

A large offshore oil platform is engulfed in intense orange and yellow flames, with thick black smoke billowing into the sky. In the background, a white supply vessel is spraying a powerful stream of water onto the burning structure. The overall scene is one of a major industrial disaster at sea.

# **Genomic Responses to the Deepwater Horizon event and development of high-throughput biological assays for oil spills**

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BITMaB-2 Texas A&M Corpus Christi 2018



**Deepwater Horizon (DWH) – April 2010**

Core samples from the seafloor of the Gulf of Mexico shows a 5 cm layer of oily material.

Researchers are finding oil on the seafloor miles away

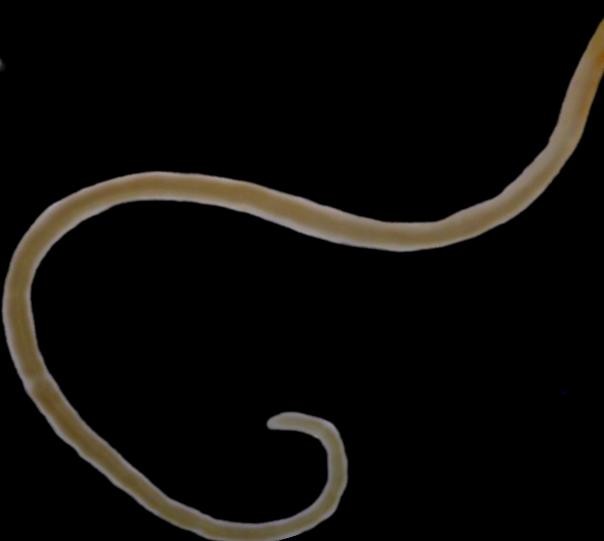
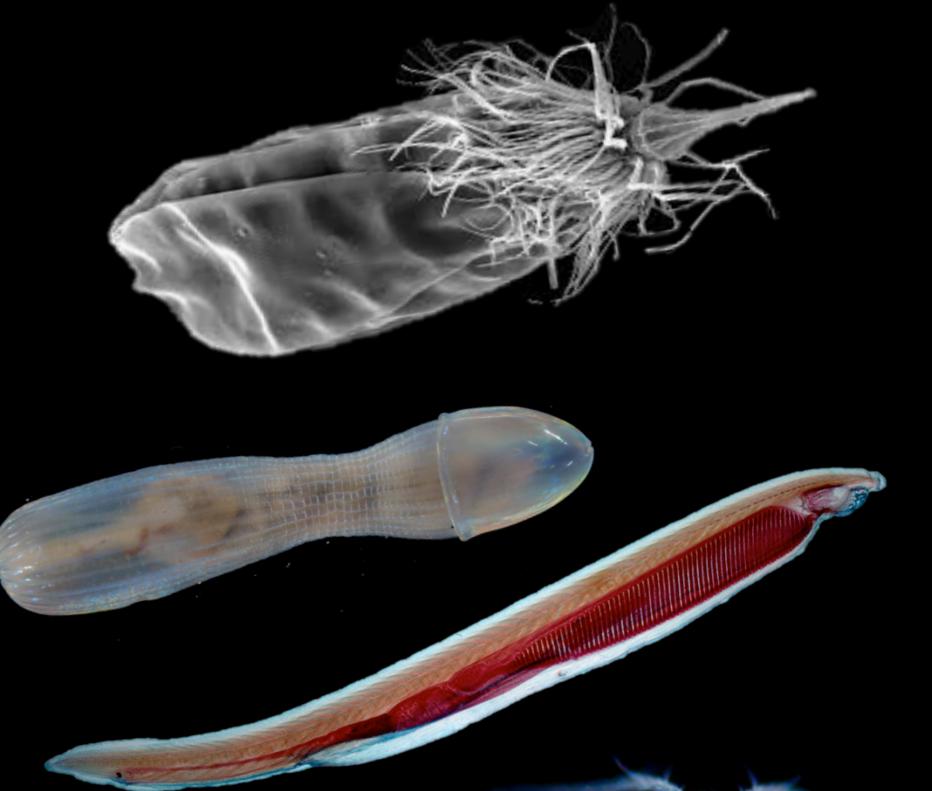


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How the community composition changes in response to a stress

