

SHE Analysis: A New Tool For Use In Biostratigraphy and Hydrocarbon Exploration

*“ . . . fervently wish that your journey may be long,
full of adventures and with much to learn.”*

“Ithaca”, Constantine P. Cavafy, 1863-1933



Dr. Brent Wilson FGS

Petroleum Geoscience Programme

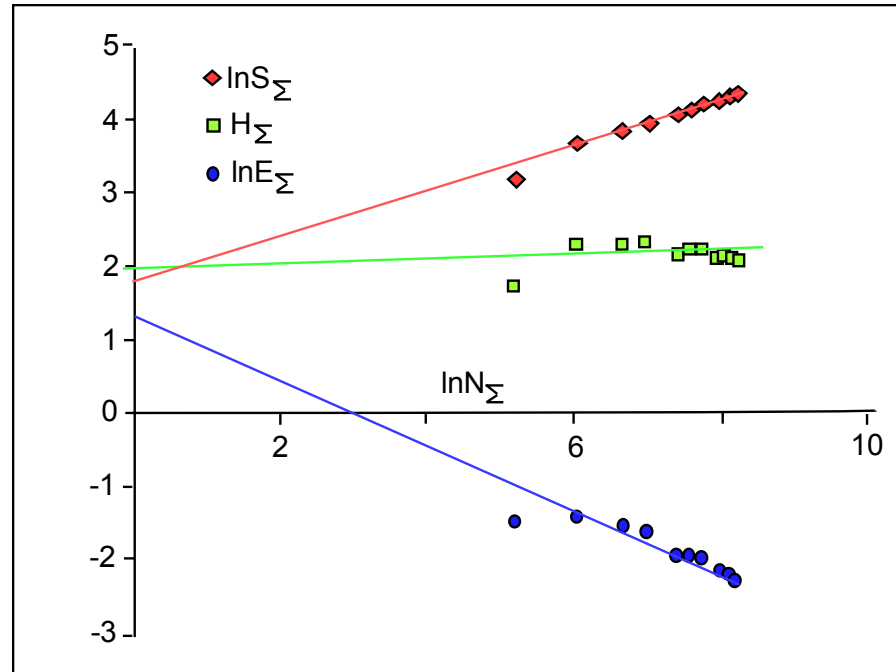
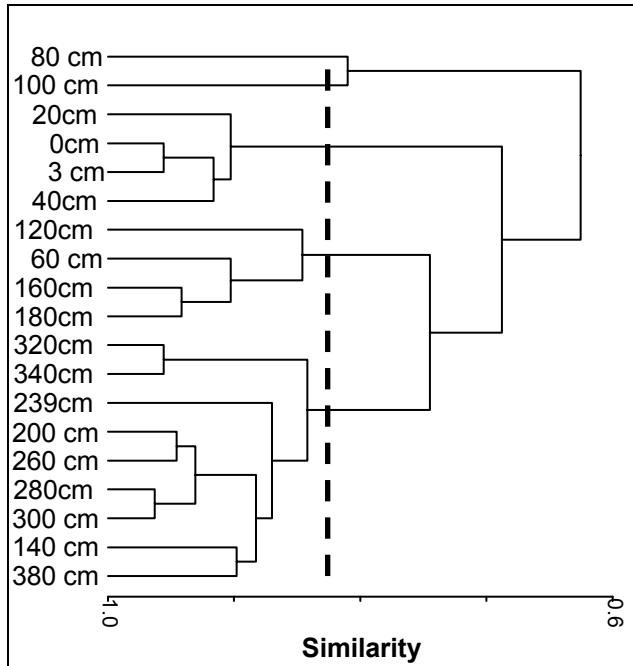
Faculty of Engineering

The University of the West Indies

St. Augustine

Trinidad and Tobago

Ways to discover if samples of fossils contain similar assemblages



Cluster Analysis

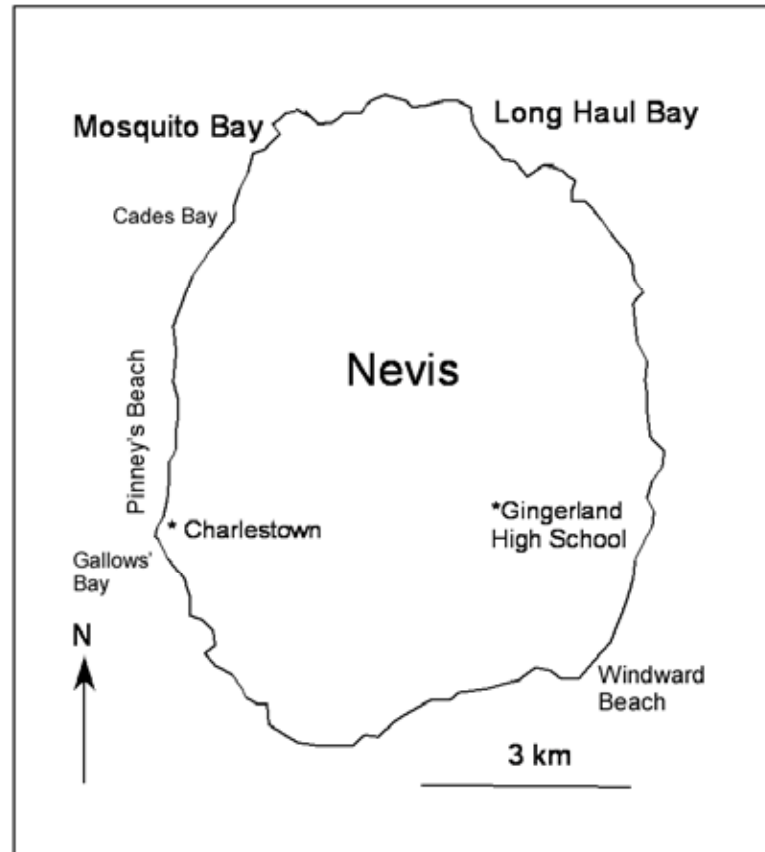
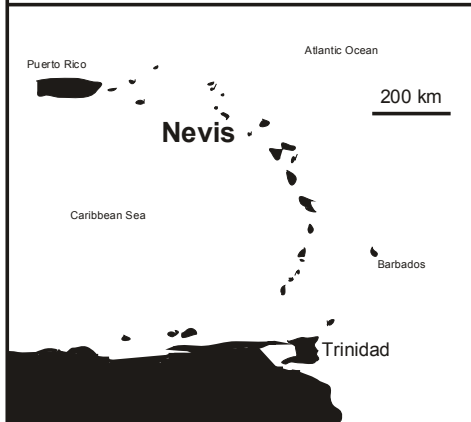
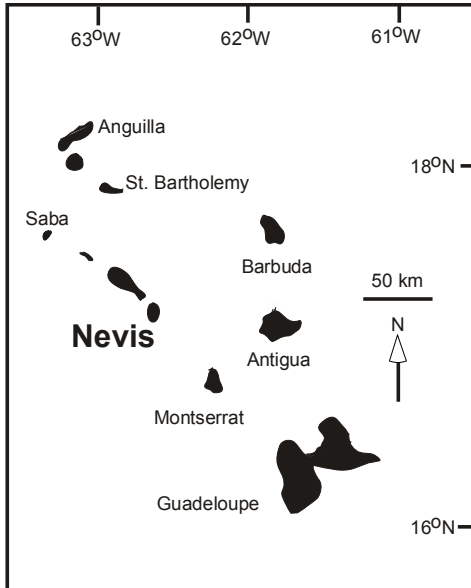
- Produces a *dendrogram*
- **Advantage:** Compares all samples at once
- **Disadvantage:** Compares all samples at once

SHE Analysis

- Produces a *biodiversitygram*
- **Advantage:** Accumulates samples one by one
- **Disadvantage:** Tedious to construct

So where is Nevis?

About 30 miles NE of Redonda!



And what is Nevis like?



A young man at
a loose end

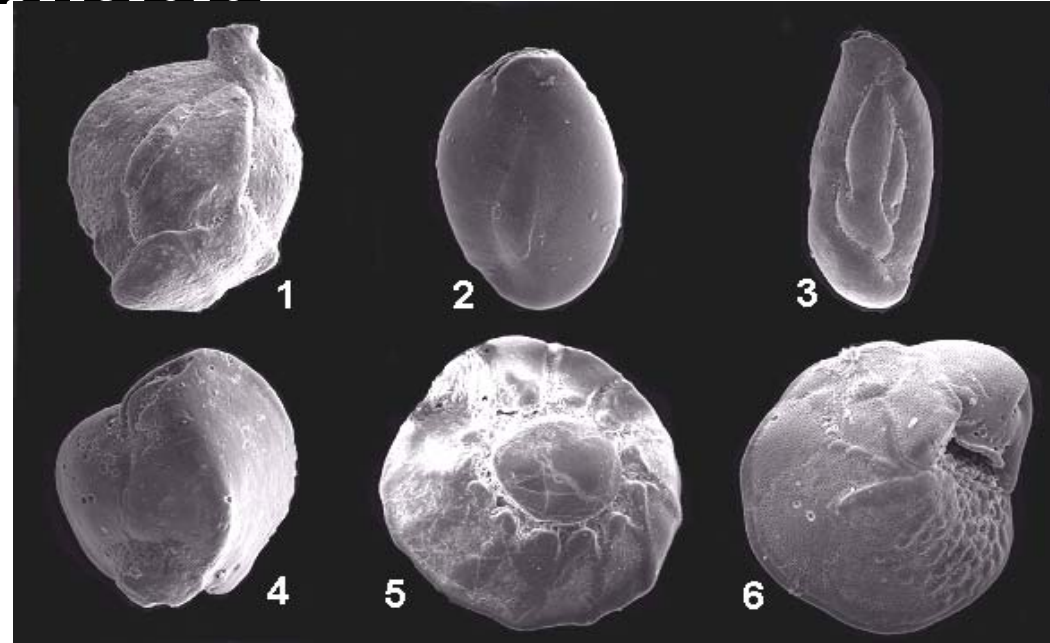
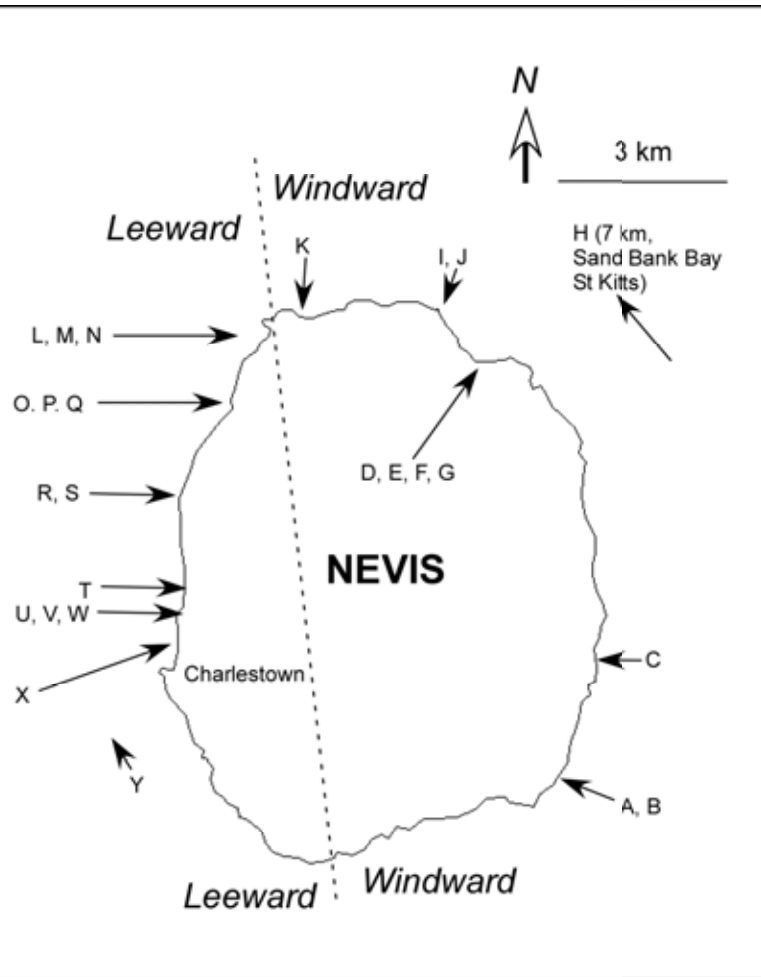


