Spatial and Bathymetric Variation of Meiofauna Community Structure and Function in the Northern Gulf of Mexico Deep Sea

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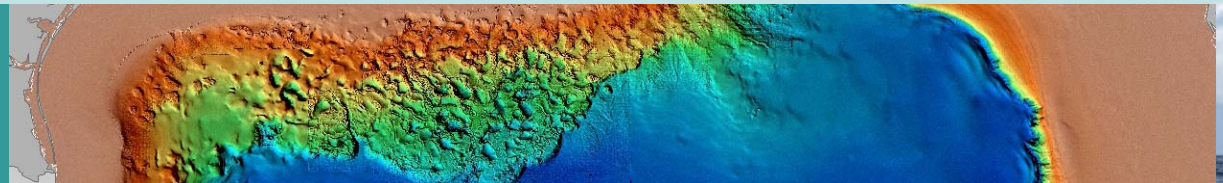
MMS



What Are Meiofauna?

- Community of small metazoan and Protistan fauna
  - 0.040 mm to 0.500 mm
  - 20 of the 34 recognized animal phyla
  - 5 phyla are exclusively meiofauna
  - Dominant taxa are the phylum **Nematoda**, and the order **Harpacticoida** (Copepoda)
  - Abundance ranges from 10^7 m^{-2} (shallow) to 10^4 m^{-2} (abyssal plain)

Meiofauna

- Small
- Slow movement
- No planktonic larval stage

Limited dispersal

- Higher metabolic rates
- Shorter generation times

Increased potential for speciation

Deep Sea Unknowns

Summarized by Etter & Mullineaux 2001

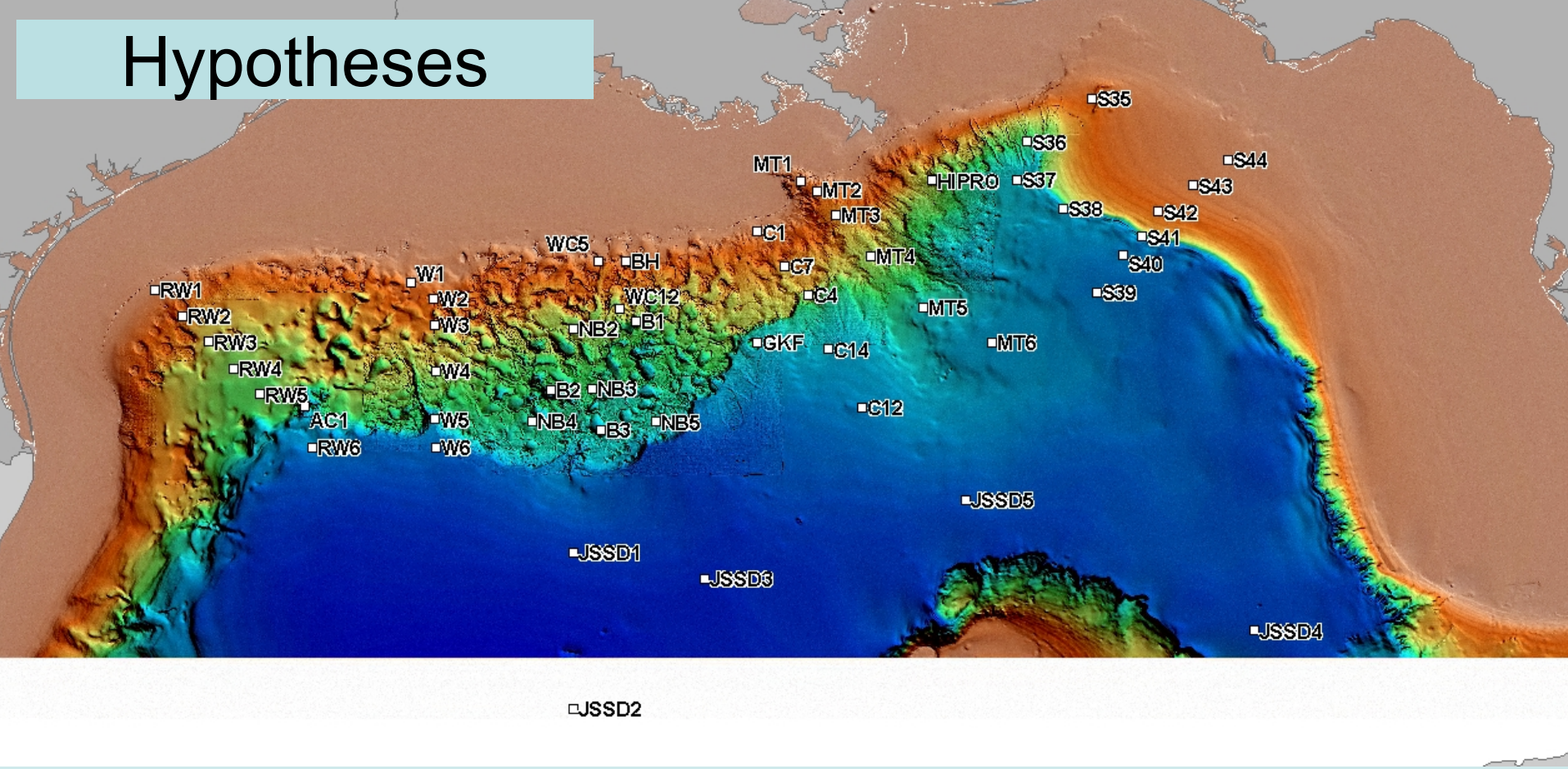
- Distributions of organisms and how they respond to topographic & geochemical features
- Mechanisms that regulate community structure, especially trophic interactions
- Knowledge of regional species pools, dispersal capabilities, and process structuring communities on various scales

Experimental Design Goals

- Environmental Variables
  - Geochemistry
  - Trace Metals
  - Organic Contaminants
  - Sediment Characteristics
- NGOM Regional Patterns
  - Slope Topography
    - Basins
    - Canyons
    - Escarpment
  - River Outflow
  - Loop Current

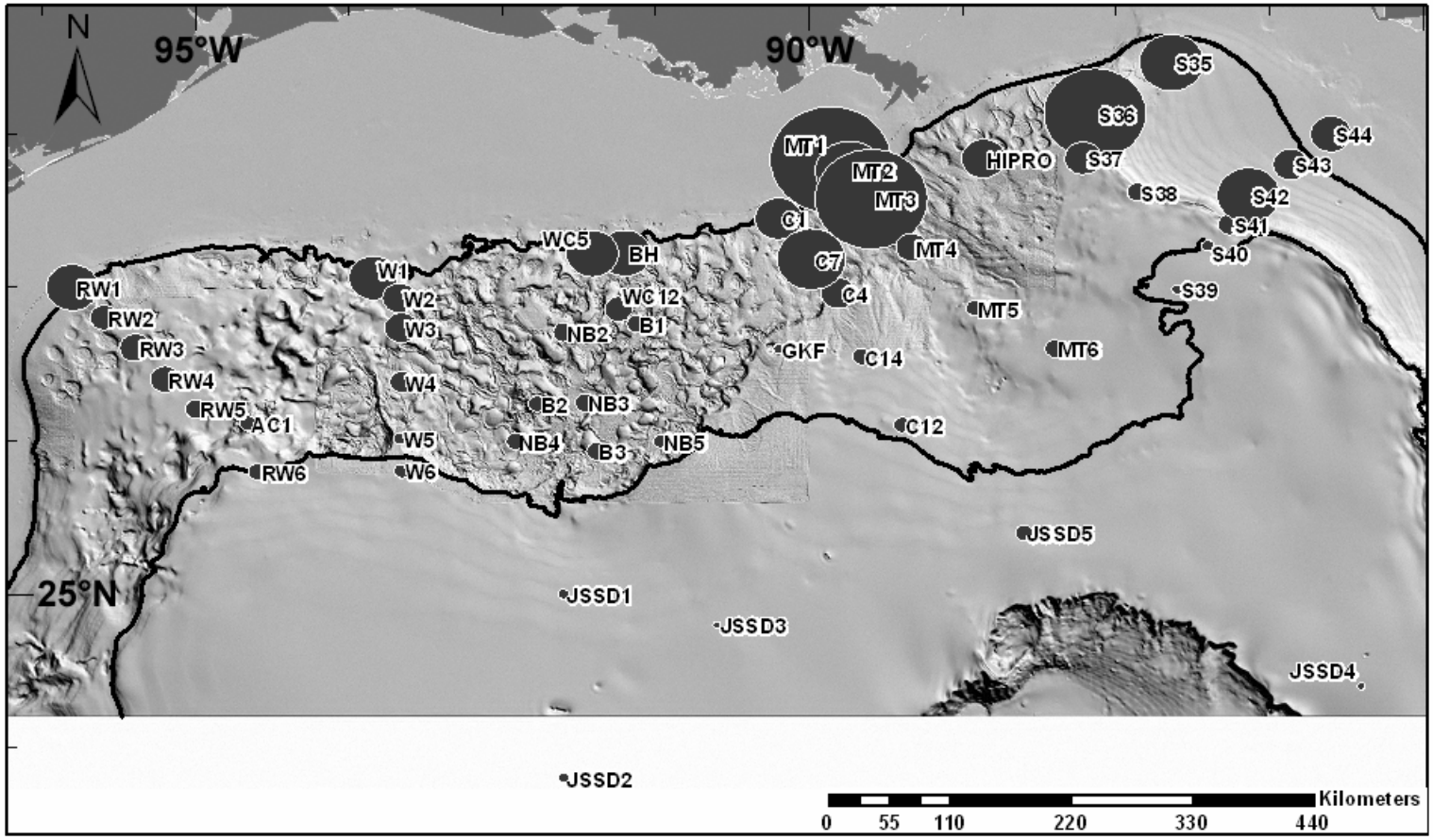
What influences community structure and function on regional and local scales?