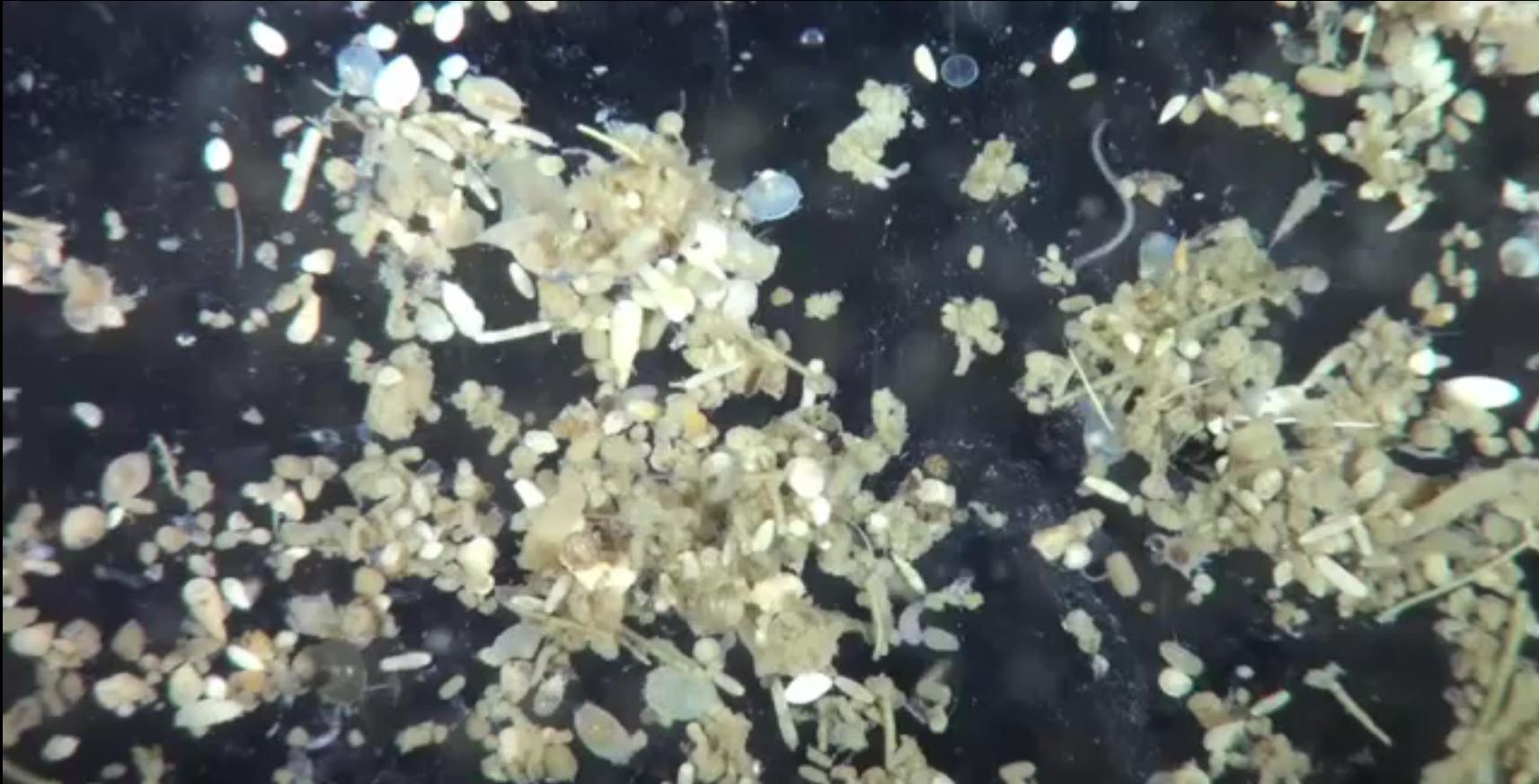
What biomarkers (genes) respond to a hydrocarbon contamination



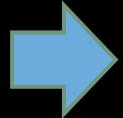
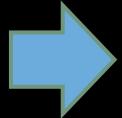


# Ecological Role

Video Credit:  
Stockholm University Systematic Zoology



- Hyperdiverse, ubiquitous and abundant
- Low dispersal potential
- Stimulate mineralization of organic matter and bacterial production
- Trophic Links
- High sensitivity to anthropogenic inputs
- Different responses to environmental stressors