St. George Gingerland
Parish Church—the
main entertainment?



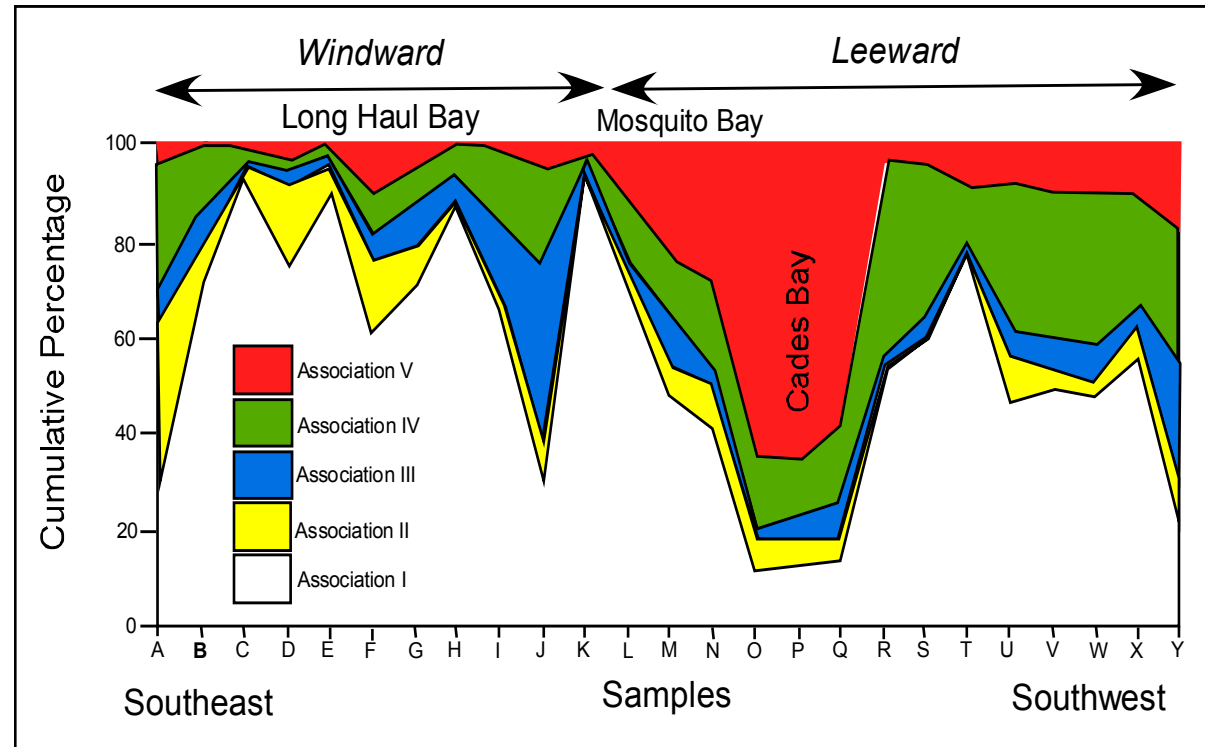
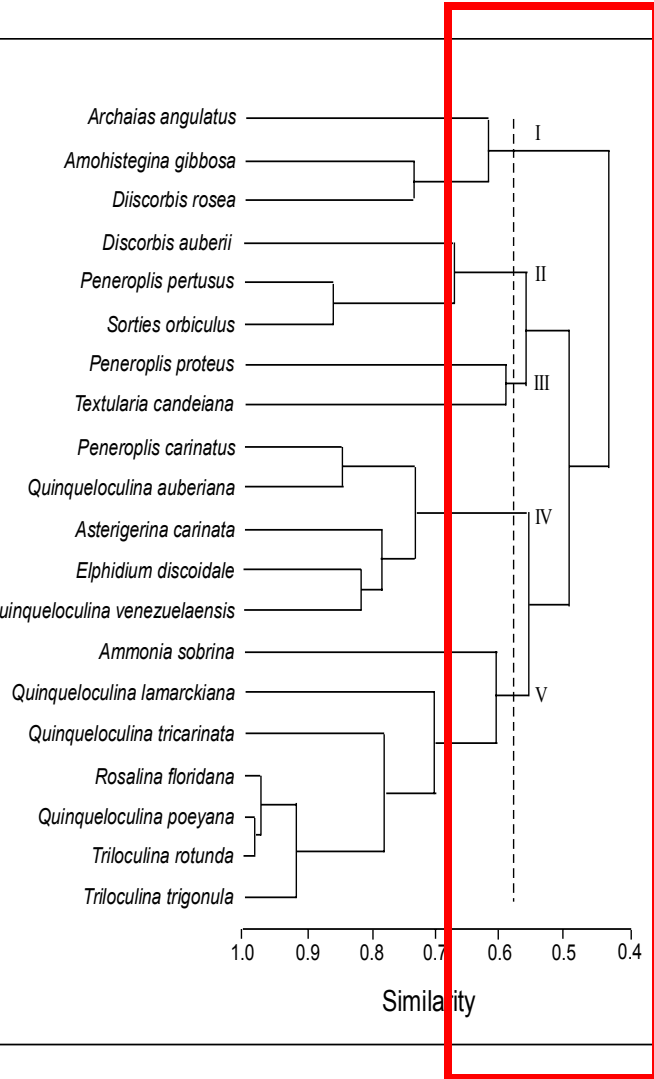
Typical Nevisian chattel
houses

How did it start? With a few sediment samples from around the island

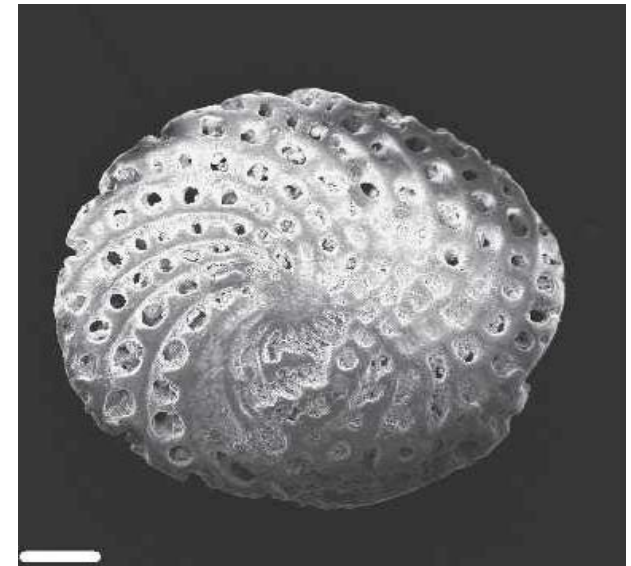
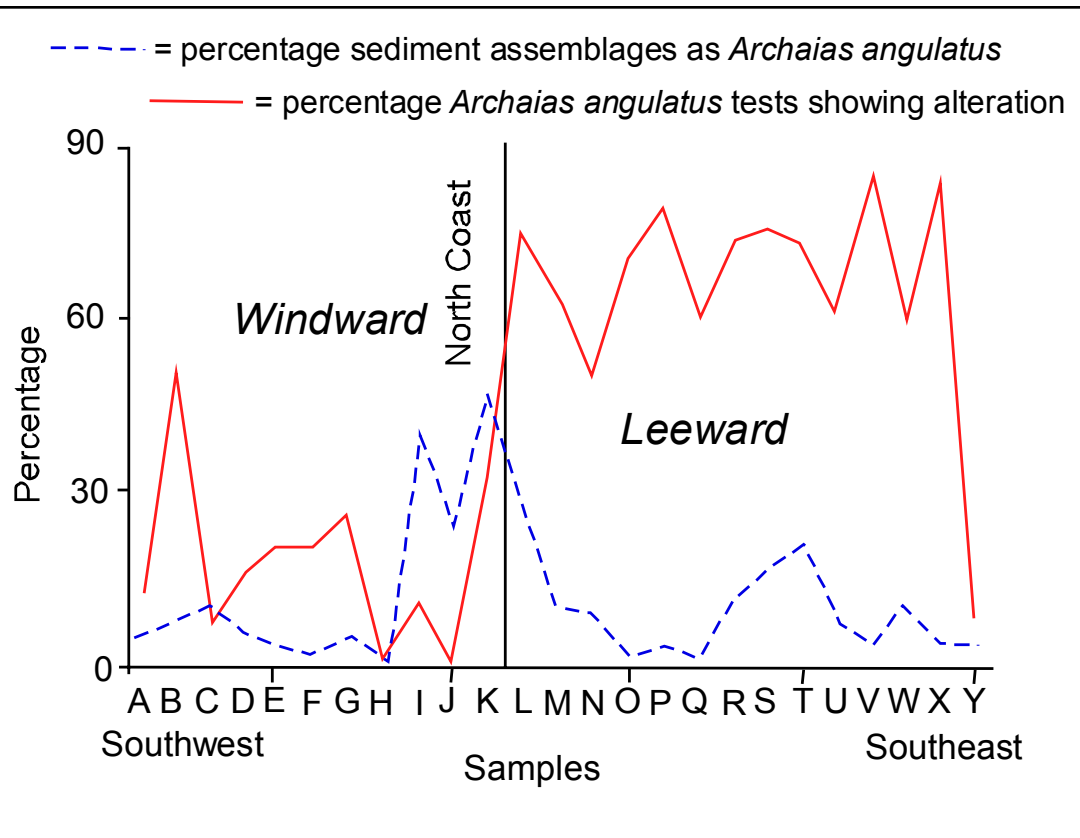