Hypotheses



- H_{01} – Depth
- H_{02} – Longitude
- H_{03} – Basins
- H_{04} – Canyon
- H_{05} – Escarpment
- H_{06} – Primary Prod

Meiofauna Abundance

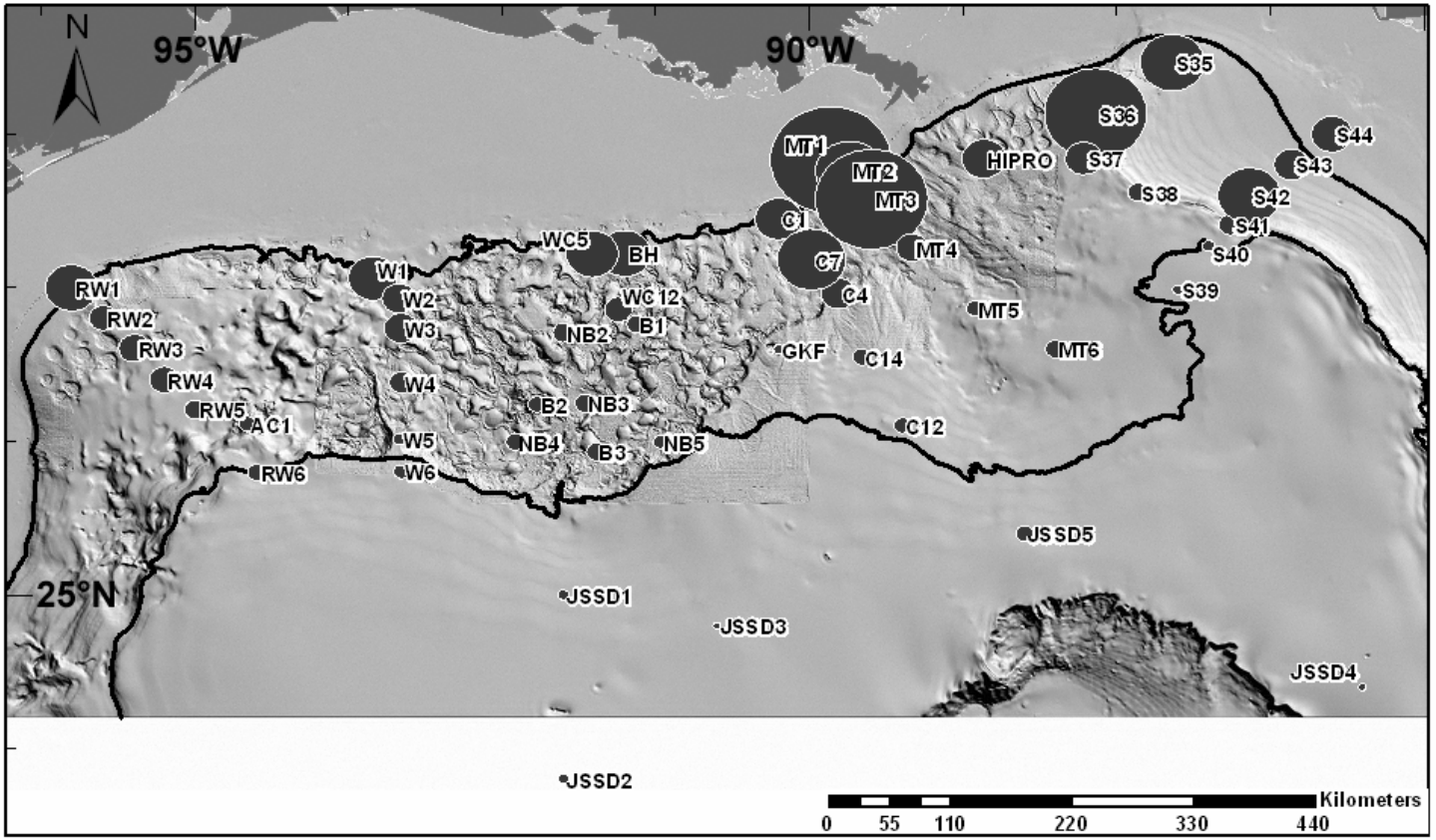


- Taxa dominance
  - **Nematoda (62%)**
  - **Harpacticoida & nauplii (24%)**
  - **Polychaeta (2%)**
  - **17 other taxa (12%)**

Baguley et al. 2006b

Meiofauna Abundance

- Hypothesis Testing
  - H_{01}/H_{02} – Significant depth*longitude interaction (P<0.0001)
  - H_{03} – No significant basin effect
  - H_{04} – Significant depth*canyon interaction (P=0.002)
  - H_{05} – Significant escarpment*dffs interaction (P<0.006)



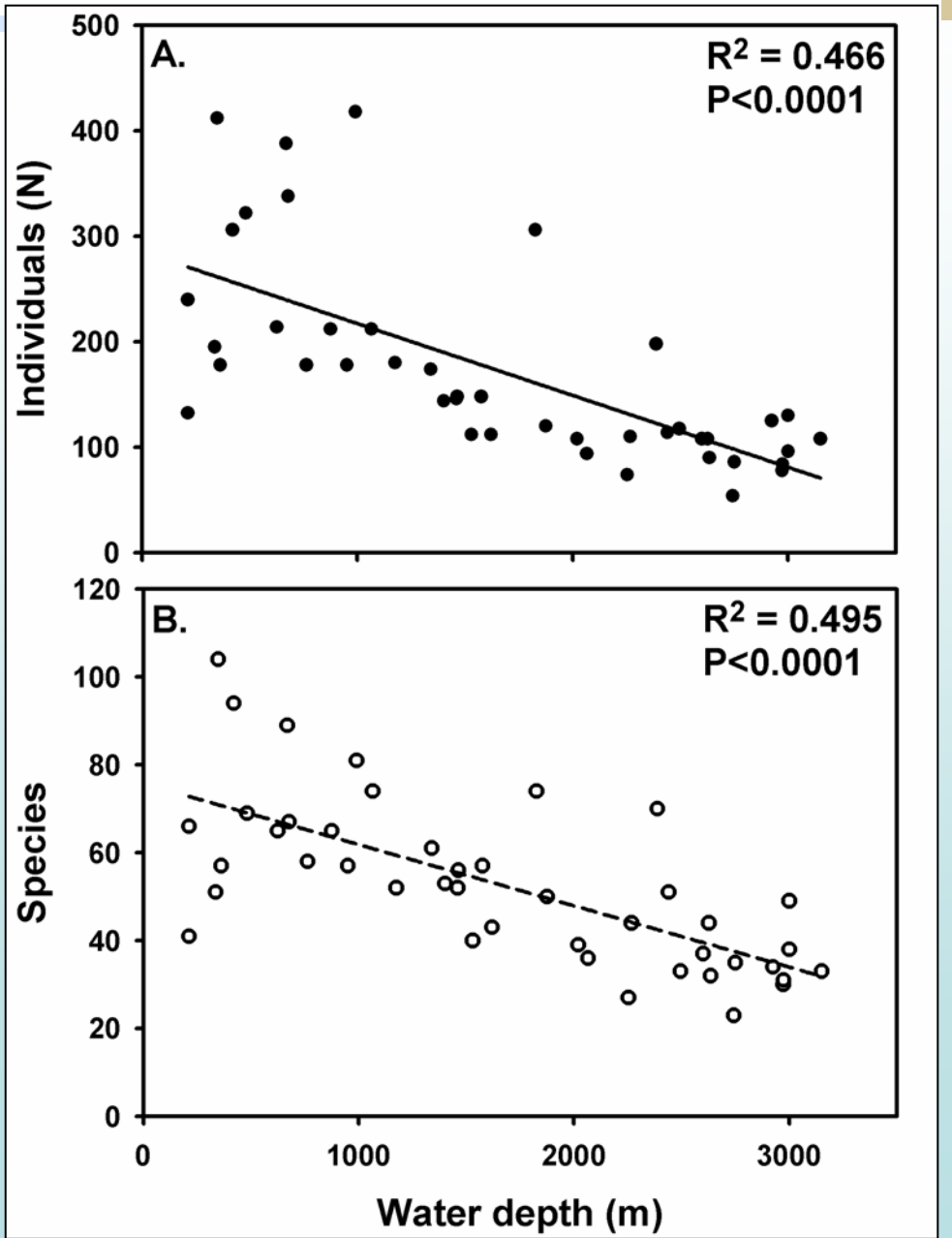
Harpacticoida Diversity

Bathymetric trends

22 Families
175 Genera
696 Species
3680 Individuals

76% undescribed

→The number of species is always dependent upon the number of individuals encountered



