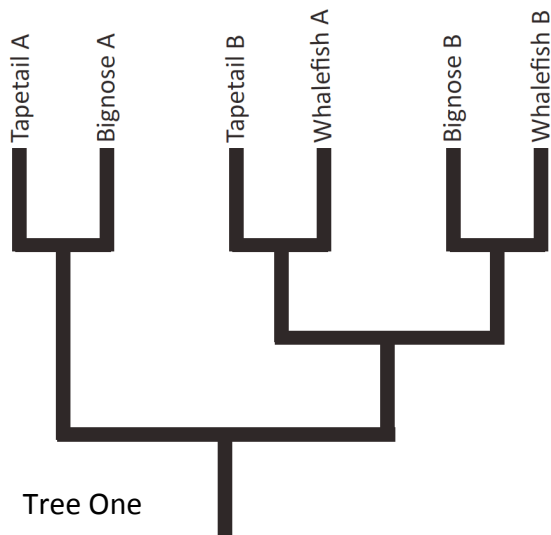
PART V - TESTING HYPOTHESES – USING PHYLOGENETIC TREES

An Exercise in Tree Interpretation

Phylogenetic trees are another line of evidence that can be used to test hypotheses about the classification and evolution of organisms. Before looking at the real fish phylogenetic data, practice your skill at tree interpretation using the two trees below.

Which tree best supports the Three Clade Hypothesis?

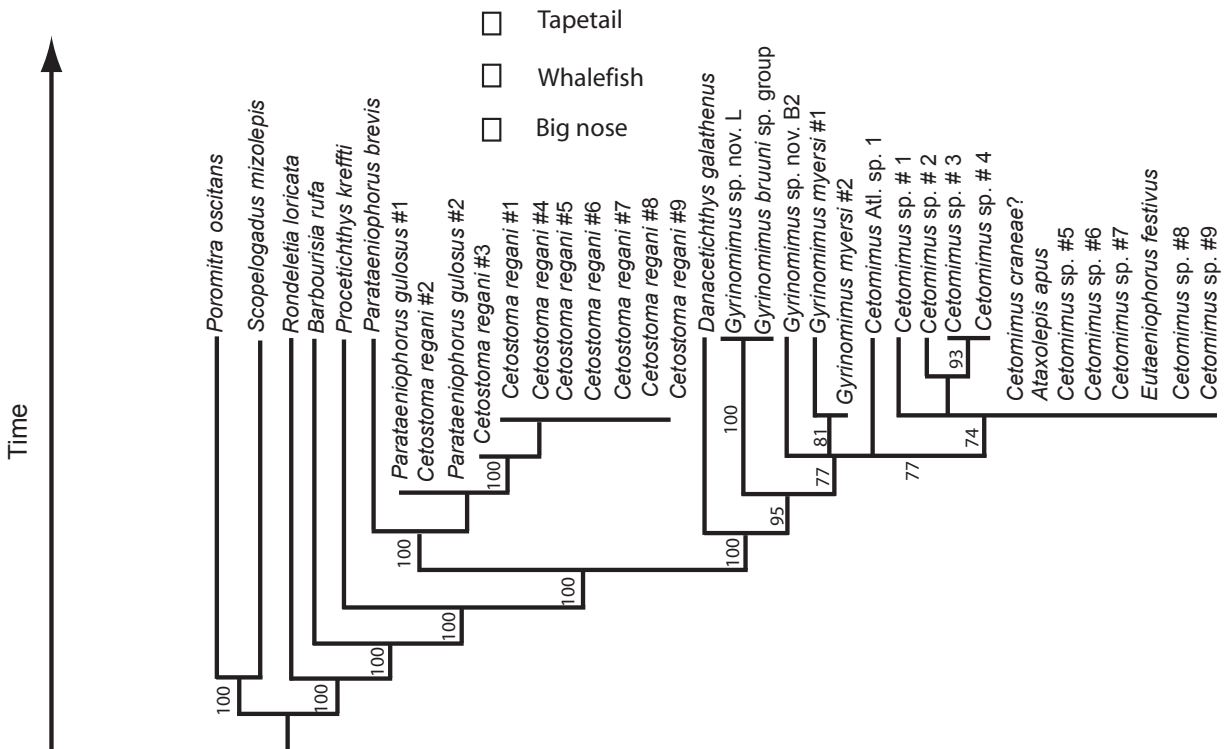
Which tree best supports the Single Clade Hypothesis?



PART V - TESTING HYPOTHESES – USING PHYLOGENETIC TREES

Phylogenetic Trees

The following is a real phylogenetic tree based on ribosomal DNA. Create a color-coded key for each of the fish groups; Whalefishes, Bignose fishes, and Tapetails, and then use the Deep Sea Specimen Key to identify each fish species in the tree by color.



Maximum Likelihood tree based on partial 16s ribosomal DNA sequences. Numerals beside internal branches indicate bootstrap values (only 50% and above are shown) based on 1000 replicates.

Look closely at the patterns that appear on the tree. Which hypothesis does this tree best support?

PART VI – WRAPPING IT UP

Summary Report

Summarize your findings

Questions for future investigations