- 1, *Quinqueloculina* sp.
- 2, *Pseudolachlanella* sp.
- 3, *Lachlanella* cf. *quadrilateralis* (d'Orbigny)
- 4, *Quinqueloculina lamarckiana* d'Orbigny having a bad aperture day
- 5, *Ammonia sobrina* (Shupack),
- 6, *Asterigerina carinata* d'Orbigny

Distribution of associations in sediments



Significance of chemically altered *Archaias angulatus* (Fichtel and Moll, 1798)



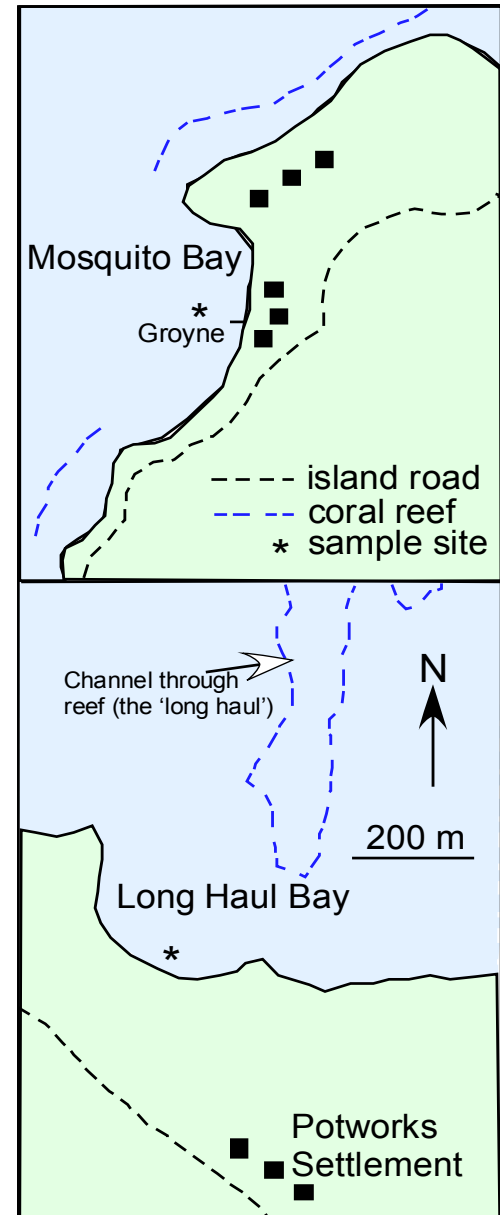
A worn *A. angulatus*
Scale bar 100 μm

What to do next?

- No regular pattern of inter-annual fluctuations occurs in benthonic fauna in sediments within seagrass beds (Buzas et al., 1977)
- In northern Caribbean Sea, nearshore benthonic foraminifera dwell mostly on marine plants
- Foraminifera do not eat the plants, but other epiphytes (bacteria, diatoms, algae)
- **Monitor the epiphytal fauna**, using mass of detritus on plants as an independent variable!

Methodology

- Mosquito Bay (polluted from leaking septic tank)
- Long Haul Bay (pristine)
- 3rd Thursday of every month
- Pseudoreplicate samples
- Stained with **very strong** rose Bengal (*Discorbis rosea* has reddish test--difficult to see protoplasm without very strong stain)
- Excepting for seagrass leaves, washed over 63 μm mesh, then detritus dried
- Mass of dried detritus used as independent variable

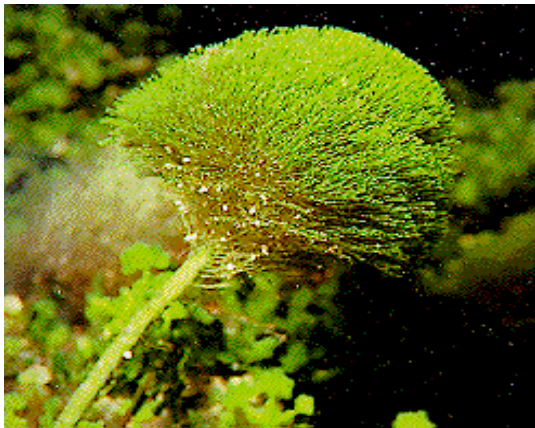


Phytal Substrates Sampled

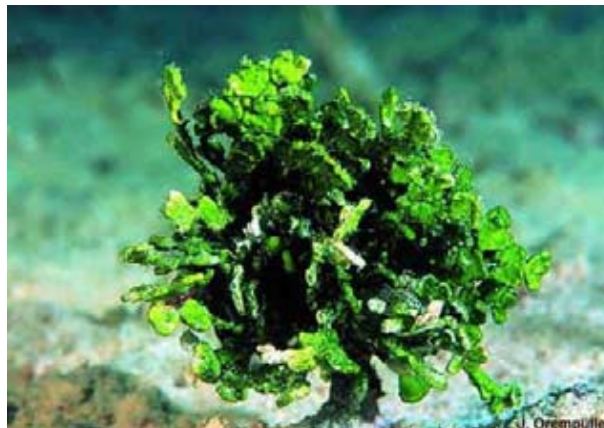
6 substrates sampled

- Mosquito Bay: *P. capitatus* heads (capitulae), *Syringodium filiforme* rhizomes, *Halimeda opuntia* growing on a groyne
- Long Haul Bay: *Penicillus capitatus* heads, *Thalassia testudinum* rhizomes, *T. testudinum* leaves

Penicillus capitatus



Halimeda opuntia



Seagrasses: *Thalassia testudinum* & *Syringodium filiforme*

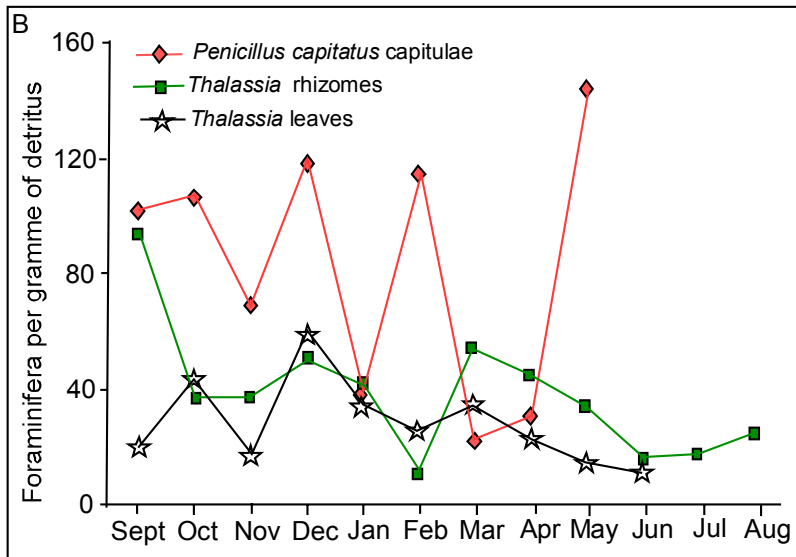
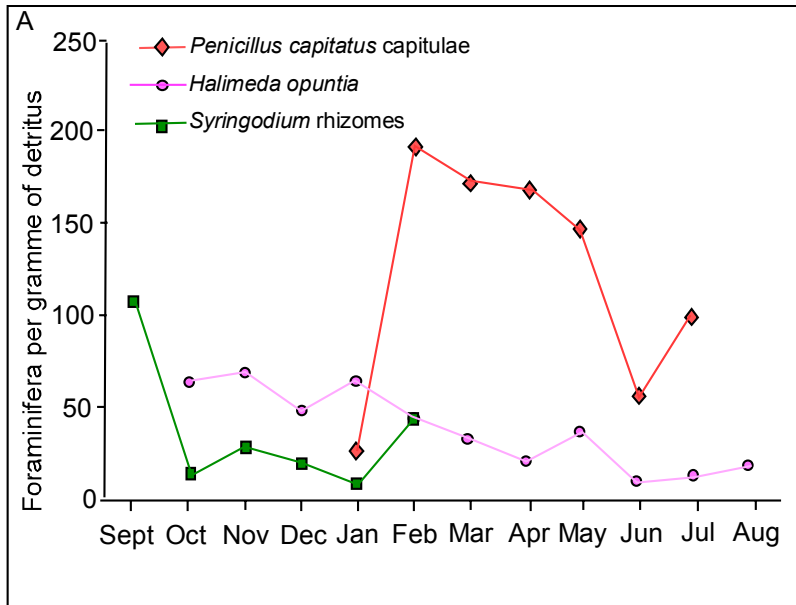


Statistical Measures Calculated For Each Sample

- Foraminiferal population density (foraminifera per gram of detritus)
- Species richness per sample (S)
- Information Function ($H = -\sum p_i \cdot \ln[p_i]$), where p_i = proportional abundance of *i*th species
- Equitability Index ($E = e^H/S$)