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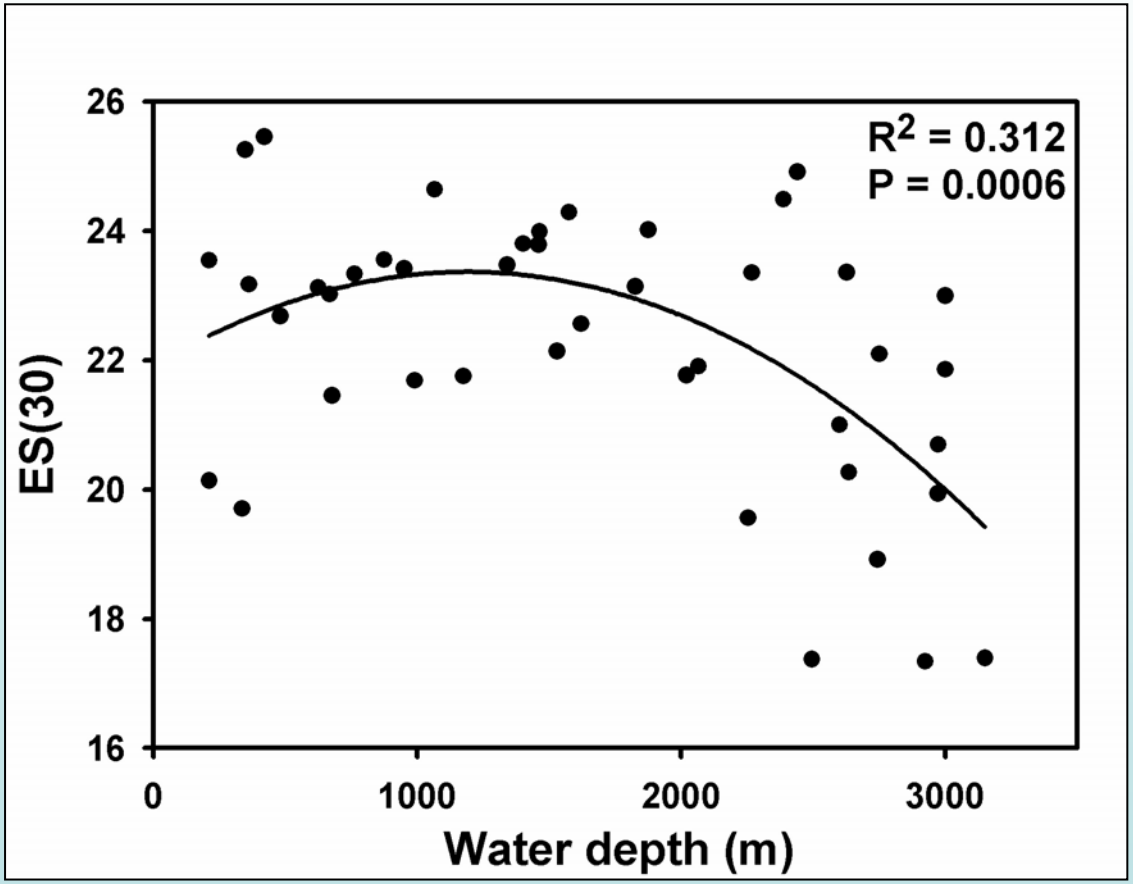
Expected Number of Species

Hurlbert's Rarefraction Index (1971)

The expected # of species found in a sample of ***n*** individuals drawn from a population of ***N*** total individuals distributed among ***S*** species.

The standard index used by deep-sea ecologists to account for differences in abundance over bathymetric gradients.



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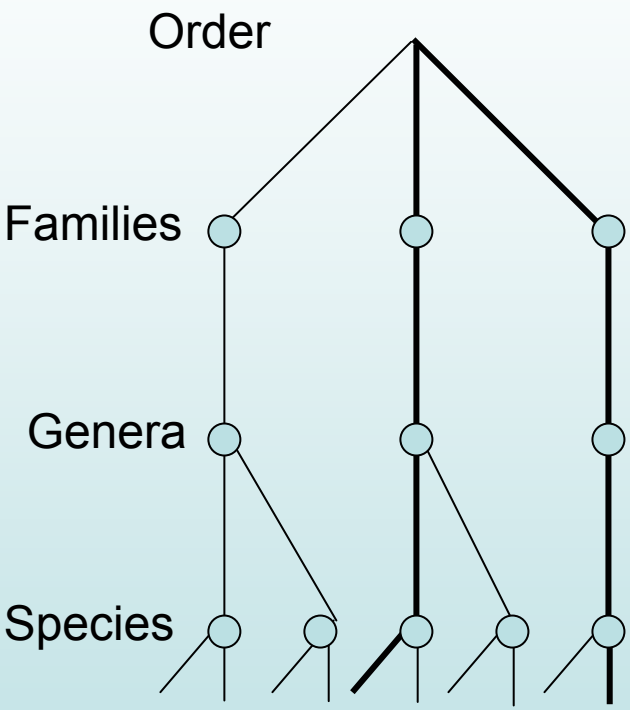
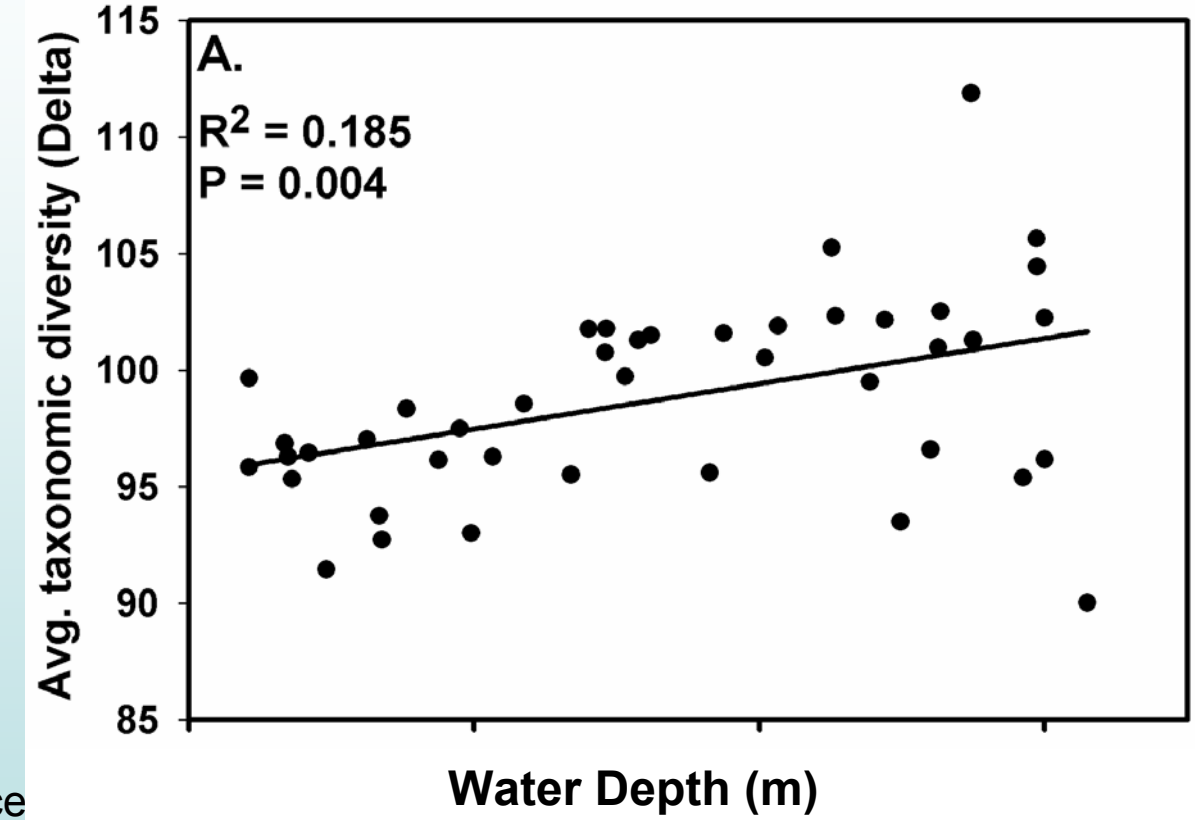
Average Taxonomic Diversity (Δ)