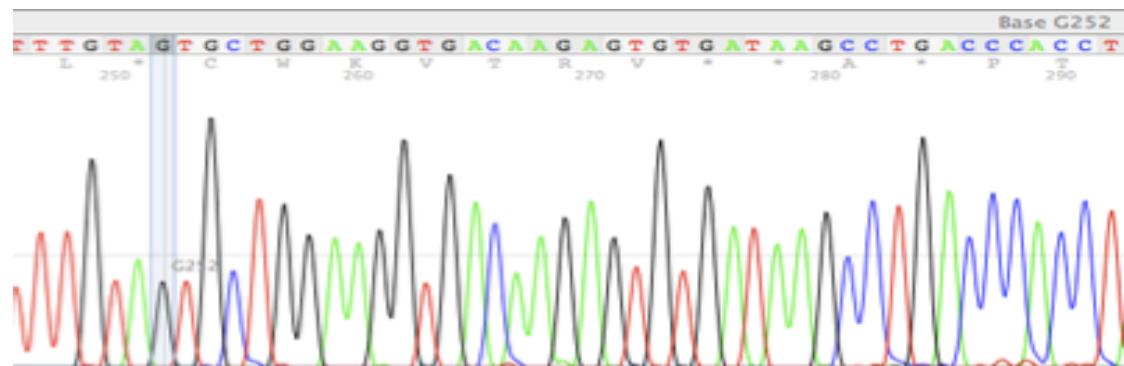


Time-consuming  
Limited taxonomic expertise  
Phenotypic plasticity  
Cryptic species