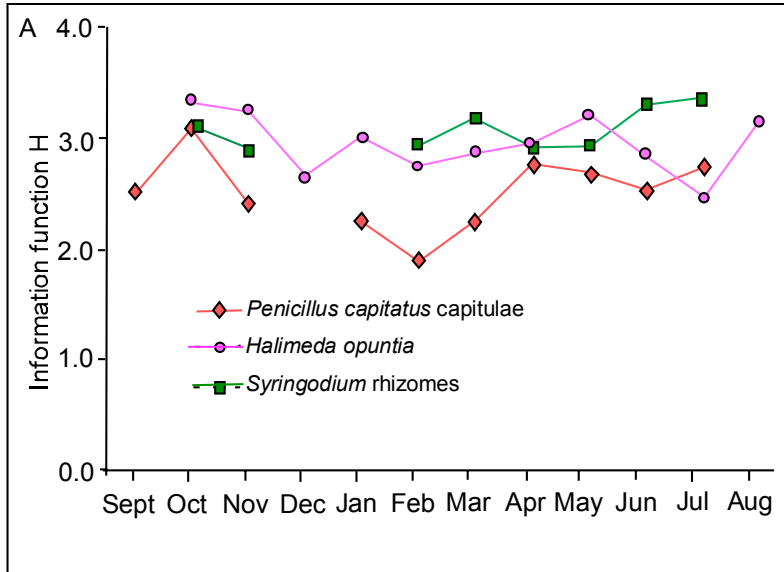
Comparison Between Bays 1—Population

Densities



- A = Mosquito Bay
- B = Long Haul Bay
- Mean population density on *P. capitatus* ~2-3 times that on other substrates
- No difference in mean population densities on *P. capitatus* or seagrass rhizomes between the two bays
- Linear regression suggests overall decreases in population densities in Mosquito Bay—reaction of fauna to onset of pollution?
- No such trends in Long Haul Bay

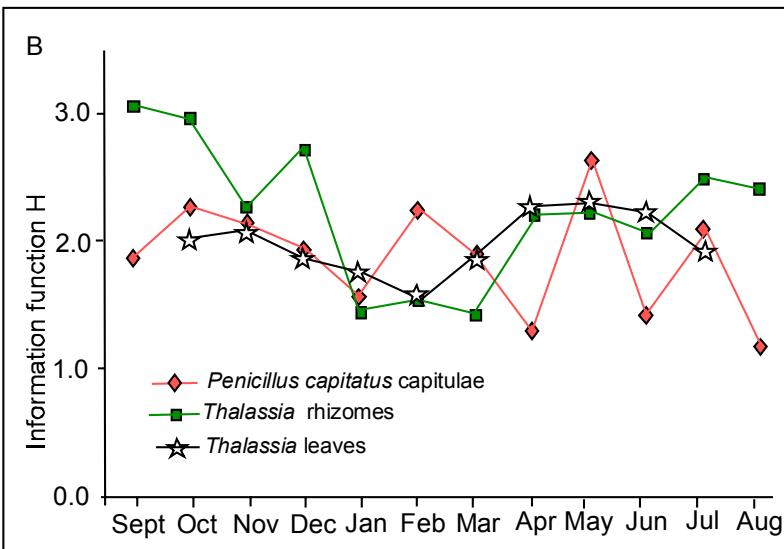
Comparison Between Bays 2—Information Function



- A = Mosquito Bay
- B = Long Haul Bay

- Diversity measured using H

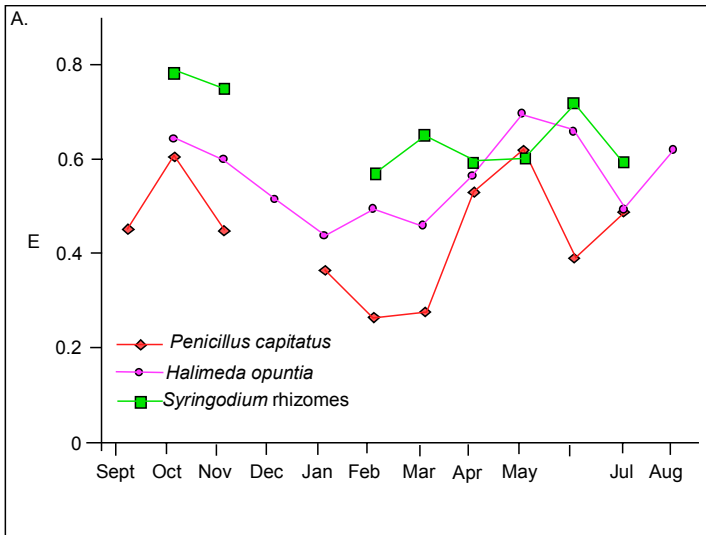
- No correlation between fluctuations in H on substrates in either the same or different bays



- No obvious inter-annual periodicity in H

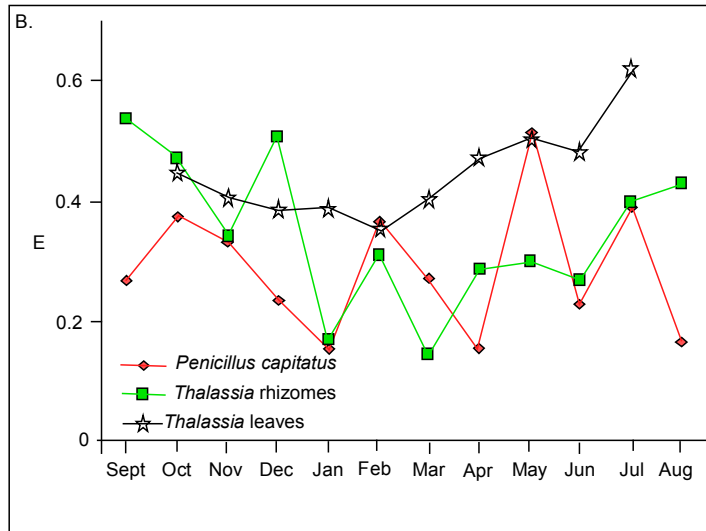
- Diversities generally higher in Mosquito Bay

Comparison Between Bays 3—Equitability Index



A: Mosquito Bay
B: Long Haul Bay

- Dominance measured using equitability index E
- In MB, mean E on all plants significantly different
- Species least equitably distributed on *Penicillus*, most equitably distributed on *Syringodium rhizomes*



- In LHB, the mean E on *Thalassia* leaves higher than on *Thalassia* rhizomes and *Penicillus*, but mean on last two substrates not significantly different

- Comparison between MB and LHB indicates mean E significantly lower in LHB when similar substrates compared

No correlation between monthly E and population densities on any substrate

And now?—Determine Epiphytal Population Structures Using SHE Community Structure Investigations (SHECSI)

For any sample, $\ln S = H - \ln E$

Holds true as several samples are accumulated, for which written as $\ln S_{\Sigma} = H_{\Sigma} - \ln E_{\Sigma}$

For a population with a logarithmic series structure:

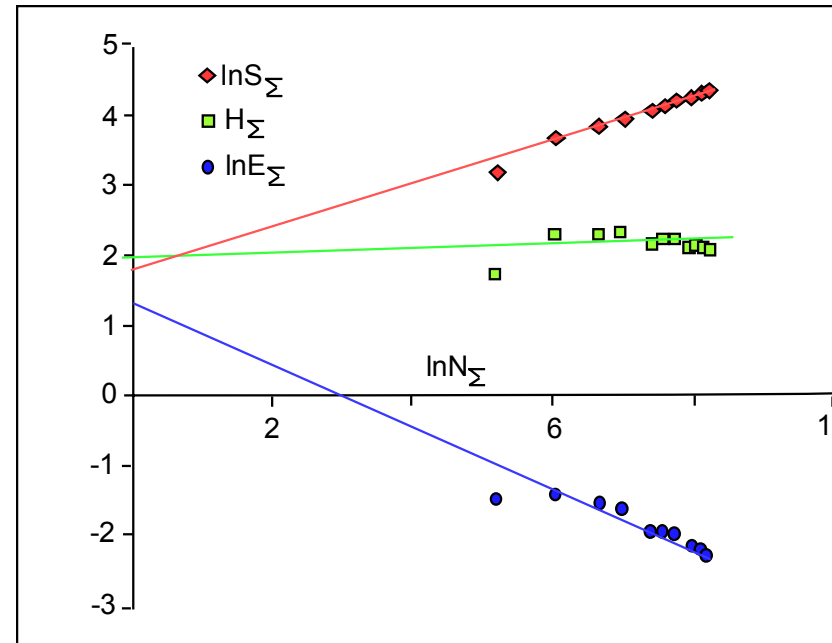
H_{Σ} fluctuates around a constant (may not be fulfilled until several samples accumulated)

Linear regressions of $\ln S_{\Sigma}$ and $\ln E_{\Sigma}$ vs. $\ln N_{\Sigma}$ have equal but opposite slopes (accepted as fulfilled if absolute values of 95% confidence limits entrain same value)

Regression coefficient (slope) or linear regression of $\ln S_{\Sigma}$ vs. $\ln E_{\Sigma}$ ~ -1.0 , while constant (intercept) close to final H_{Σ} (accepted as fulfilled if 95% confidence interval for constant entrains final H_{Σ} and those of regression coefficient entrain -1.0)

Population Structures in Epiphytal Foraminifera

- 5 of 6 plants had logarithmic series distributions of species abundances
- Slopes of $\ln S$ vs. $\ln E$ for 5 time-series within -1 ± 0.3
- 3 time-series within -1.0 ± 0.05

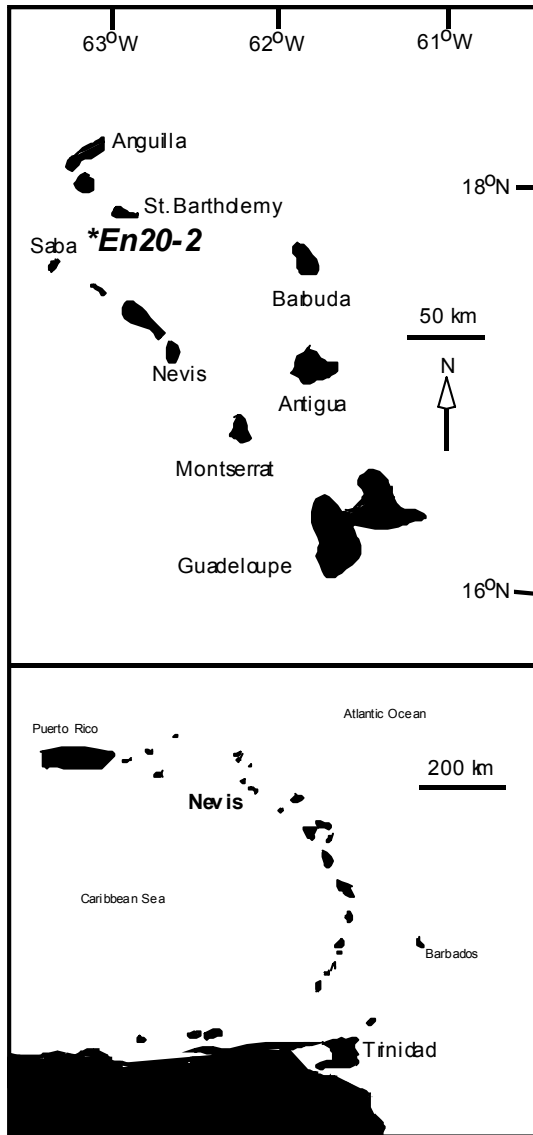


Biodiversitygram, *P. capitatus* in Long Haul Bay

Comparison of species richness trends on substrates, within and between bays

- Mean H_{Σ} higher in Mosquito Bay
- Rate of increase in $\ln S_{\Sigma}$ vs. $\ln N_{\Sigma}$ does not differ between *Penicillus*
- Rate of increase in $\ln S_{\Sigma}$ vs. $\ln N_{\Sigma}$ on *Halimeda* in Mosquito Bay < *Penicillus* in Long Haul Bay
- All other confidence intervals overlap
- No clear indication that rate of increase in $\ln S_{\Sigma}$ vs. $\ln N_{\Sigma}$ differs between bays, despite differences in H_{Σ}

Moving on — Core En20-2



- $17^{\circ}49.9'N$, $63^{\circ}02.4'W$, water depth 680 m (Reid and others, 1996)

- Mostly chalky. Sampled every 20 cm. Sample 120-121 cm from calcareous turbidite

- Pleistocene-Holocene boundary at 107cm

- Yielded deep-water association (DWA) of middle bathyal benthonic foraminifera and shallow-water association (SWA; up to 56% of total recovery) of back-reef, epiphytal aspect—transported on floating seagrass debris?

