

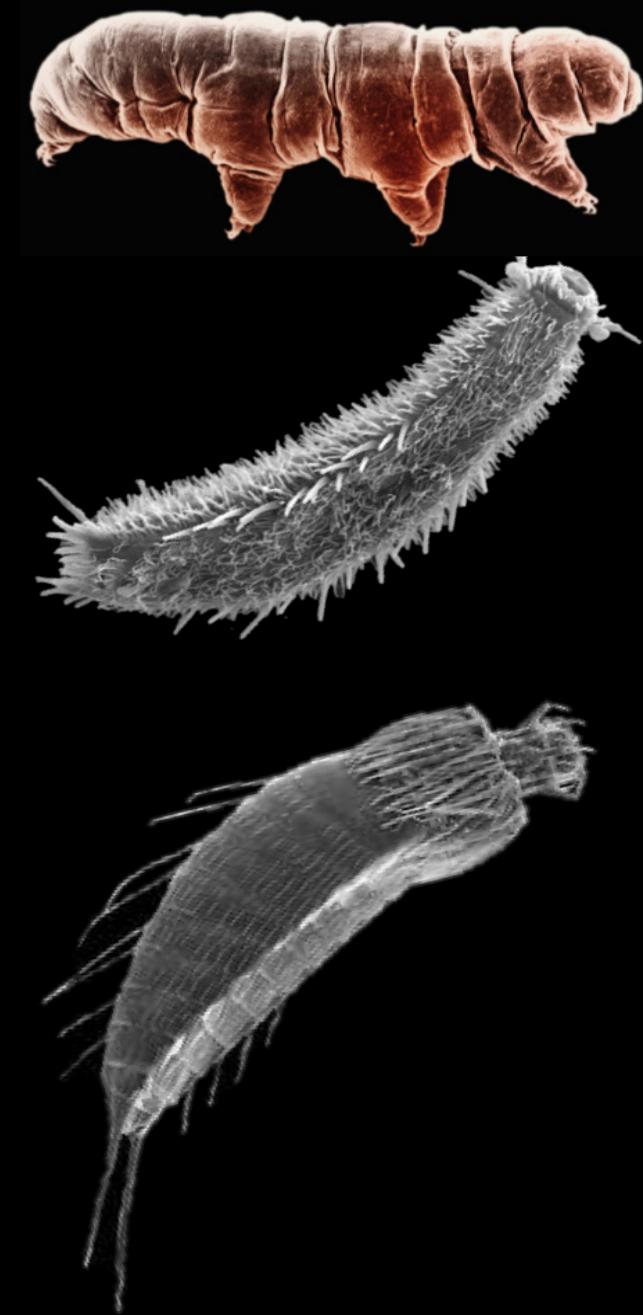
Goals of the workshop in the context of the research project

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

Francesca Leasi
Smithsonian Institution National Museum of Natural History
University of New Hampshire

PHYLA OF THE KINGDOM ANIMALIA

| PHYLA | FREE-LIVING | | | SYMBIOTIC |
|---------------------------------------------------------------------------------------------------------|-------------|------------|-------------|------------------|
| | Marine | Freshwater | Terrestrial | |
| Porifera | Yes | Yes | No | No |
| Placozoa | Endemic | No | No | No |
| Cnidaria | Yes | Yes | No | Yes |
| Ctenophora | Endemic | No | No | No |
| Platyhelminthes | Yes | Yes | Yes | Yes |
| Orthonectida | No | No | No | Endemic (Marine) |
| Rhombozoa | No | No | No | Endemic (Marine) |
| Cyclophora | No | No | No | Endemic (Marine) |
| Acanthocephala | No | No | No | Endemic |
| Nemertea | Yes | Yes | Yes | Yes |
| Nematomorpha | No | No | No | Endemic |
| Gnathostomulida | Endemic | No | No | No |
| Kinorhyncha | Endemic | No | No | No |
| Loricifera | Endemic | No | No | No |
| Nematoda | Yes | Yes | Yes | Yes |
| Rotifera | Yes | Yes | Yes | Yes |
| Gastrotricha | Yes | Yes | No | No |
| Entoprocta | Yes | Yes | No | Yes |
| Priapulida | Endemic | No | No | No |
| Pogonophora | Endemic | No | No | No |
| Echiura | Endemic | No | No | No |
| Sipuncula | Endemic | No | No | No |
| Annelida | Yes | Yes | Yes | Yes |
| Arthropoda (Copepoda, Halacaroidea, Ostracoda, Mystacocarida, Tantulocarida) | Yes | Yes | Yes | Yes |
| Tardigrada | Yes | Yes | Yes | No |
| Onychophora | No | No | Endemic | No |
| Mollusca | Yes | Yes | Yes | Yes |
| Phoronida | Endemic | No | No | No |
| Bryozoa | Yes | Yes | No | No |
| Brachiopoda | Endemic | No | No | No |
| Echinodermata | Endemic | No | No | No |
| Chaetognatha | Endemic | No | No | No |
| Hemichordata | Endemic | No | No | No |
| Chordata | Yes | Yes | Yes | Yes |