Warwick and Clarke (1995)



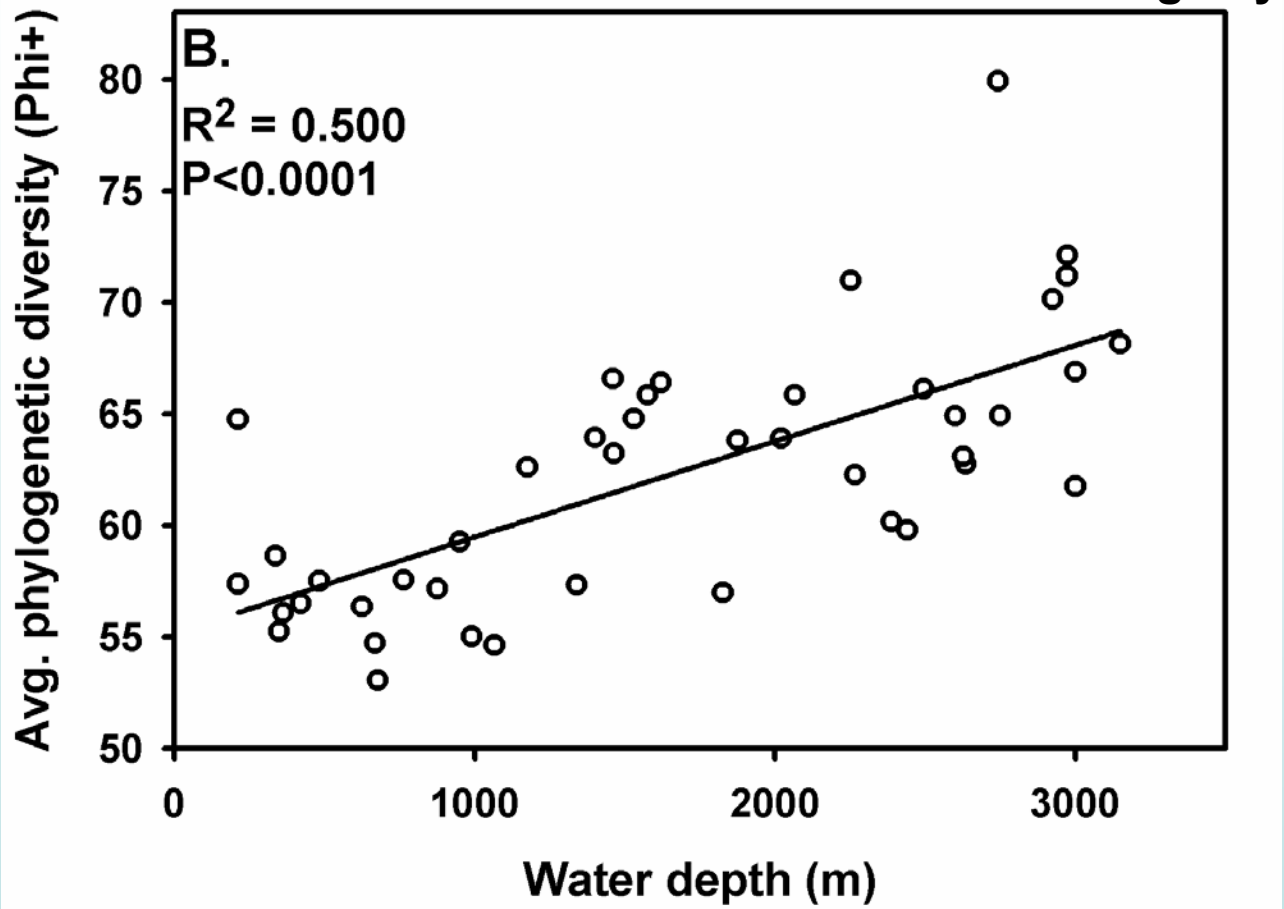


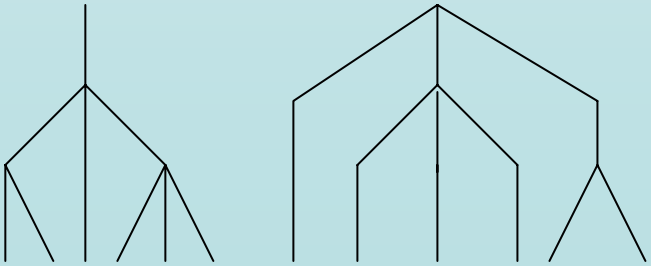
Δ is the average taxonomic distance apart of every pair of individuals in the sample, or the expected path length between two individuals chosen at random

Baguley et al. 2006a

Average phylogenetic diversity (Φ^+)

Baguley et al. 2006a





order

family

genus

species

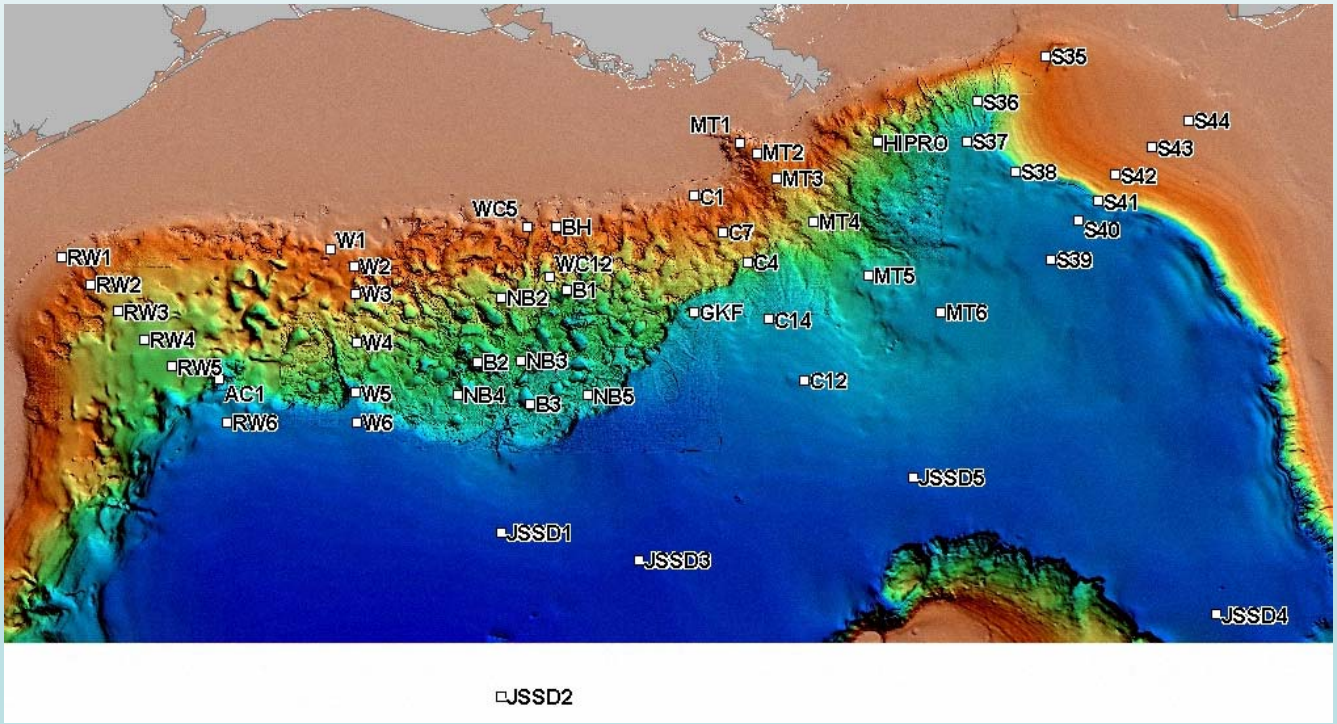
Φ^+ is the cumulative branch length of the entire tree, normalized to the number of species present

Warwick and Clarke (1995)

Hypothesis Testing

Dependent variable = average phylogenetic diversity

- H_{01}/H_{02} – Significant depth*longitude interaction ($P<0.05$)
- H_{03} – No significant basin effect
- H_{04} – Significant depth effect only ($P<0.0001$)
- H_{05} – Significant escarpment*dffs interaction ($P<0.001$)