- Percentage abundances of species calculated separately for DWA and SWA

- 70 significant correlations found between percentage abundances of DWA and SWA species

SHE Analysis for Biozone Identification (SHEBI)

Within a **perfect logarithmic series population**, as $\ln N_{\Sigma}$ increases:

- H_{Σ} fluctuates around a constant
- $\ln S_{\Sigma}$ increases linearly

Because $\ln S_{\Sigma} = H_{\Sigma} - \ln E_{\Sigma}$, the increase in $\ln S_{\Sigma}$ is matched by a decrease in $\ln E_{\Sigma}$

At the junction between two populations:

- Species change in proportional abundance (p_i)
- Some leave or join the community

This forces non-linear changes in $\ln S_{\Sigma}$, H_{Σ} or $\ln E_{\Sigma}$ vs. $\ln N_{\Sigma}$. ($\ln E_{\Sigma}$ is the best marker)

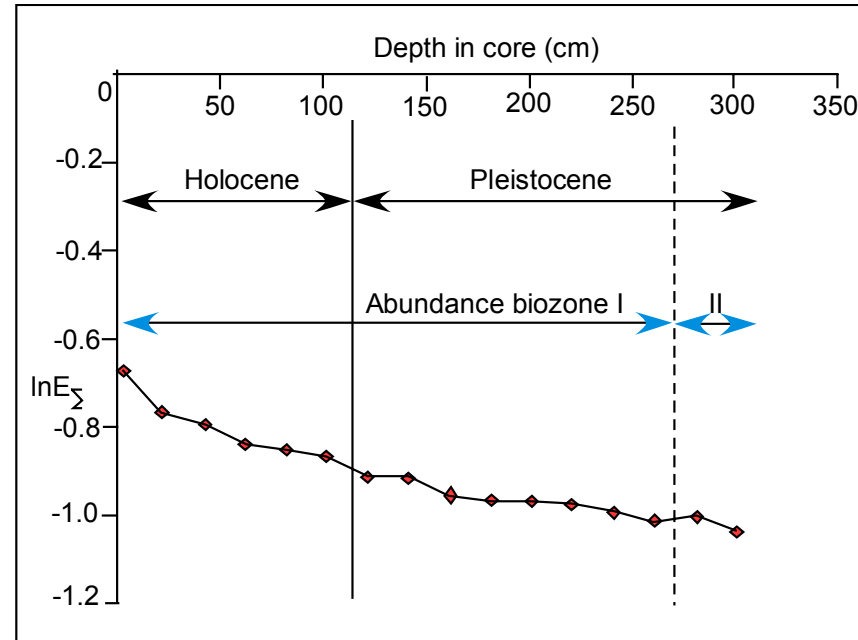
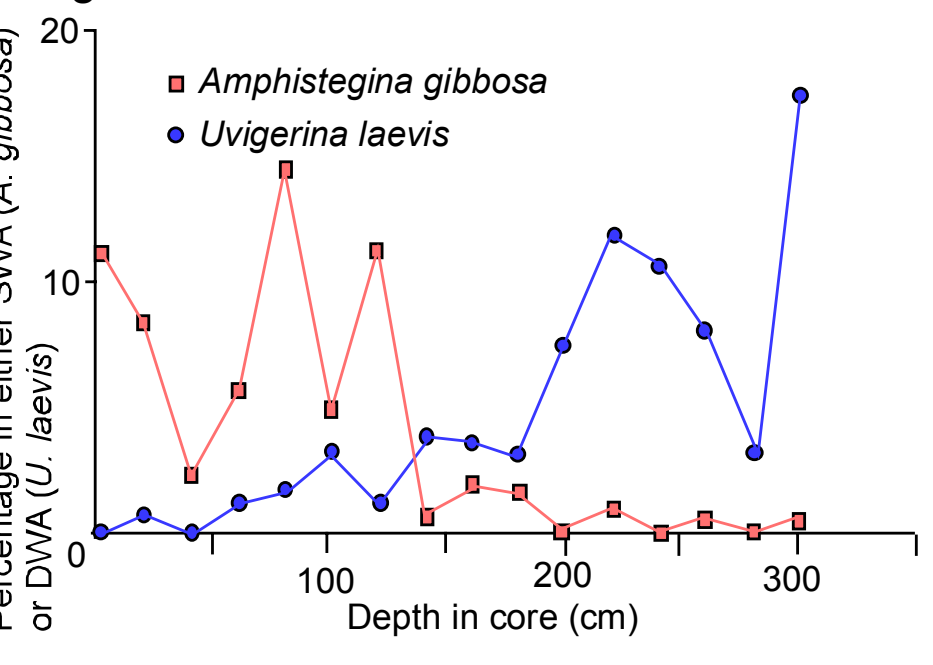
- **Abundance Biozone (AB)**: An area within which population structure is constant
- **AB Boundary**: the junction between two adjacent ABs

Trends in Core En20-2

DWA, gradual change from higher-productivity fauna at base to lower-productivity fauna at top

inverse correlation between SWA *Amphistegina gibbosa* and DWA *Uvigerina laevis*

change in nutrient flux affected SWA & DWA



- SHEBI conducted using DWA from top downwards, shows AB boundary at ~270 cm

- AB boundary not at Pleistocene/Holocene boundary

- Why accumulate samples from top down?

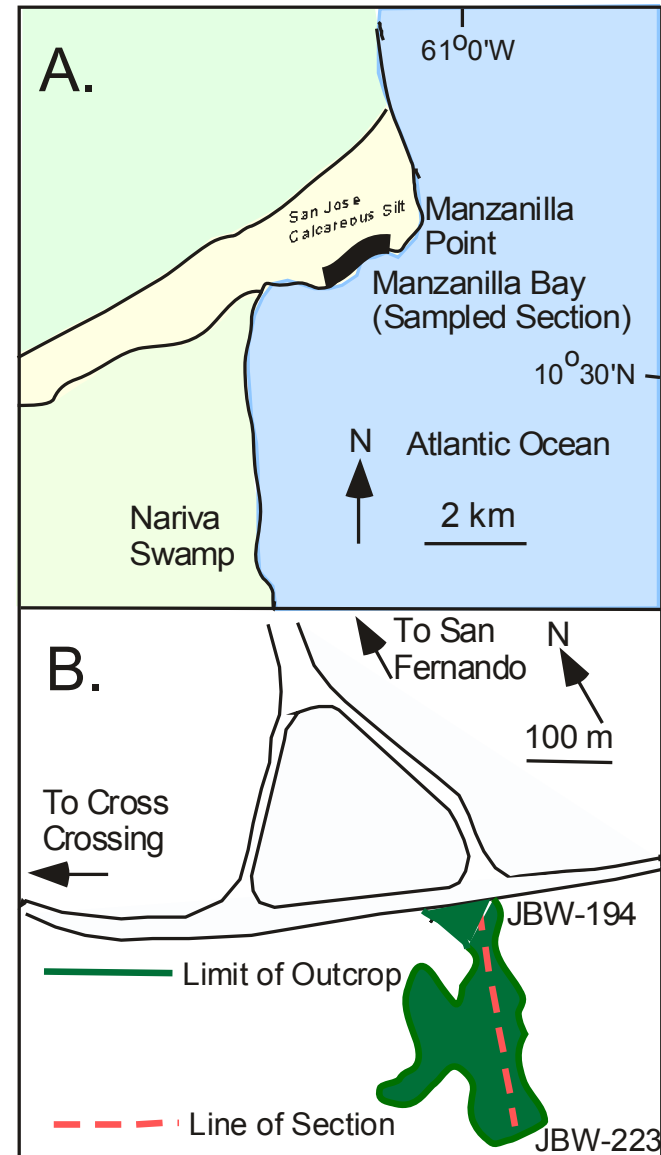
Top-down or Bottom-up? 1

Does accumulating samples from top down indicate same AB boundaries as when samples accumulated from bottom up?