## BIOLOGICAL ASSAY – TRADITIONAL TAXONOMY



# BIOLOGICAL ASSAY – DNA TAXONOMY

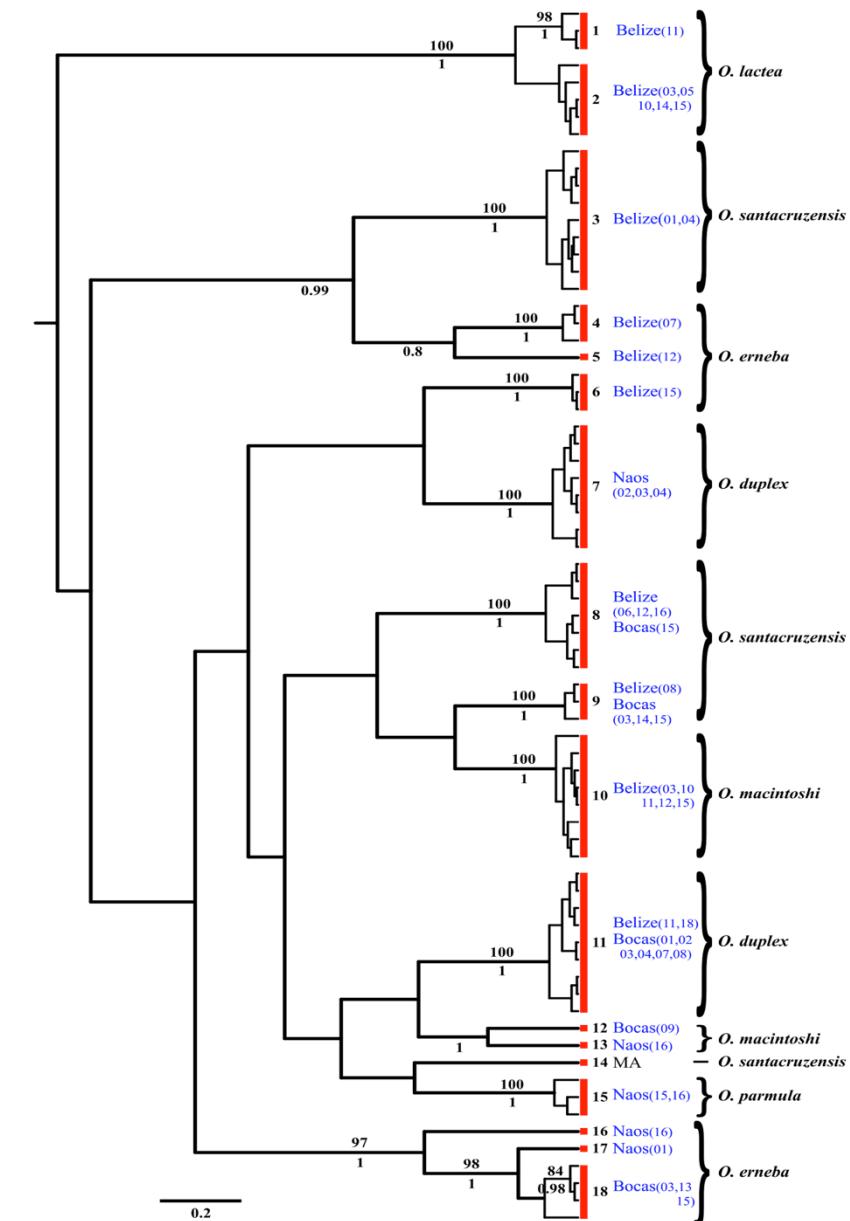


**ABGD** Automatic Barcode Gap Discovery (Puillandre *et al.* 2012)

**bPTP** Bayesian implementation of Poisson Tree Processes (Zhang *et al.* 2013)

**GMYC** General Mixed Yule-Coalescent model (Pons *et al.* 2006)

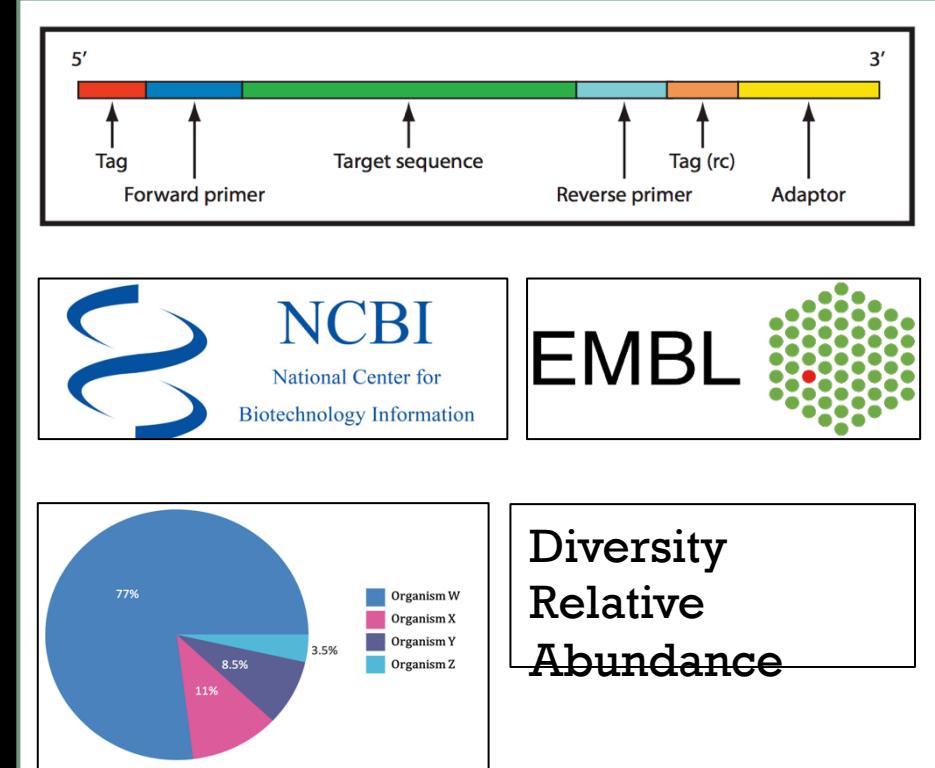
**BPP** Bayesian Phylogenetics and Phylogeography (Rannala & Yang 2003)