Non-parametric Multivariate Cluster Analysis

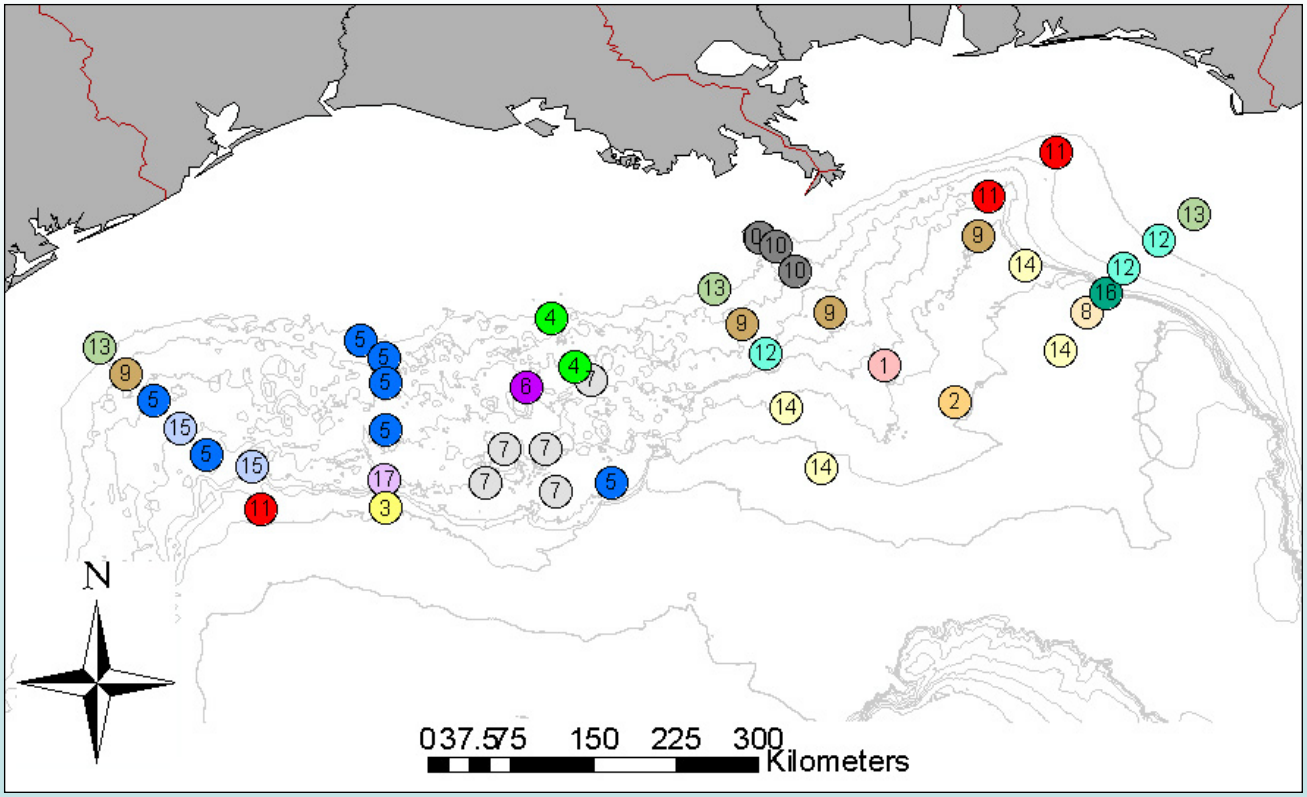
Zones (20% species similarity)

Found at all stations (25%)

Neozosime bisetosa
Neozosime trisetosa
Halectinosoma aff. gothiceps
Bradya aff. congenera

Zone 5 (34%)

Neozosime bisetosa
Neozosime trisetosa
Halectinosoma aff. gothiceps
Bradya aff. congenera
Ameira aff. parvula



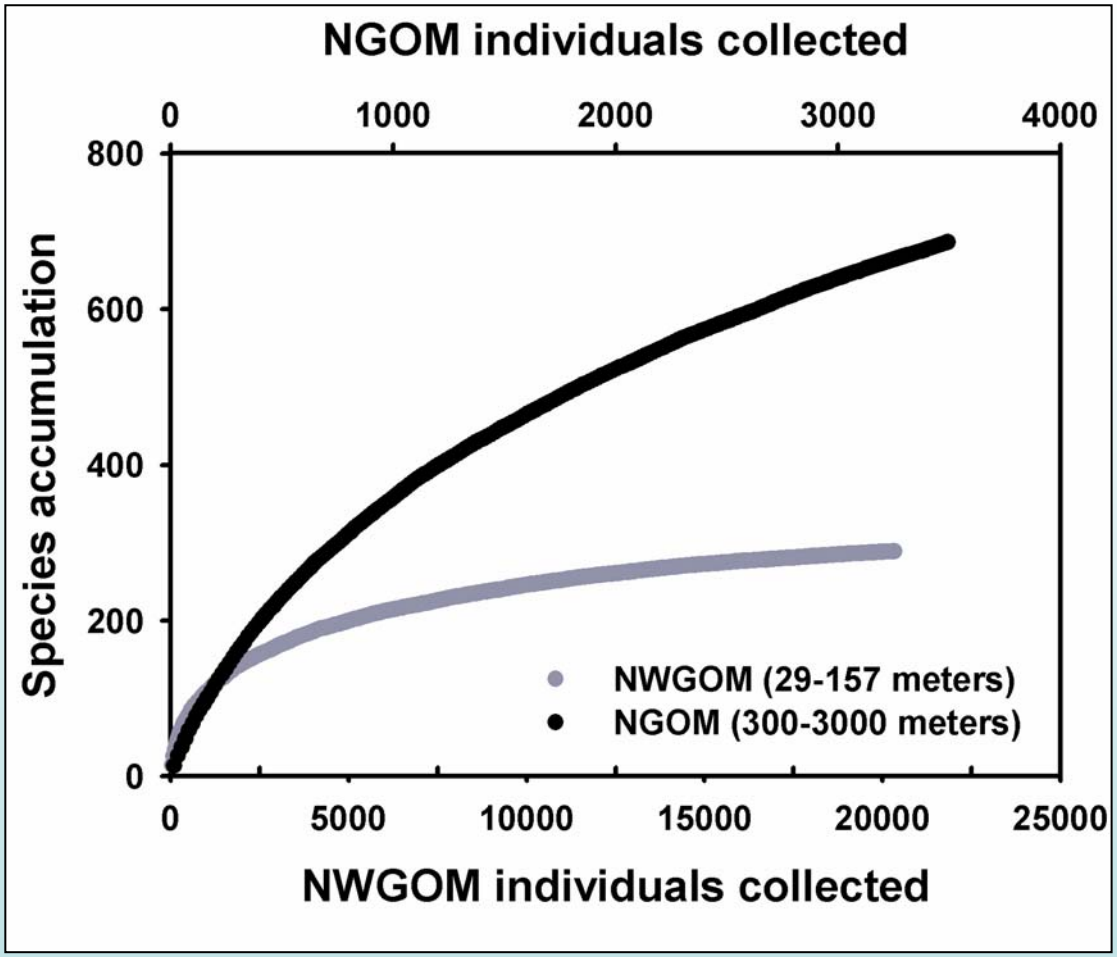
Baguley et al. 2006a

Regional & Global Extrapolations

- Species Accumulation
- $y = (ab + cx^d)/(b + x^d)$
- Model regional estimates
  - NGOM = 2241 species
    - $R^2 = 0.99996$
  - NWGOM = 457 species
    - $R^2 = 0.99980$
  - Total ≈ 2700
  - Approx. regional area = 1.5×10^6 km^2

  Approx. global area = 3.61×10^8 km^2

  - Est. Global Biodiversity = 6.5×10^5 !!!!