San José Calcareous Silt at Manzanilla Point (upper Miocene);

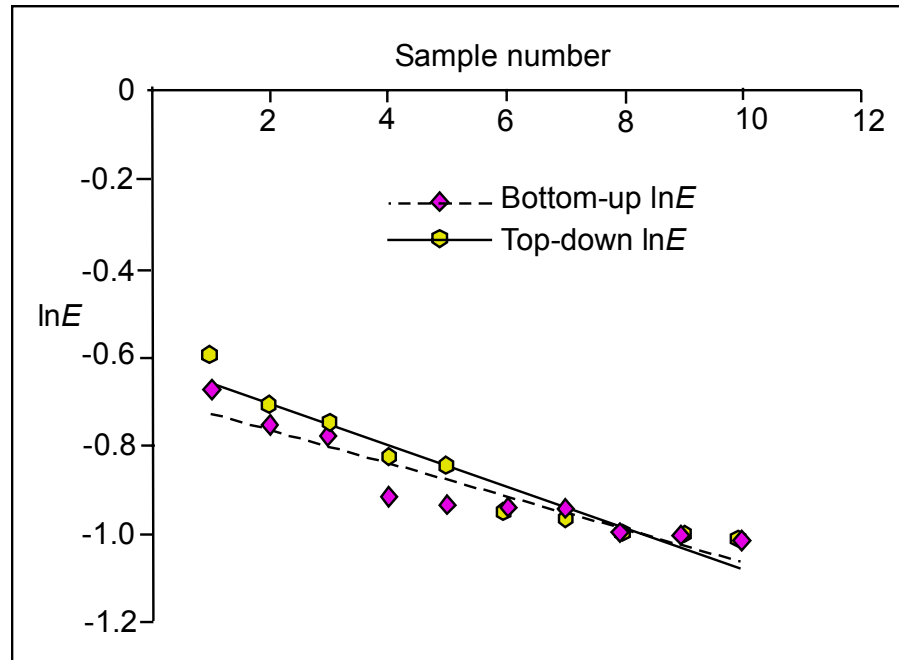
Cipero Formation at San Fernando Bypass (lower Miocene)



Top-down or Bottom-up? 2

Sample	Stratigraphic distance above base of section (metres)	Per sample N	<i>Cyrtodactylus cf. soldanii</i>	<i>Globocassidulina subglobosa</i>	<i>Normalinella umbonifera</i>	<i>Siphonodorsaria nivalis aculeata</i>	<i>Siphonodorsaria nivalis gracillima</i>	Bottom-up: Abundances Biotones	Top-down: Abundances Biotones
223	161	139	4.3	2.9	0.0	0.7	25.2	III	A
222	156	181	4.4	0.0	0.0	6.1	47.5		
221	152	129	4.7	0.0	0.0	2.3	7.0		
220	148	183	7.7	3.3	0.0	11.5	8.2	B	
219	143	337	3.0	3.9	9.8	0.0	26.7	II	C
218	138	225	3.1	2.2	0.9	0.0	2.7		
217	133	199	9.0	0.0	0.0	6.0	0.5		
215	122	250	4.4	0.0	14.0	4.4	1.6		
214	117	313	5.1	1.3	15.3	1.0	7.7		
213	112	66	6.1	3.0	1.5	9.1	13.6		
212	107	197	5.6	5.1	0.5	1.0	0.5	I	D
211	102	293	3.4	1.4	0.7	1.4	11.6		
210	97	176	0.0	0.0	0.6	12.5	1.7		
209	92	296	3.7	1.4	2.0	3.4	0.0		
208	87	342	4.1	7.9	0.3	2.0	5.0		
207	82	62	14.5	0.0	1.6	1.6	1.6		
206	77	326	12.0	1.8	1.8	3.7	6.7		
205	71	204	5.9	2.9	3.4	0.0	1.5		
204	66	161	4.3	0.6	2.5	0.0	5.6		
203	61	283	2.8	5.7	4.6	1.8	0.4		
202	56	274	9.9	2.2	0.0	1.8	6.9		
201	50	235	7.7	0.4	3.8	2.6	0.4		
200	45	205	3.9	0.0	3.4	0.5	1.0	E	
199	41	232	3.9	6.0	6.5	1.7	1.3	F	
198	37	293	3.4	1.7	8.2	0.0	0.3		
197	33	254	2.8	7.9	2.0	1.6	3.1		
196	29	220	5.0	6.4	0.0	1.4	2.7		
195	26	201	8.5	9.5	2.5	0.0	0.0		
194	0	230	4.8	4.3	0.0	0.0	6.5		

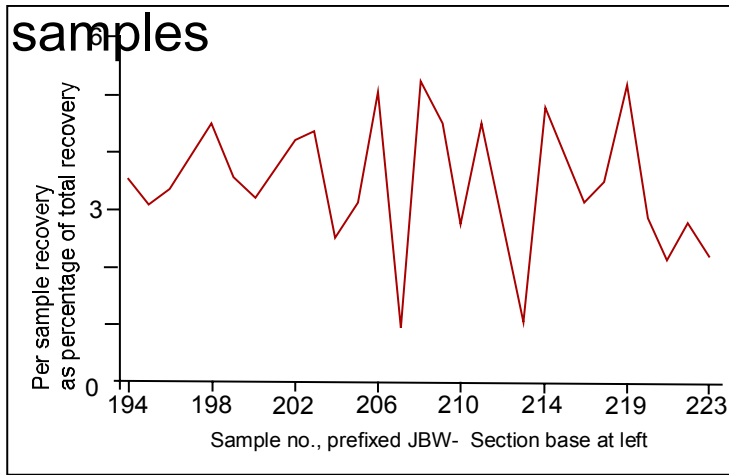
- Different top-down and bottom-up AB boundaries in both sections
- Ciperó Section: 3 bottom up ABs, 6 top-down
- No AB boundaries from the two analyses coincided



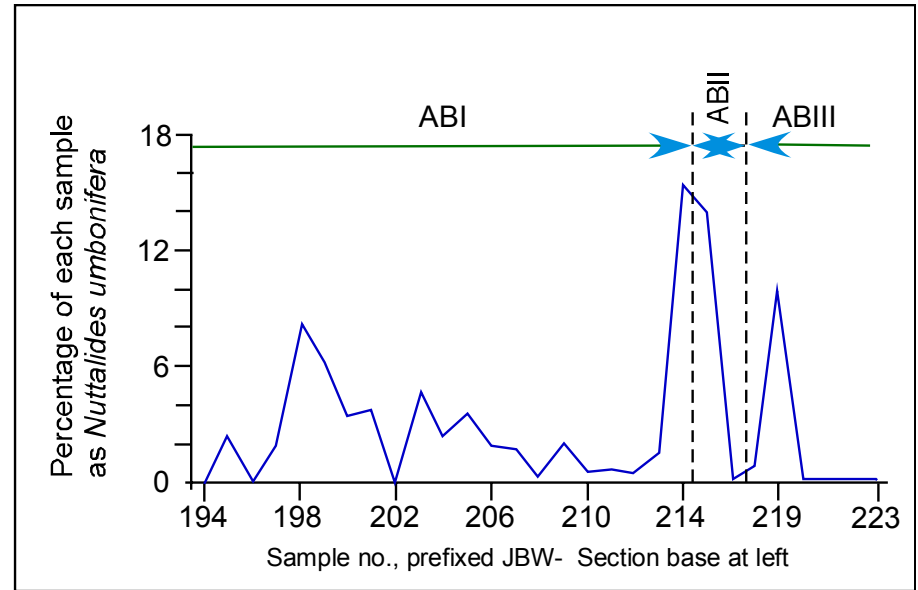
ABD examined from top down and bottom up, showed same population structure

Top-down or Bottom-up? 3

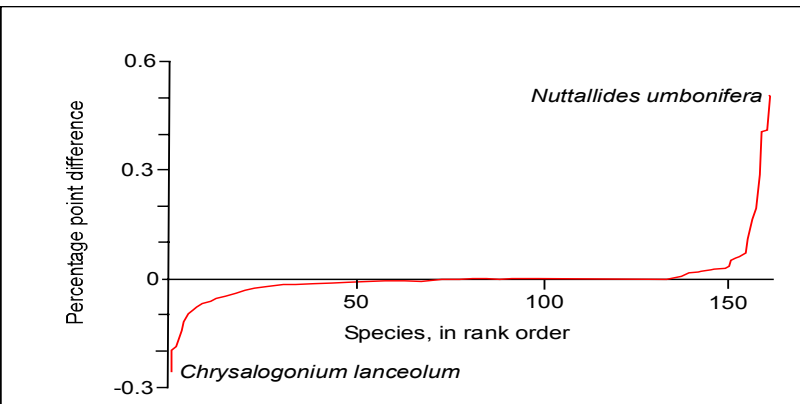
1. Benthonic foraminiferal recovery fluctuated widely between samples



3. But ABI/ABII boundary does not coincide with base of increase in *N. umbonifera*



2. *Nuttallides umbonifera* shown to increase at AbI/ABII boundary



Why not? Do fluctuations in sample size lead to misplacement of AB boundaries?

And so? Can SHE Analysis be modified for use with samples with differing numbers of specimens?

Introducing Modified SHE Analysis

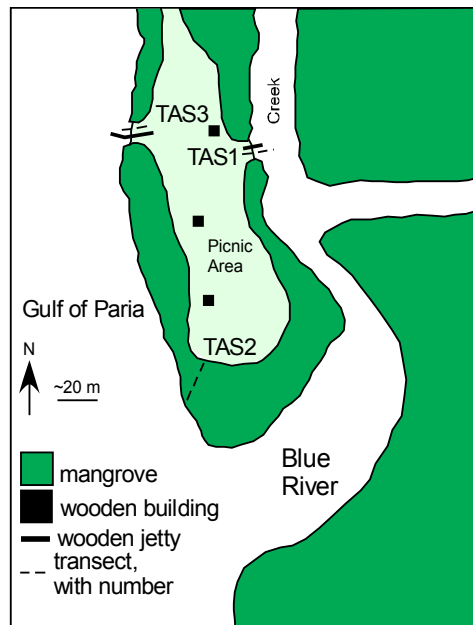
Assumption: p_i per species is relatively constant within an AB, changes at AB boundary for some species at least

Modified SHE Analysis begins with a table of proportional abundances, so for each sample $\sum p_i = 1$:

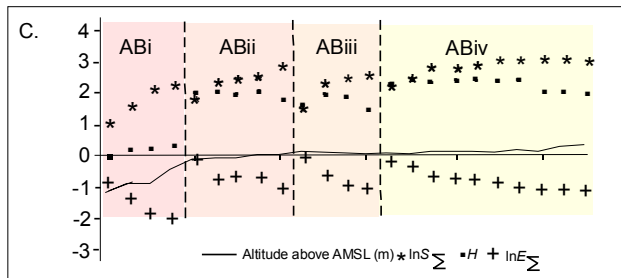
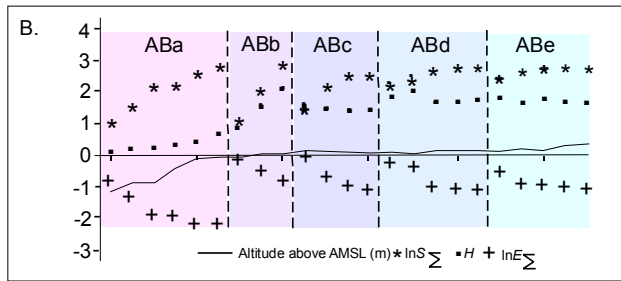
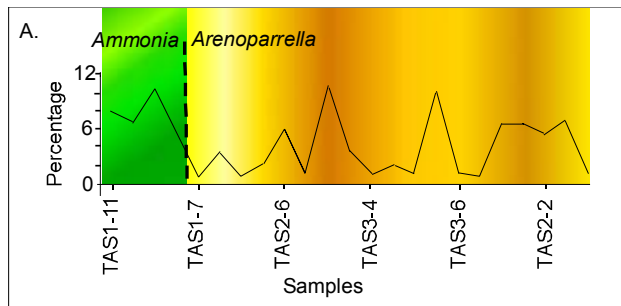
- S and S_Σ remains the same as for Classical SHE Analysis
- H (per sample) remains unchanged
- H_Σ is now calculated using the mean p_i per species across the samples
- Differences in H_Σ between the Classical and Modified methods are matched by differences in E_Σ