Ubiquitously and abundantly found on the bottom of beaches, mud flats, and deep sea

Important role as a trophic link between bacteria and larger fauna

Facilitate biomineralization of organic matter and enhance nutrient regeneration

Exhibit high sensitivity to anthropogenic inputs, making them excellent sentinels of pollution

Short lifecycles, the effects of a contaminant on the entire life-history can be assessed within a relatively short time

MEIOFAUNA

Pollution

Dwarfism

Abnormalities

Maturity Index

Diversity

Density

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Deepwater Horizon (DWH) – April 2010

A core sample 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

QUESTIONS

How the community composition changes in response to a stress

What biomarkers (genes) respond to a hydrocarbon contamination



Kimes et al. (2013) Frontiers in Biology 50: 100-117

MEIOFAUNA COMMUNITY DIVERSITY

MORPHOLOGY – TRADITIONAL TAXONOMY

LIMITATION:

- FEW INDIVIDUALS AT THE TIME
- OPERATOR BIAS
- DIFFICULTY IN QUANTIFYING DIVERSITY
- MORPHOLOGY IS PLASTIC
- CRYPTIC SPECIES

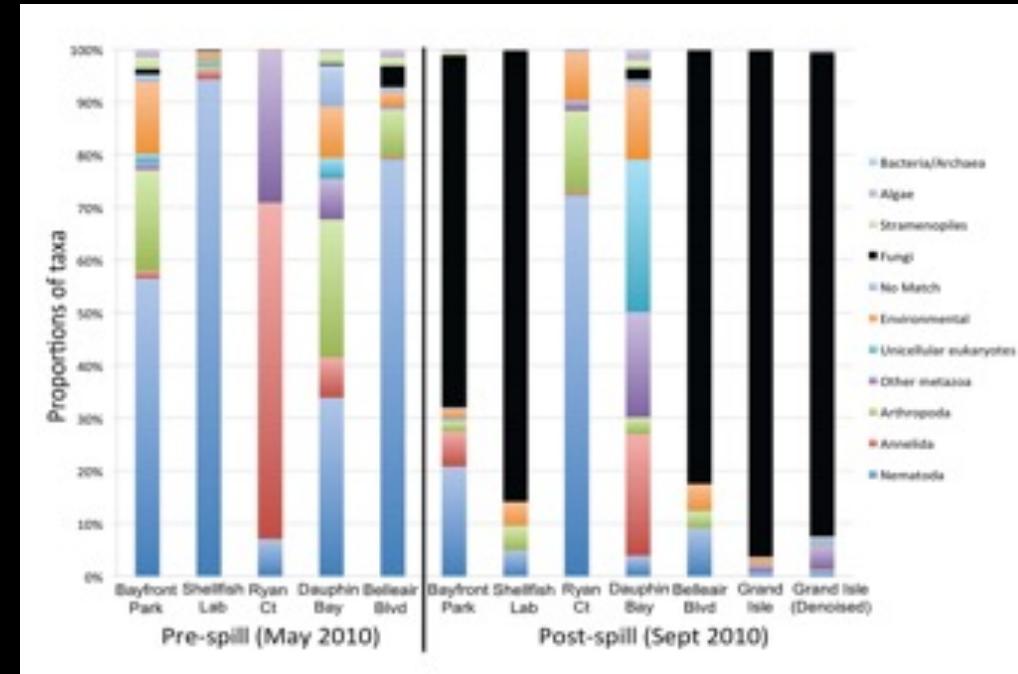
DNA TAXONOMY

LIMITATION:

- ANALYSIS AT INDIVIDUAL LEVEL

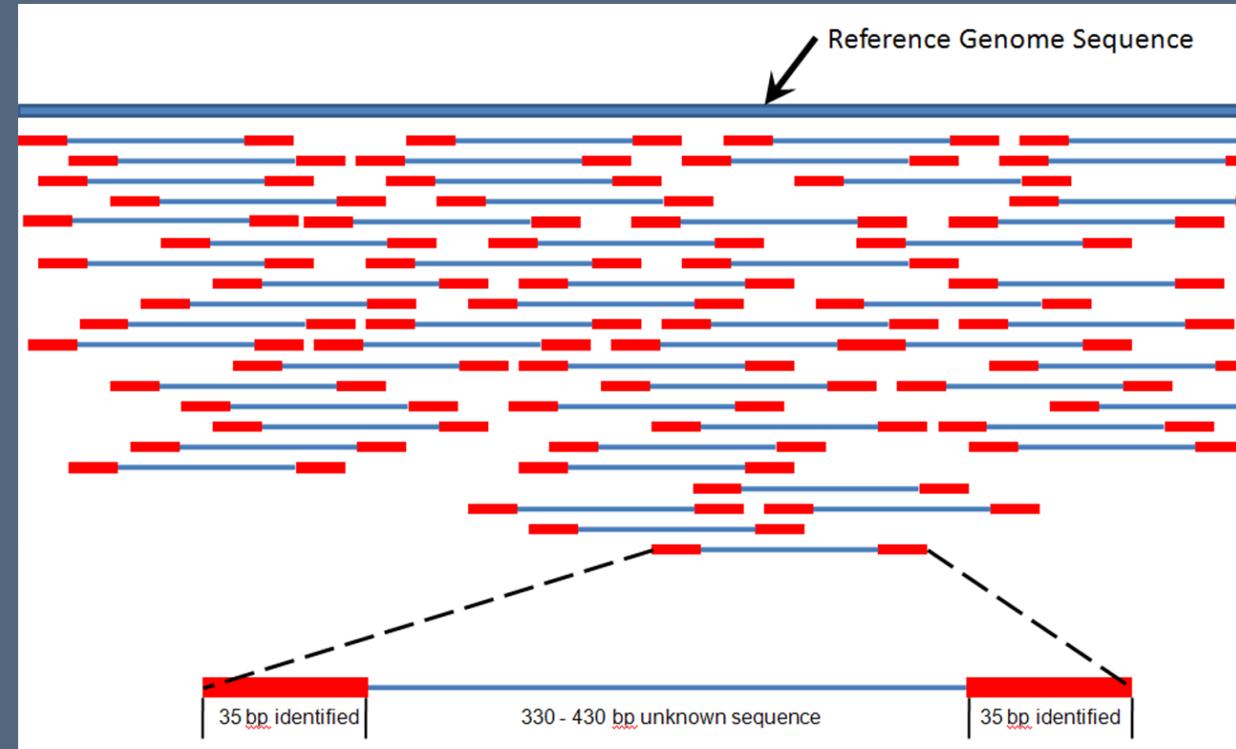
NEXT GENERATION SEQUENCES ON ENVIRONMENTAL SAMPLES

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
- Most of the biomarkers are neglected
- Need for additional resources and infrastructure to make more comprehensive comparisons

Metagenomics



Major Limitation: lack of database matches

| Phylum | Estimated Species (Appeltans et al. 2012) | Genomes/ Assemblies | Mitochondrial Genomes |
|-----------------|----------------------------------------------|------------------------|--------------------------|
| Arthropoda | 1,134,000 | 308 | 1169 |
| Chordata | 100,000 | 375 | 3801 |
| Mollusca | 112,000 | 8 | 250 |
| Annelida | 17,000 | 2 | 47 |
| Brachiopoda | 300 - 500 | 1 | 4 |
| Cnidaria | 11,000 | 12 | 124 |
| Echinodermata | 7,000 | 7 | 43 |
| Entoprocta | 150 | 0 | 2 |
| Gastrotricha | 690 | 0 | 1 |
| Gnathostomulida | 100 | 0 | 2 |
| Kinorhyncha | 150 | 0 | 0 |
| Loricifera | 122 | 0 | 0 |
| Nematoda | 80,000–1,000,000 | 74 | 122 |
| Nemertea | 1,200 | 0 | 17 |
| Platyhelminthes | 25,000 | 16 | 84 |
| Priapulida | 16 | 1 | 2 |
| Rotifera | 2,000 | 2 | 4 |
| Sipuncula | 144–320 | 0 | 2 |
| Tardigrada | 1,000 | 1 | 2 |

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**Greater taxon sampling and additional loci are needed
to achieve higher resolution**

| | | | |
|-----------------|------------------|----|-----|
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GoMRI Goals

- 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

METHODS

Single individuals as well as environmental samples are collected

Shotgun metagenomics is performed to retrieve the genome from both selected taxa and bulks of sediments

Sequences are appropriately revised with bioinformatics pipelines (trimmed, filtered, assembled, etc.)

Genomic information are compared to identify taxa and biomarkers that reflect ecology