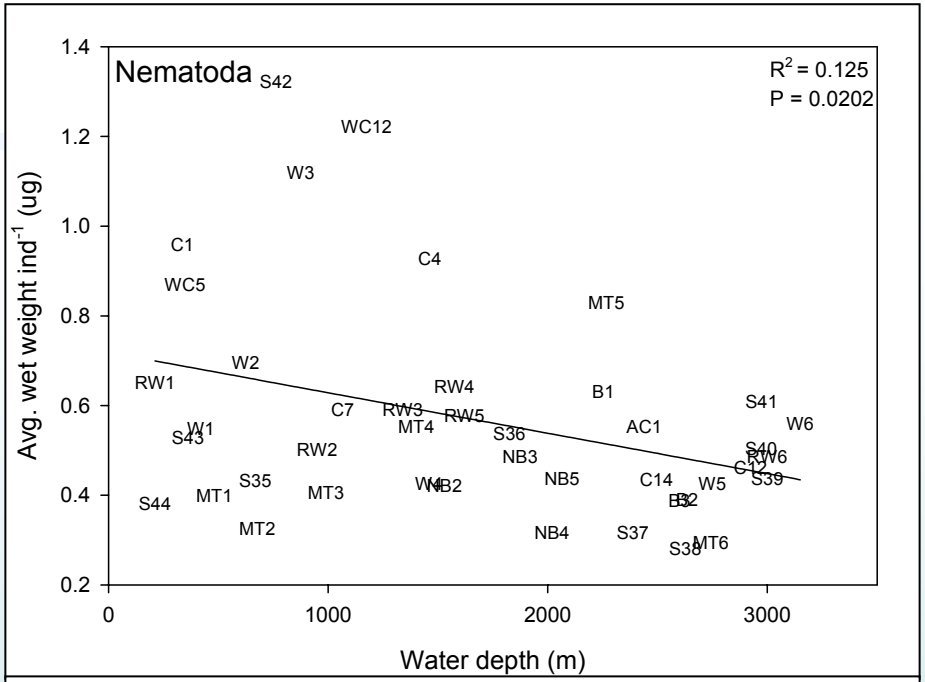
NWGOM - Montagna & Harper 1996

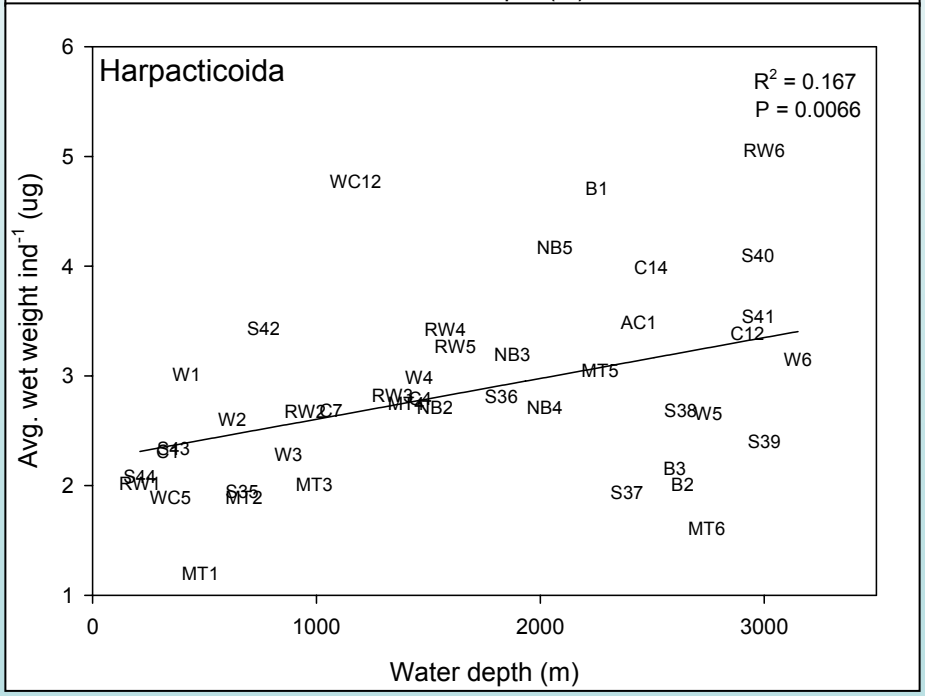
NGOM = DGoMB Harpacticoids

Baguley et al. 2006a

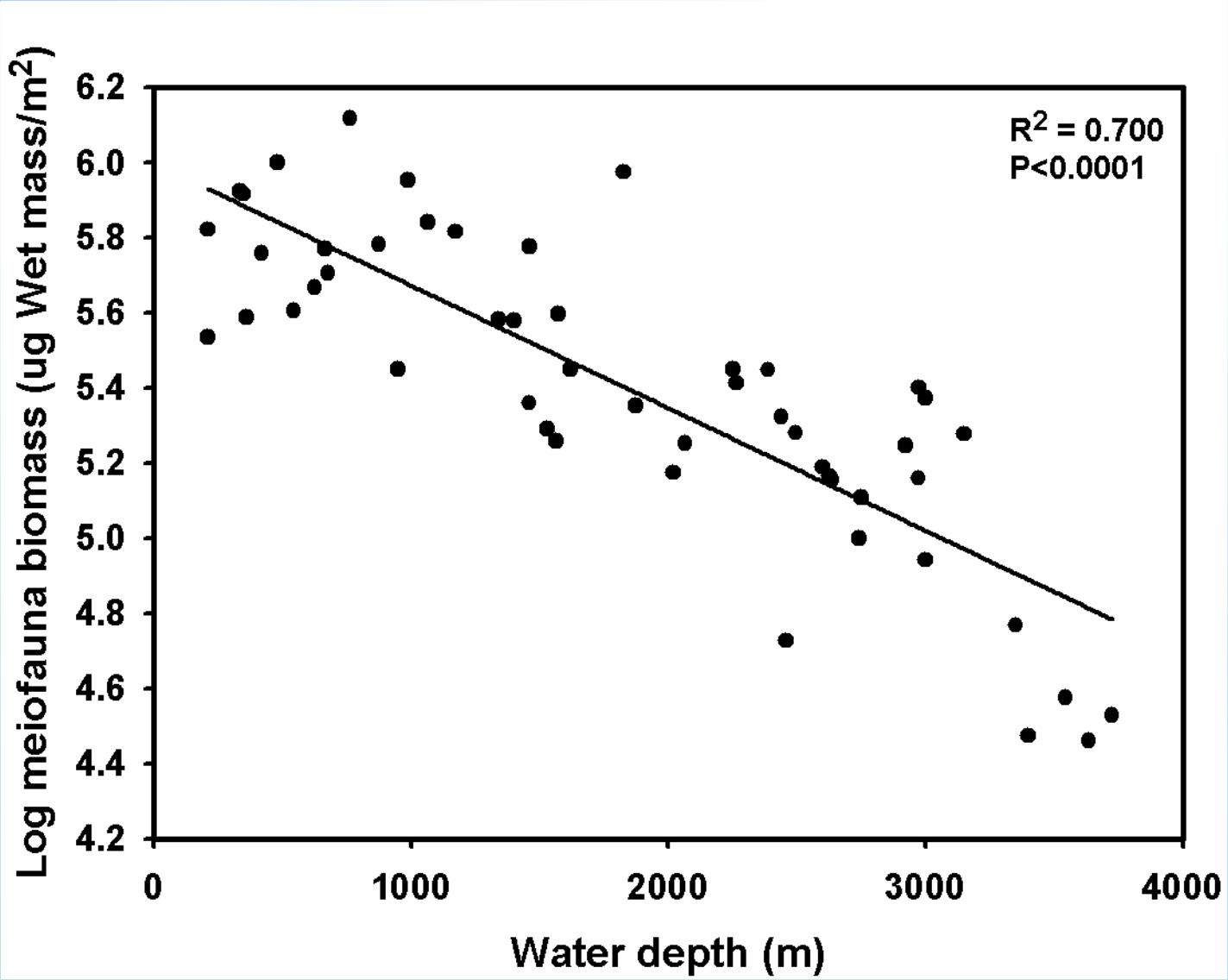
Biomass

Baguley, Hyde, & Montagna (2004)