A Case Study in Using Modified SHE Analysis: Intertidal Foraminifera in the Caroni Swamp, Trinidad

- 3 transects (TAS1 to TAS3) taken in Caroni Swamp, a mangal on Trinidad
- Samples ranged in altitude from -1.18 m to 0.34 m relative to annual mean sea level
- Only samples with $N \geq 20$ used in analysis
- Mean per sample $N = 154$ (S.D. = 121): S.D. $\sim 78\%$ of the mean



The research team: Sherezz, Taneja and Arianna at sample location

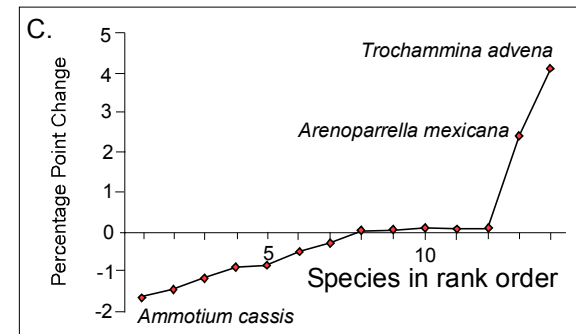
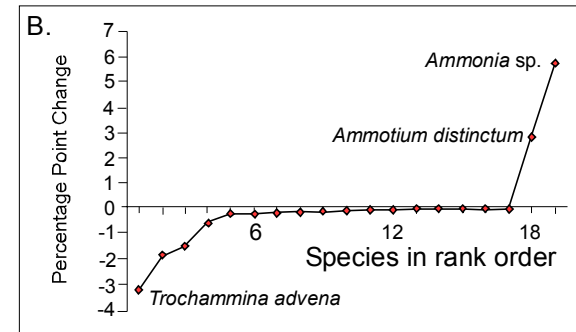
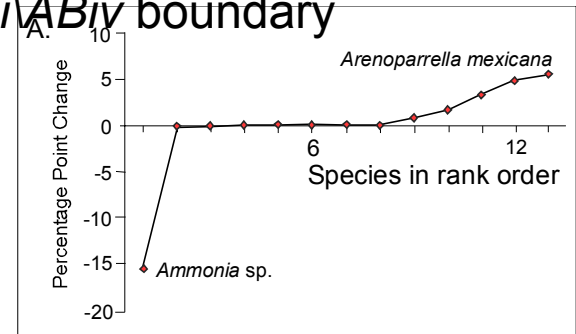


Patterns of species change at AB boundaries:

A. *ABi*\(*ABii*) boundary

B. *ABii*\(*ABiii*) boundary

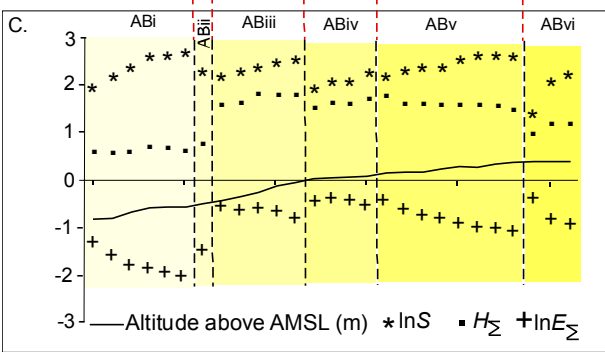
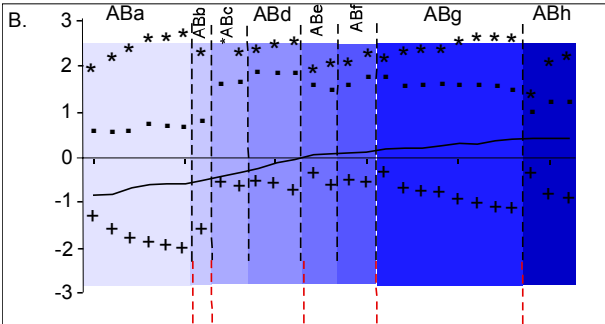
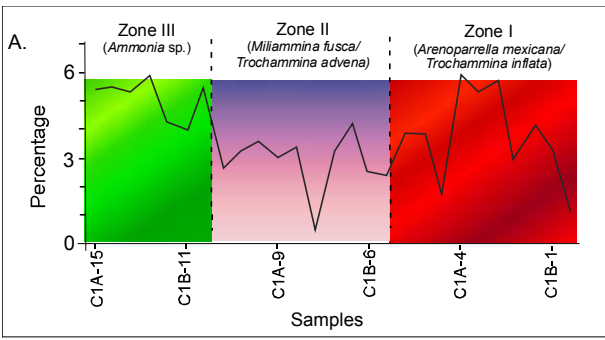
C. *ABiii*\(*ABiv*) boundary



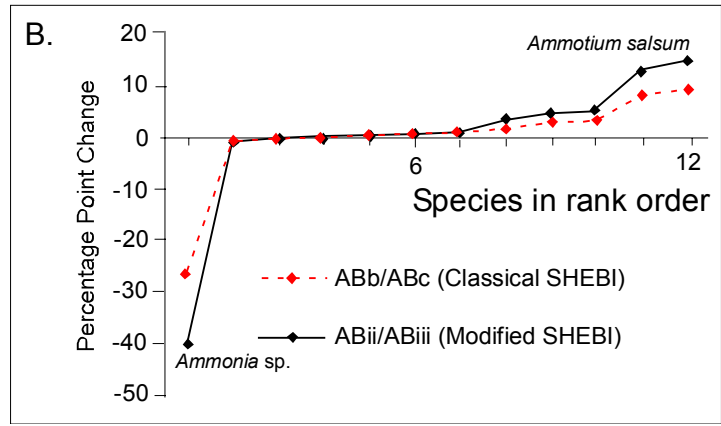
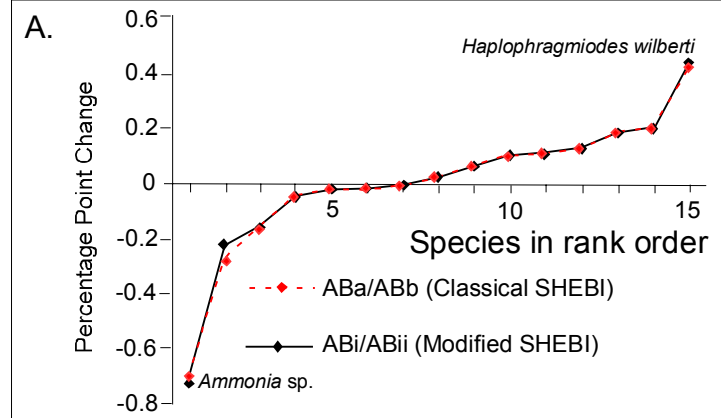
A. Per sample recovery as a percentage of total recovery, boundary between *Ammonia* and *Arenoparrella* dominated areas.

B. ABs from Classical SHEBI. Note placement of *ABa*\(*ABb*) boundary.

C. ABs from Modified SHEBI. Note placement of *ABi*\(*ABii*) boundary. *ABv* comprises *ABd* and *ABe* from Classical SHEBI