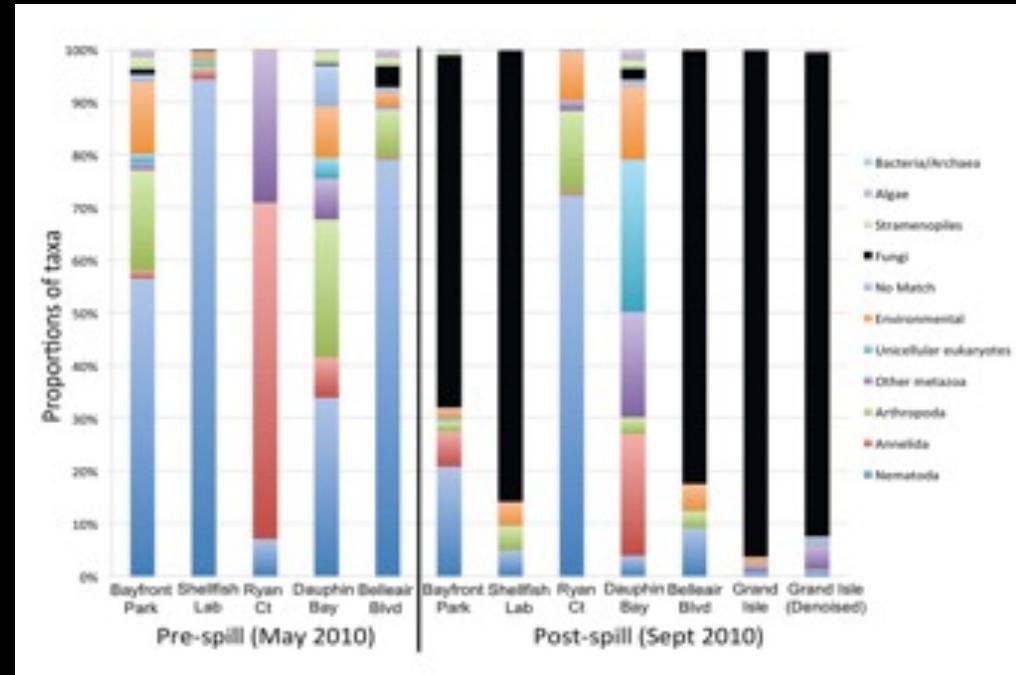


# BIOLOGICAL ASSAY – METABARCODING

- Rapid and inexpensive
- Investigation at the community level
- Taxonomists are not required