Meiofauna Biomass



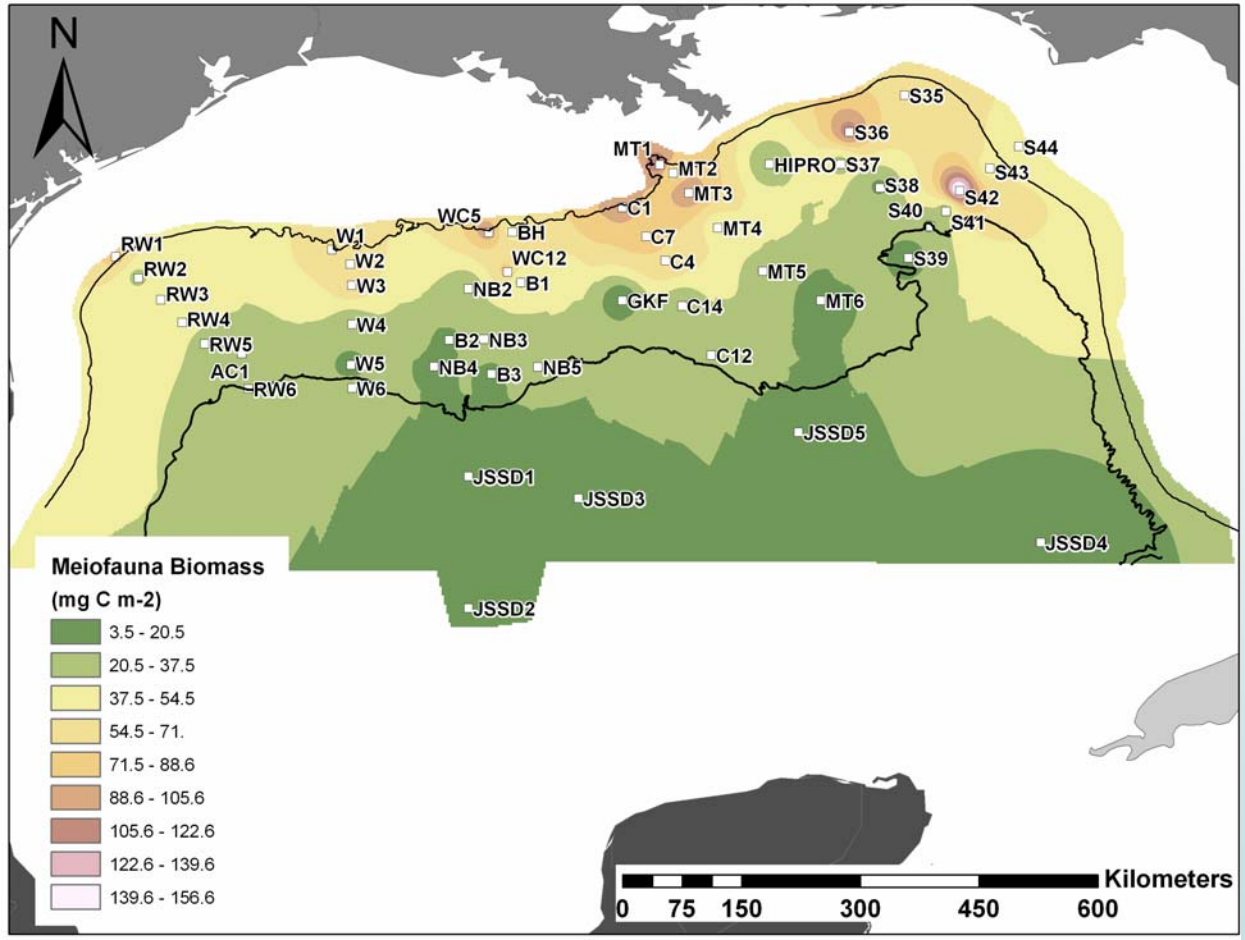
Baguley et al., in prep

Meiofauna Biomass

<u>Model</u>
Inverse Distance Weighted,
Variable search radius,
Cell Size = 2.8 Km^2

<u>Total Meiofaunal Carbon</u>
= Mean (Kg C Km^{-2}) x
Area (Km^{-2})

= 2.1 10^7 ± 1.2 10^7 Kg C

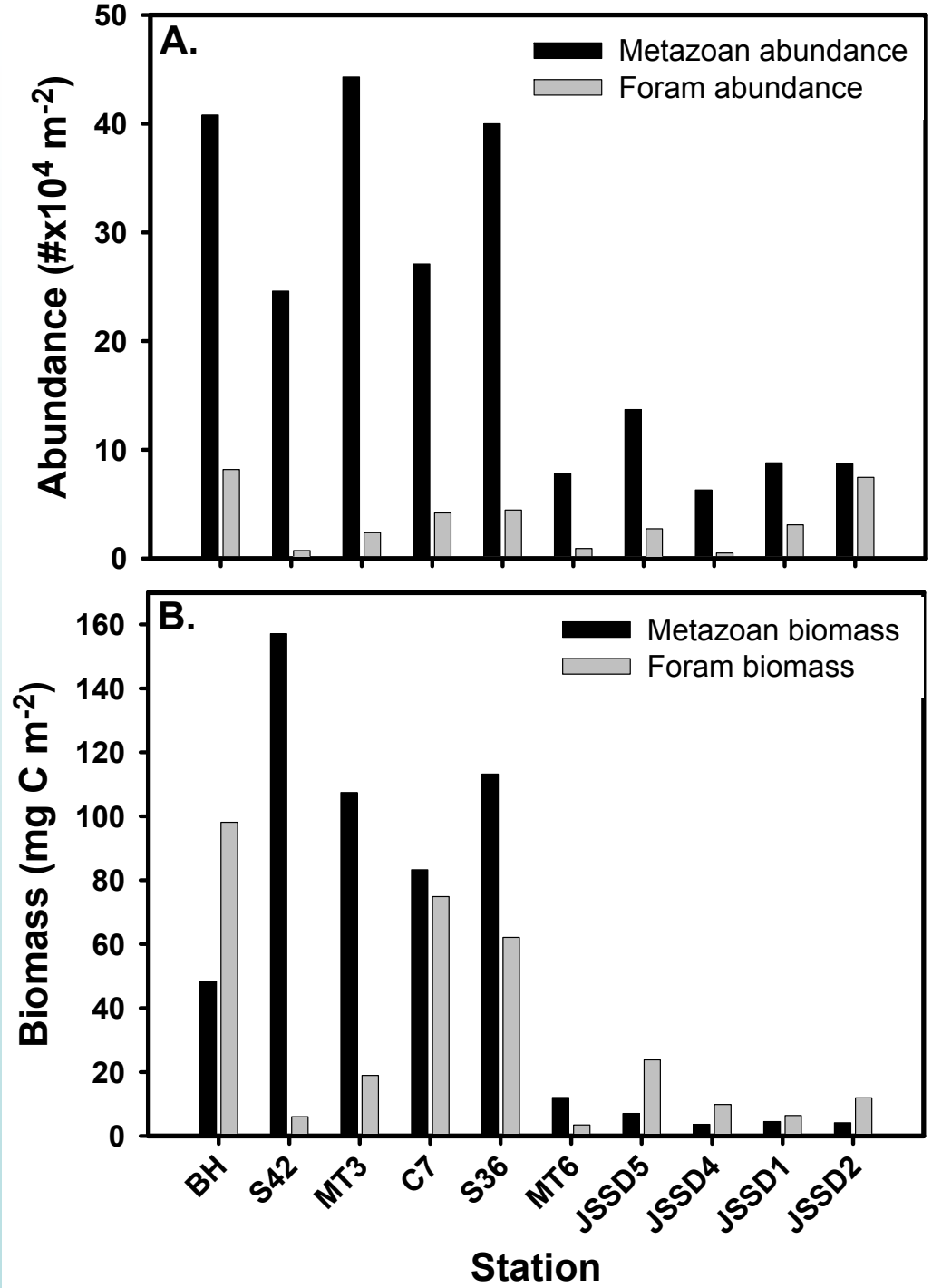


Baguley et al., in prep

Metazoan & Foram Biomass

Comparison of foraminiferal and metazoan meiofaunal abundance and biomass.

Note that metazoa are more abundant, but foraminiferal biomass exceeds that of metazoan meiofauna at half the sites.



Bernhard et al., in press

Meiofauna Respiration (O_2 Flux)