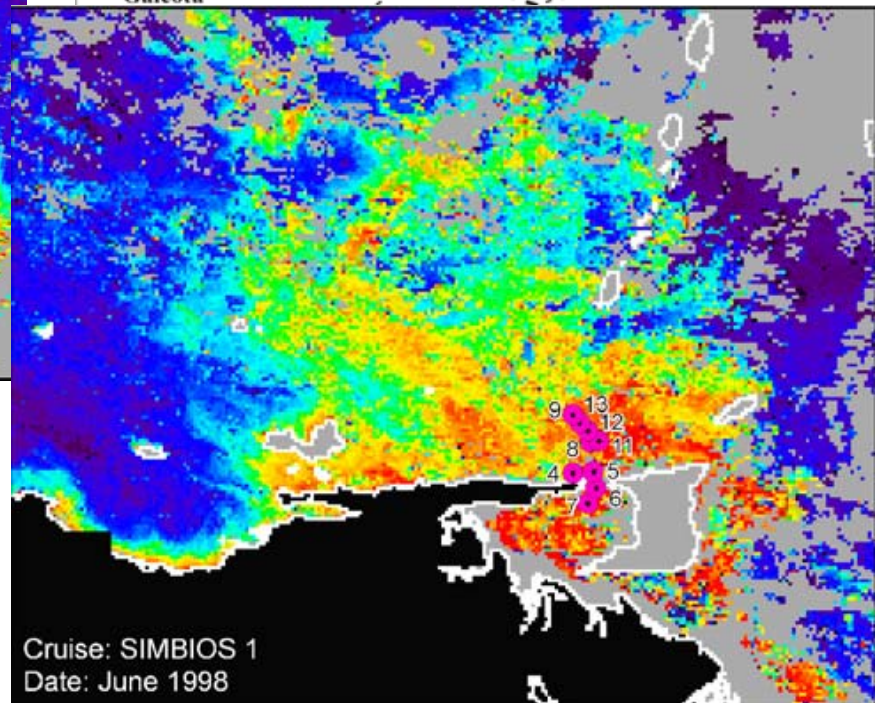
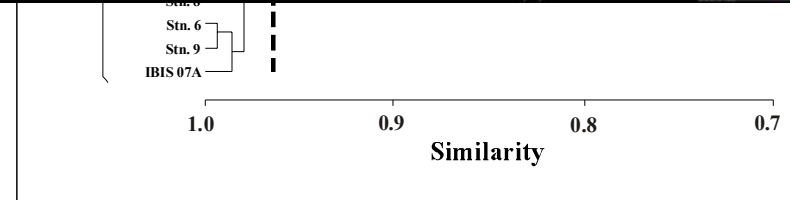
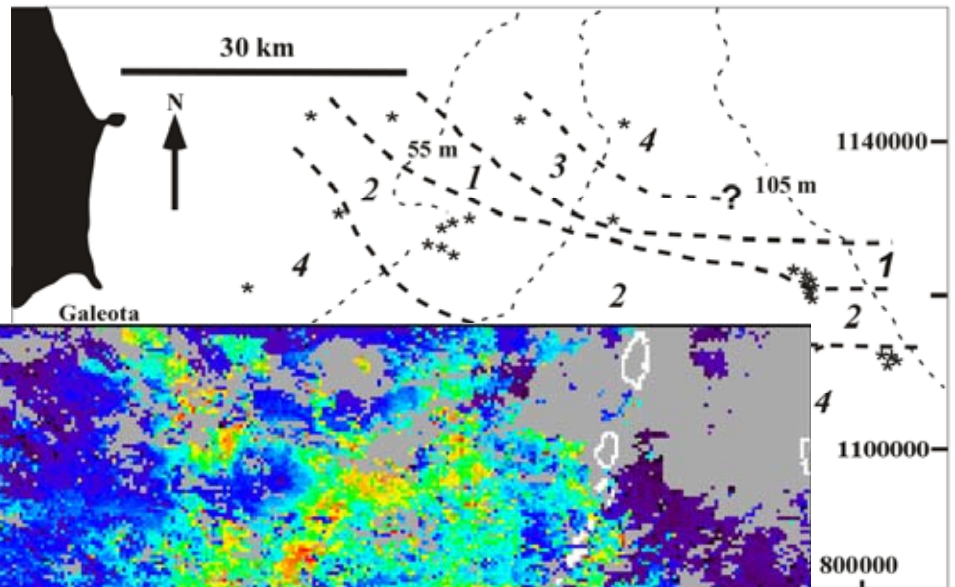
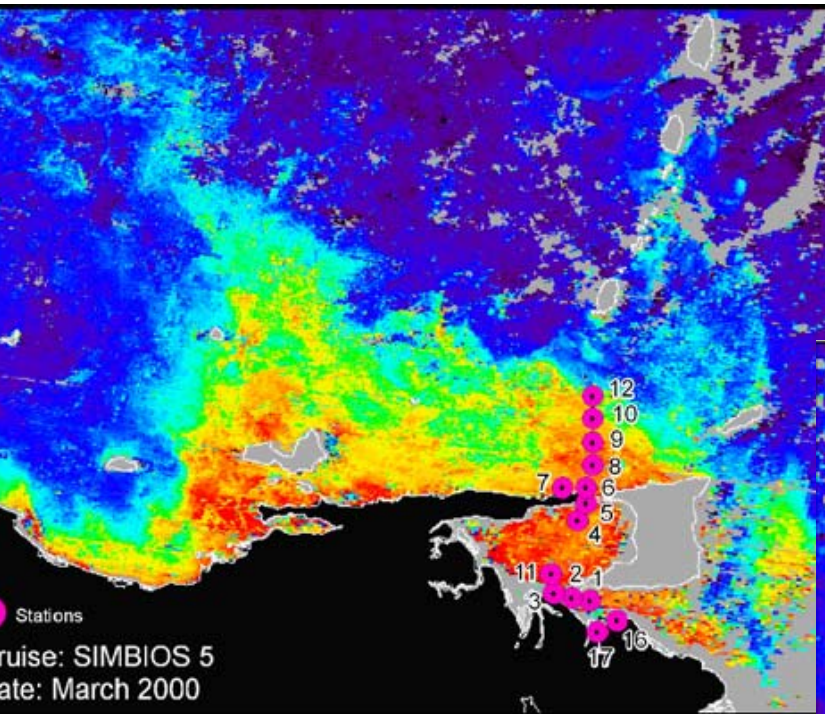


Species causing changes at some AB boundaries, data from Classical and Modified SHEBI. Note general similarities in curves. Percentage point changes from Modified SHEBI show greater range in both cases.



An earlier study for comparison. Only 4 of six AB boundaries from Classical SHEBI (B) detected by Modified SHEBI (C)

Ostracoda Off SE Trinidad: Indicators of an Offshore Front—1



Ostracoda Off SE Trinidad: Indicators of an Offshore Front—2

Biofacies 1

Depth range: **47-78 m** (4 samples)

Not amenable to SHECSI

Biofacies 2 - AB1

Depth range: **54 m** (2 samples)

Not amenable to SHECSI

Biofacies 2 - AB2

Depth range: **54 - 75 m** (5 samples)

Biofacies 2 - AB3

Depth range: **76-78 m** (3 samples)

Not a good fit for a logarithmic series model

Biofacies 3 - AB1

Depth range: **60-77 m** (4 samples)

Biofacies 3 - AB2

Depth: **78 m** (1 sample)

Not amenable to SHECSI

Biofacies 4 - AB1

Depth range: **47-71 m** (4 samples)

Biofacies 4 - AB2

Depth range: **72-101 m** (6 samples)

Biofacies 4 - AB3

Depth range: **102 m** (2 samples)

Not amenable to SHECSI

Conclusions



More content, but older & greyer
OW

- On phytal substrates around Nevis, **rate of increase** in $\ln S_{\Sigma}$ vs. $\ln N_{\Sigma}$ **same** at different sites, *despite* **different** overall **diversities**.
- **No AB boundaries** in core EN20-2 at Pleistocene/Holocene boundary.
- **AB boundaries differ** when successions analysed from **top-down and bottom-up**. Bottom-up is preferred.
- **Modified SHEBI** where SD approaches mean N may indicate boundaries more

Acknowledgements

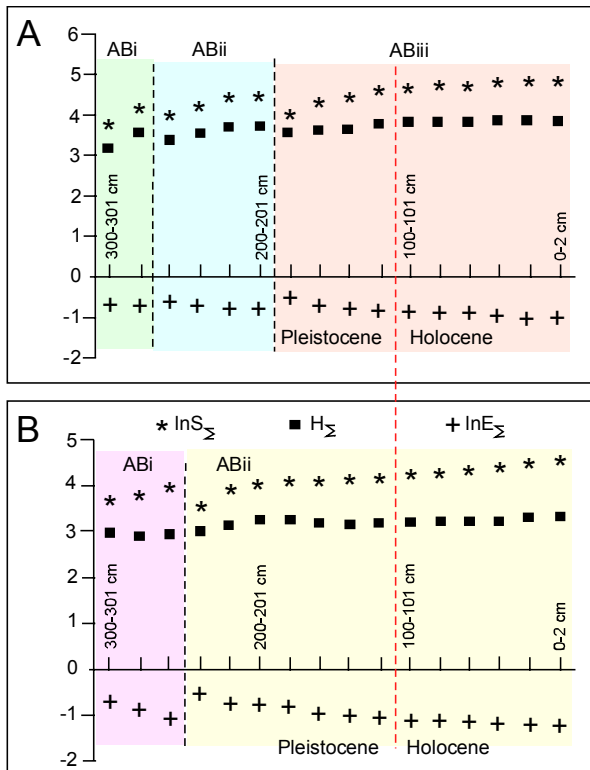
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- Any questions?
- Any at all? 😊

Answering Some Unanswered Questions—1



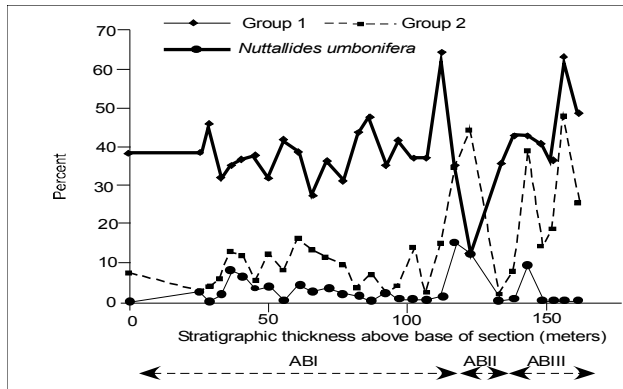
Core En20-2 Sample	Modified SHEBI, Bottom up Abundance		Modified SHEBI, Top-down Abundance			
	Biozones	H_{Σ}	$\ln E_{\Sigma}$	Biozones	H_{Σ}	$\ln E_{\Sigma}$
0-2 cm	ABii	3.856	-0.988	ABa	3.085	-0.677
20-21 cm		3.864	-0.965		3.325	-0.769
40-41 cm		3.857	-0.939		3.495	-0.809
60-61 cm		3.804	-0.906		3.582	-0.849
80-81 cm		3.799	-0.883		3.668	-0.875
100-101 cm		3.815	-0.829		3.740	-0.895
120-121 cm		3.780	-0.795		3.792	-0.944
140-141 cm		3.628	-0.754		3.329	-0.583
160-161 cm		3.592	-0.712		3.502	-0.717
180-181 cm		3.536	-0.508		3.628	-0.754
200-201 cm	ABi	3.700	-0.843	ABb	3.651	-0.756
220-221 cm		3.687	-0.824		3.737	-0.785
240-241 cm		3.610	-0.796		3.732	-0.842
260-261 cm		3.575	-0.756		3.746	-0.888
280-281 cm		3.522	-0.653		3.766	-0.898
300-301 cm		3.147	-0.614		3.740	-0.933

In Core En20-2, mean $N = 258$, S.D. = 104. If core re-examined using bottom-up Classical SHEBI (Fig. A), does it pick out Pleistocene/Holocene boundary?

No.
Does SWA show same AB pattern? No.

3. If DWA is examined from bottom-up using Modified SHEBI (Fig. B), does it pick out the Pleistocene/Holocene boundary? No.
4. If DWA examined from top down using Modified SHEBI (Table above), does it produce the same results as bottom up? No.

Answering Some Unanswered Questions—2



Does using Modified SHEBI on the Cipero Formation (bottom-upwards analysis) pick out the peak in *N. umbonifera* more precisely?

No. Sigmoidal curve at the **ABi/ABii boundary** indicates two groups of foraminifera that first change in percentage abundance in the sample **below** the boundary:

Group 1: Decrease: *Chrysalogonium lanceolum*, *Globocassidulina subglobosa*, *Pullenia bulloides*, *Gyroidinoides* cf. *soldanii* Galloway and Heminway, *Pleurostomella* cf. *alternans*, *Gyroidinoides complanata*, *Melonis barleeanus*, *Pleurostomella cubensis*, *Stilostomella matanzana*, *Nodosaria longiscata*, *Siphonodosaria nuttalli gracillima*.

Group 2: Increase: *Uvigerina gallowayi basicordata*, *Entosolenia staphyllearia*, *Uvigerina auberiana attenuata*, *Stilostomella subspinoso*, *Brizalina plicatella*, *Nuttalides umbonifera*.

Why the offset from the start of change in both groups (sample JBW-214)?

Change not caused by *N. umbonifera* alone. Not until JBW-215 have both groups changed in abundance sufficiently to cause non-linear change