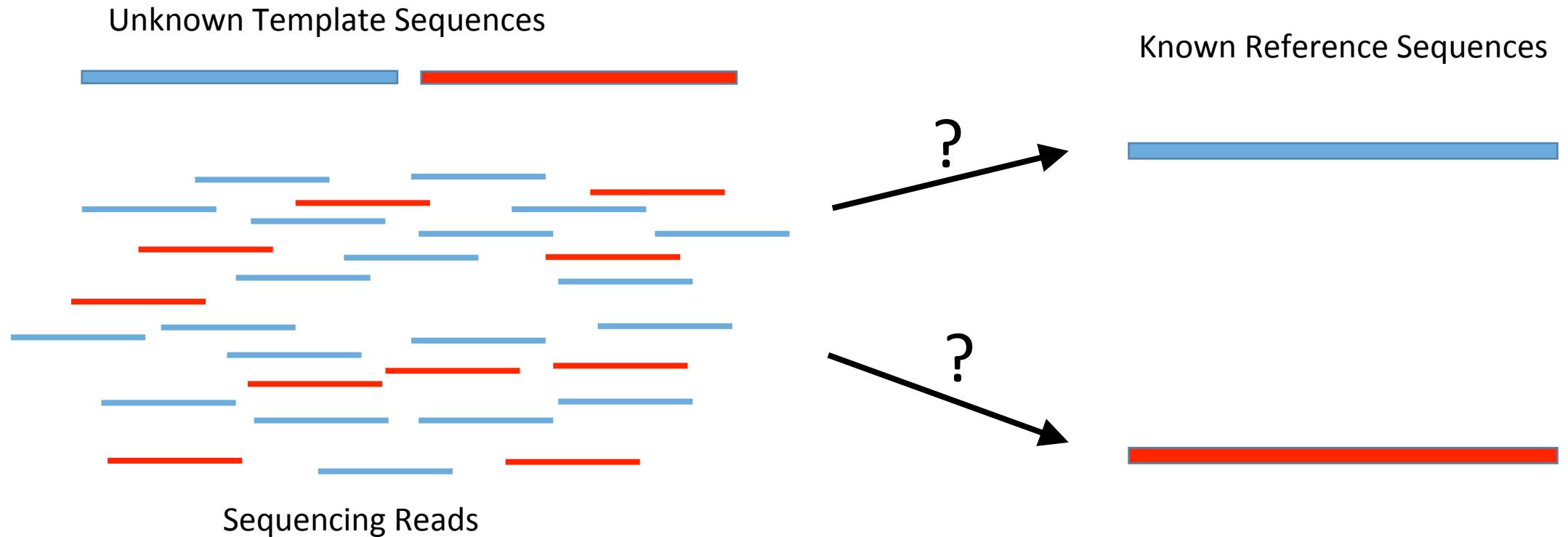


# Pilot Studies – Metabarcoding (18S)



- Significant changes in microscopic eukaryotic communities across an oiling event
- Based solely on 18S gene, which is known to **LARGELY** underestimate diversity
- Need for additional resources and infrastructure to make more comprehensive comparisons

# FURTHER STEPS



**Whole Genome Shotgun Sequencing  
and Read Mapping**

# Gulf of Mexico Research Initiative Project

- Sequence and assemble draft genomes of unrepresented meiofauna organisms
  - Establish a standard operating procedure for sample collection, sequencing, and assembly
- Determine an extended set of nuclear and mitochondrial loci useful for examining both closely and distantly related meiofauna
- Assess the community structure of meiofauna organisms throughout the Gulf of Mexico both pre and post oil spill via metagenomic sequencing