Mahaut *et al.* 1995

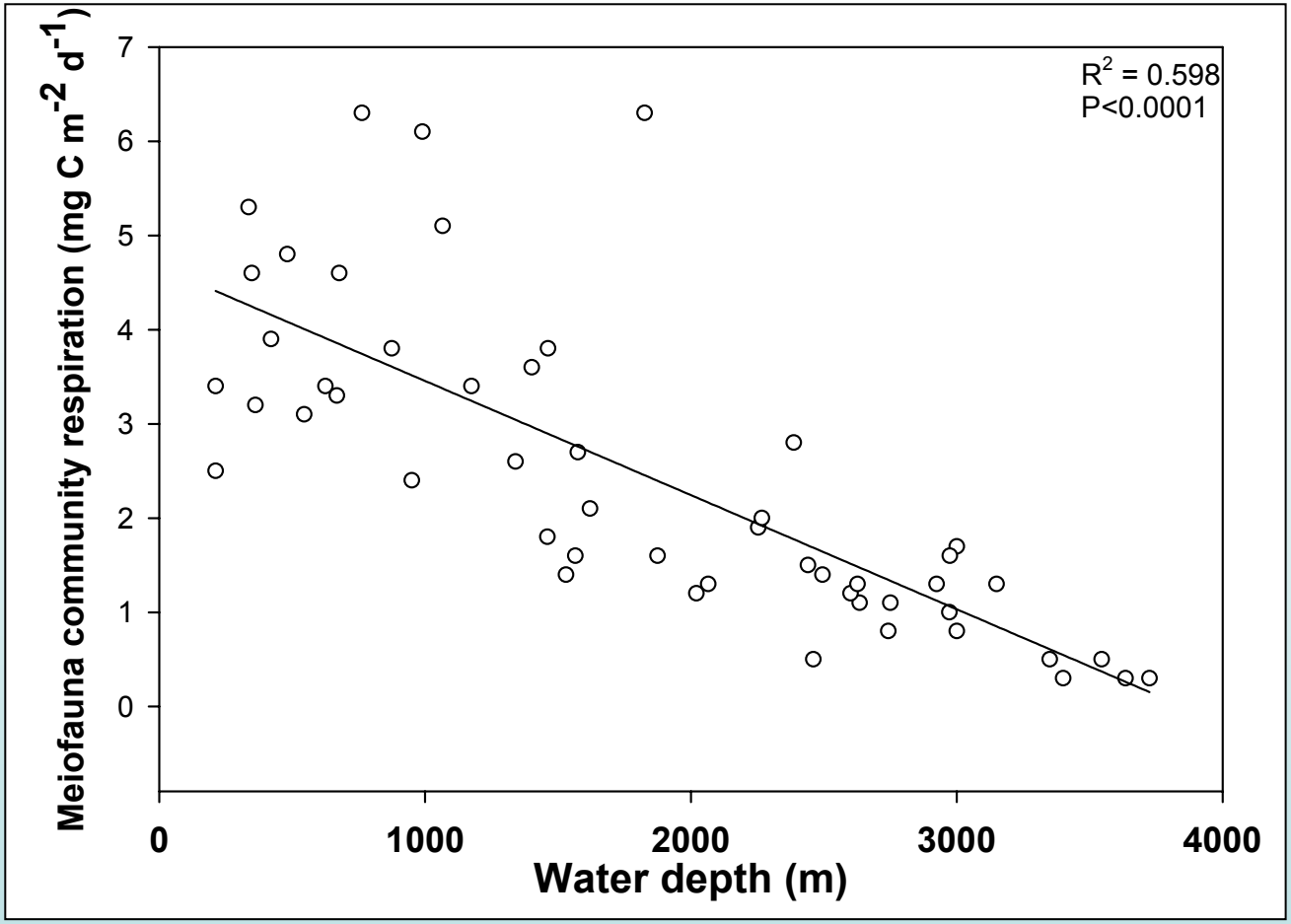
$$R = aWb$$

W = mean mass

a & *b* = Constants*

$$CO_2 = (\Sigma B_i \times R_i)$$

ΣB_i = sum of biomass
R_i = resp. rate



Baguley et al., in prep

Meiofauna Respiration (O_2 Flux)

Model

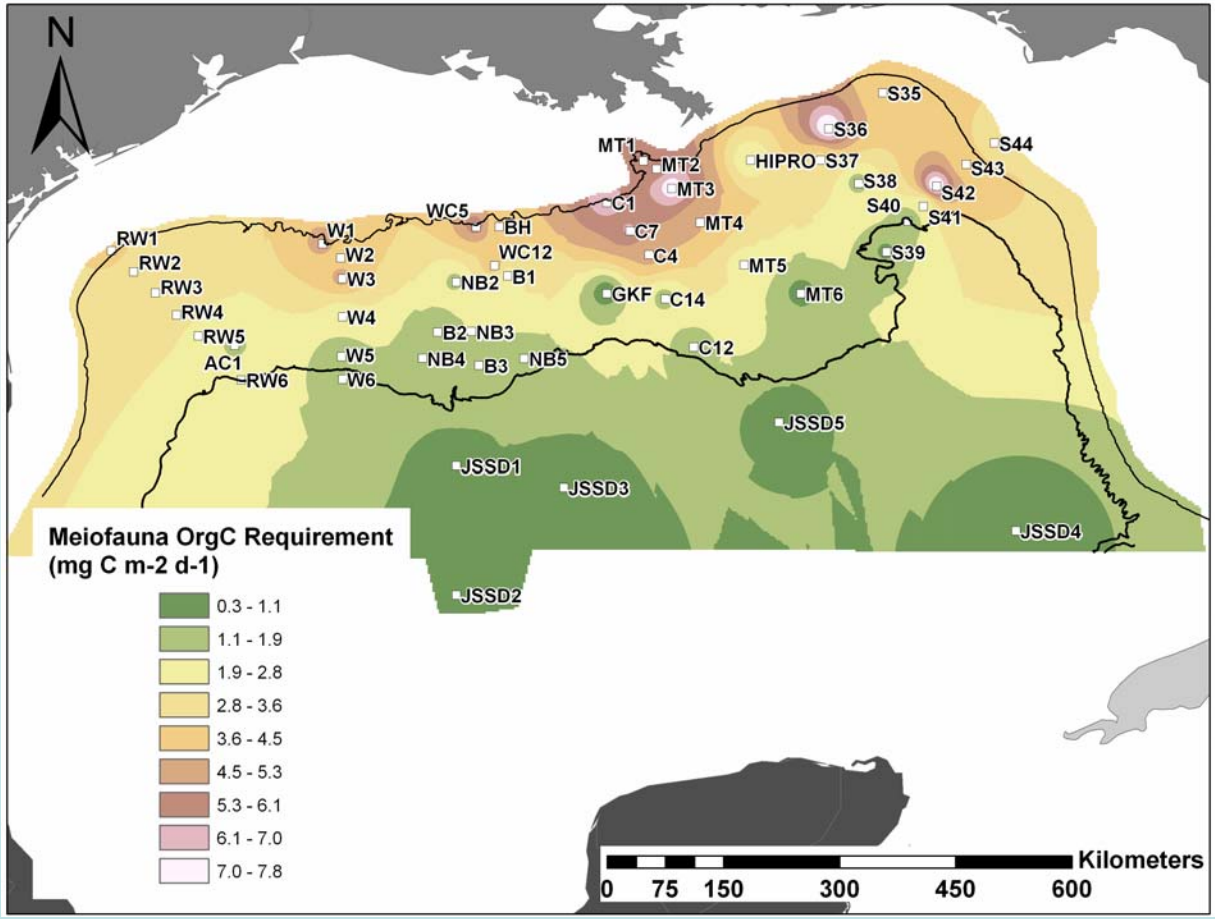
Inverse Distance Weighted,
Variable search radius,
Cell Size = 2.8 Km^2

Total Meiofaunal Carbon

= Mean (C_{org} Km^{-2}) x Area (Km^{-2})

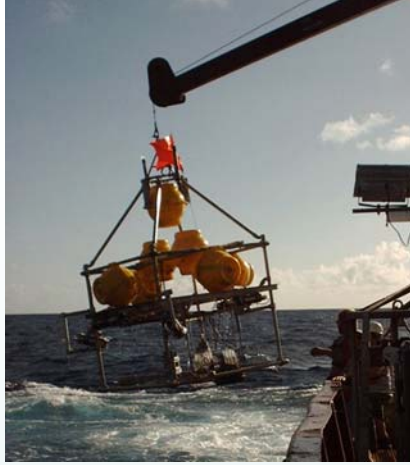
= 1.5 10^6 (± 8.4 10^5) Kg C d^{-1}

= 7% of meiofaunal biomass



Baguley et al., in prep

Total Community Metabolism



mg C m^{-2} d^{-1}

Station	Depth	Total	Meio	% Meio
S42	750	32.4	6.3	19.4
S36	1800	29.1	6.3	21.6
MT1	480	36.5	4.8	13.2
MT3	1000	28	6.1	21.8
JSSD1	3550	3.9	0.5	12.8
JSSD4	3400	3.9	0.3	7.7

8–22% of Total

Total community metabolism, converted from SCOC, measured by the benthic lander (Rowe et al., submitted)

Foraminiferal biomass is comparable to meiofaunal biomass (Bernhard et al., in press)

Bacterial biomass exceeds meiofaunal biomass by 10–100X (Deming et al., submitted)

Meiofauna require only 0.1 to 0.5% of the bacterial standing stock

Baguley et al., in prep

Summary of Results (Abundance)

- Univariate
  - Abundance patterns with depth differ among transects (interactions)
  - Large geologic features important
    - Canyon, escarpment
- Multivariate
  - Sediments are very similar on a regional scale:
    - Geochemical, geological, metals, hydrocarbons
  - Overlying Chl(a) & sediment POC are driving meiofauna abundance patterns

Summary (Diversity)

- Local (per core) diversity (α) decreases with increasing depth
  - But expected number of species is maximized in bathyal
  - And proportional number of higher taxa increases with increasing depth (Δ & Φ)
- Rate of encounter of new species (β) is high and therefore regional (γ) and global estimates are high
  - Zonation
  - Species accumulation
- Inverse relationship between taxonomic diversity and organic carbon fluxes
  - Huston (1979), Rex (1983) → Dynamic equilibrium on local scales
- High local-scale variability, meiofauna life history characteristics, and the vast area of the deep sea are likely responsible for high β & γ (Abele and Walters 1979)

Summary (Community Function)

- Meiofauna biomass decreases with depth
- Highest biomass and respiration are found in the NE GOM (Mississippi Trough, DeSoto Canyon, and above the Florida Escarpment
- Meiofauna account for 10–25% of whole-community metabolism
- Meiofauna organic carbon consumption is 7% of the standing stock (biomass) per day
- Allometric estimations suggest a carbon requirement equaling 0.1 to 0.5% of the bacterial standing stock

Advances in Deep Sea Ecology

- Demonstrated that interactions with physical processes and topographic conditions affect POM fluxes and regulate abundance, diversity, biomass, and community function
- Demonstrated that the regional species pool is large
  - Small species ranges, less species similarity with depth (high endemism)
  - High global diversity (millions of species, not thousands)
- In contrast to macrofauna, meiofauna alpha diversity is constant or decreases with depth
- Meiofauna are a good model for studying deep sea ecological and evolutionary processes because of their life history characteristics
- Small-scale heterogeneity, not constancy, affects community, structure and function

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