Genome-Enabled Environmental Biology

Advances in DNA sequencing technology have changed our ability to address fundamental biological questions.

- Truly global knowledge of Biodiversity.

- Knowing how communities of organisms function within ecosystems.
“Metagenomics: Sequencing the Genomes of an environment”

1. Marker-based Metagenomics or “Barcoding”
   Use of diagnostic sequences to discover and quantify members of a community allowing global comparisons of virtually all organisms.

2. “Metagenomics/Metatranscriptomics”
   Sequencing uncultured organisms from an environmental sample to explore function by linking the functions of individual genes to the environment.
Consequences of the DWH
RAPID: Taxonomic and metagenetic test of species distributions for marine meiofauna in the Gulf of Mexico

Logic:

1. Informed mitigation and remediation requires knowledge of the resident communities.

2. The vast majority of the organisms doing most of the “work” are microscopic.

3. We applied a marker-based metagenomic approach.
Metagenomic analysis of the meiofauna

James Baldwin and Manuel Mundo, UCR
Key questions:

1) How unique are the meiofaunal communities in the GOM?

2) How structured are the meiofaunal communities within the GOM?

3) What has been the effect of the anthropogenic disturbance on the meiofaunal communities?
RAPID: Taxonomic and metagenetic test of species distributions for marine meiofauna in the Gulf of Mexico

Holly M. Bik¹, Kenneth M. Halanych², Jyotsna Sharma³, W. Kelley Thomas¹
Metagenomic approach

- Extract DNA from environmental samples
- Target specific loci (PCR w/ conserved primers)
- Next-Generation Sequencing
- Infer biologically meaningful diversity units
- Describe community
- Go to lunch
- Publish

Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill

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Abstract

Benthic habitats harbour a significant (yet unexplored) diversity of microscopic eukaryote taxa, including metazoan phyla, protists, algae and fungi. These groups are thought to underpin ecosystem functioning across diverse marine environments. Coastal marine habitats in the Gulf of Mexico experienced visible, heavy impacts following the Deepwater Horizon oil spill in 2010, yet our scant knowledge of prior eukaryotic biodiversity has precluded a thorough assessment of this disturbance. Using a marker gene and morphological approach, we present an intensive evaluation of microbial eukaryote communities prior to and following oiling around heavily impacted shorelines. Our results show significant changes in community...
Figure 1. Pre-spill and Post-spill taxonomic comparisons of microbial eukaryote communities.

http://www.plosone.org/article/info:doi/10.1371/journal.pone.0038550
Figure 2. Phylogenetic beta diversity analysis of eukaryote communities conducted using the UniFrac distance metric.
Conclusions

1. All samples displayed significant changes in the meiofaunal communities.
2. Common loss of metazoan taxa and rise to dominance of a small number of fungi.
3. Fungal Taxa were not common to marine and well-known from sites of hydrocarbon contamination.
What’s Next?

Sequencing Fungal genomes

Monitoring “Recovery”? Does the community return to its prior state or a new state?

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Collaborative Research: RCN: EukHiTs: Eukaryotic Biodiversity Research Using High-Throughput Sequencing
Thanks,

Co-PIs

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