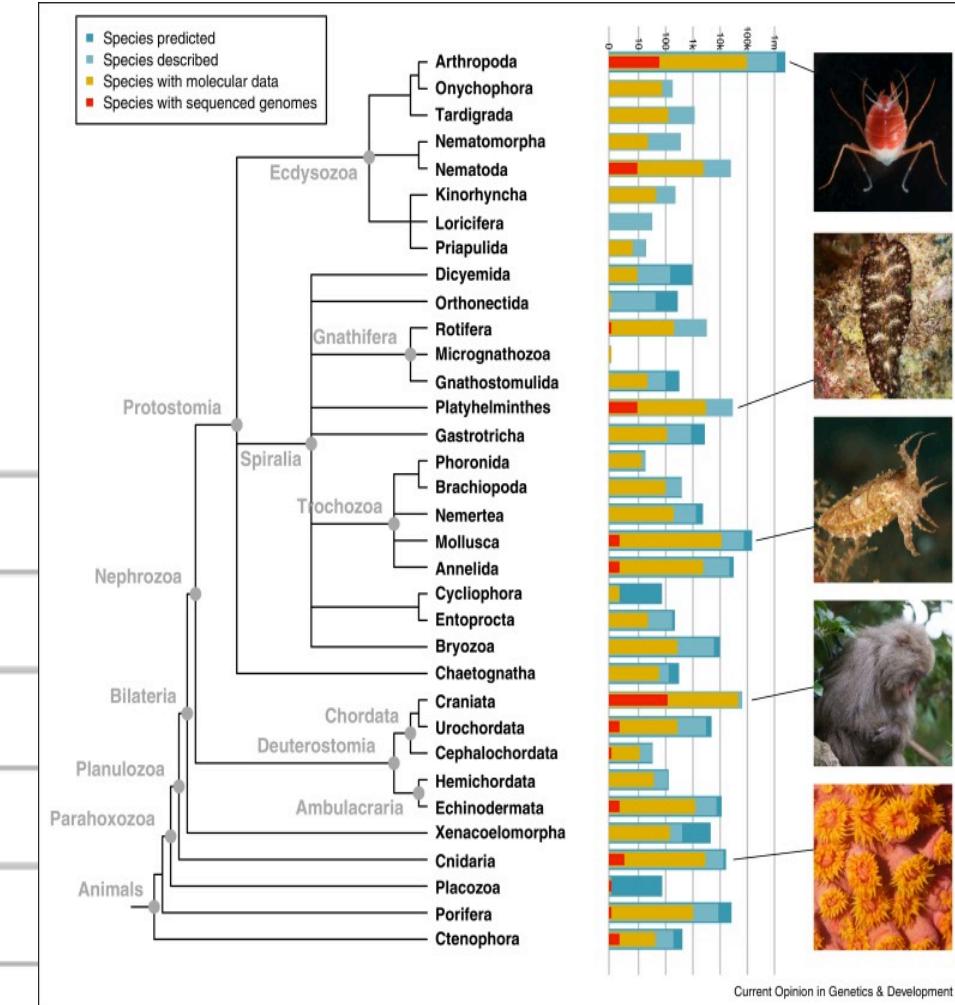
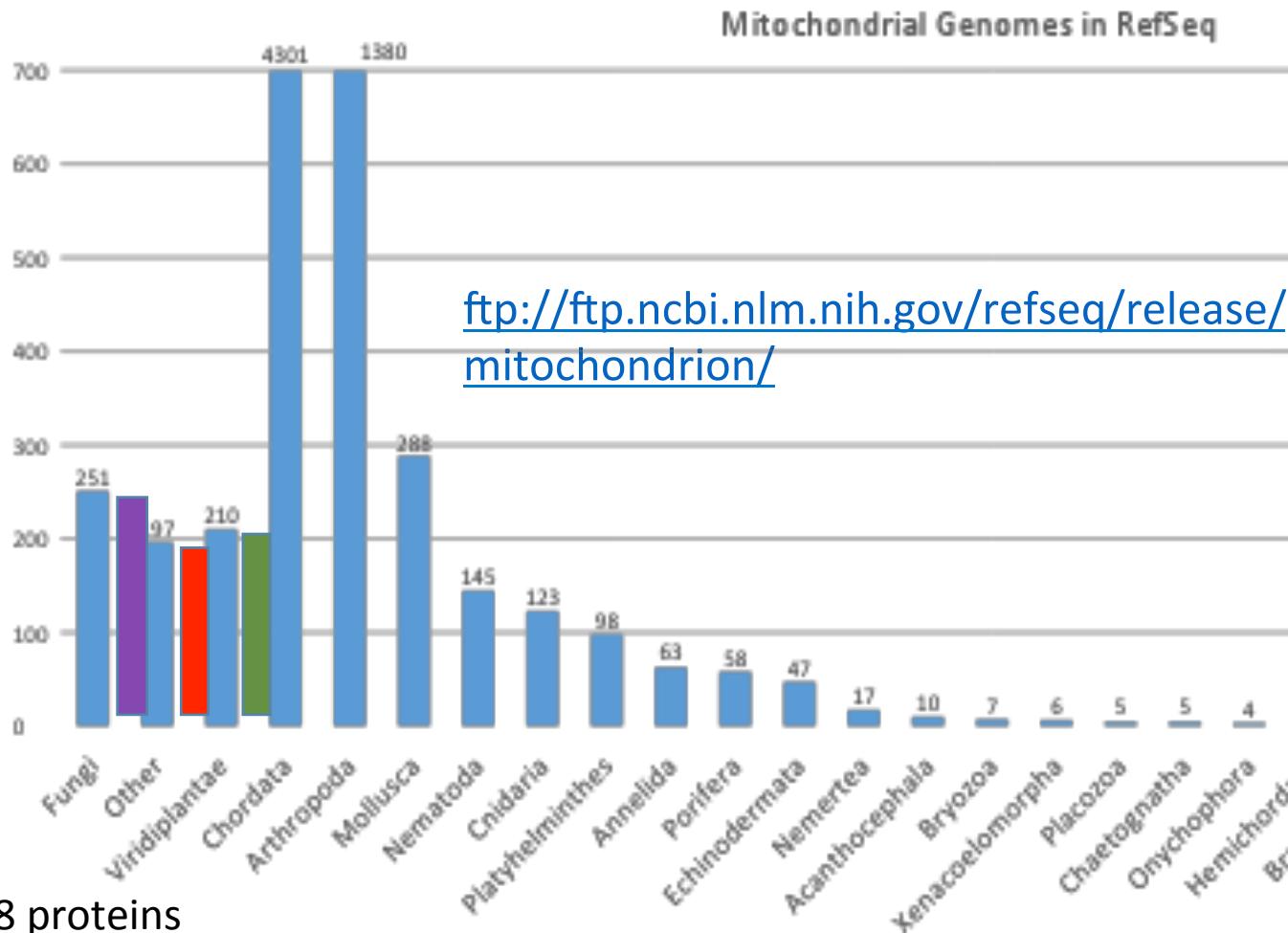
# Workforce Training – Annual Workshops

Texas A&M University, Corpus Christi – January 2017-18

Taxonomy & Bioinformatics



# 7,873 complete animal mitochondrial genomes



**ENJOY THE WORKSHOP**

**AND HAVE A GOOD WORK**