



# Spatial and Temporal Variations in the Community structure of Marine Archaea: The Gulf of Mexico



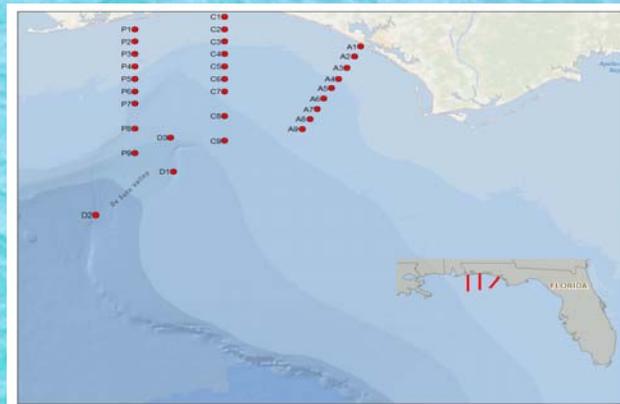
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## Abstract

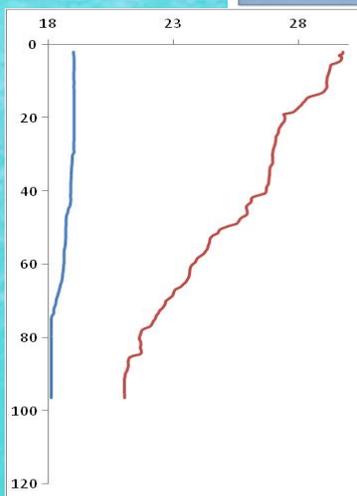
Since the Deepwater Horizon oil spill in 2010, much emphasis has been placed on understanding the processes, both physical and biological, that occur in the Gulf of Mexico. On the micro-scale, bacterioplankton and archaeoplankton play major roles in the cycling of nutrients through the microbial loop, and then the macro-scale geochemical cycles. Understanding the changes that occur in the community structure of archaea in the Gulf of Mexico over space and time has the potential to shed new light on the transfer of energy into and out of the system as well as through higher trophic levels. Using clone libraries constructed with the archaeal 16S rRNA sequence, samples collected across three transects will be compared seasonally and spatially. The libraries will also be compared by physical water column parameters during time of collection and overall current movement.

## Materials and Methods

Samples of 20L of seawater were collected on a 0.22 µm Sterivex filter. Environmental DNA was extracted with MoBio's Power Soil extraction kit, PCR amplified, cloned and sequenced. Sequencing was carried out at Beckman Coulter Genomics. Clone libraries were analyzed with Mothur. Water column parameters were collected with a Sea-Bird CTD, in addition to nutrient and production analyses.



- AR1 C5 22712 Surface
- AR2 C5 22712 Depth
- AR13 C5 71012 Depth
- AR15 C5 71012 Chlorophyll Max



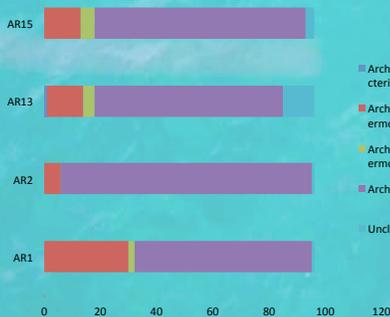
Temperature profile at station C5 in February (blue) and July (red).

The hypothesis that community structure does not remain constant over time has been explored at station C5. From these preliminary findings it can be said that the mixing/stratification of the water column plays a role in altering community structure. Many other factors play a part in successional patterns in the community structure of marine Archaea, and they will be analyzed with Primer6 or similar programming.

Tree#	Groups	UWScore	UWSig
1AR1-AR13-AR15-AR2		0.725976	<0.0010
$\alpha = 0.05$			
Tree#	Groups	UWScore	UWSig
1AR1-AR13		0.601153	0.093
<b>1AR1-AR15</b>		<b>0.665419</b>	<b>0.001</b>
<b>1AR13-AR15</b>		<b>0.754274</b>	<b>0.002</b>
1AR1-AR2		0.662716	0.016
1AR13-AR2		0.742161	0.024
1AR15-AR2		0.741975	0.012

$\alpha = 0.008333$

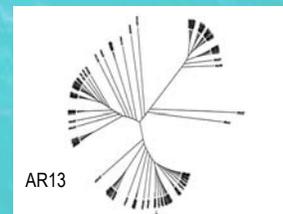
Unifrac unweighted statistical analysis of community structure similarity.



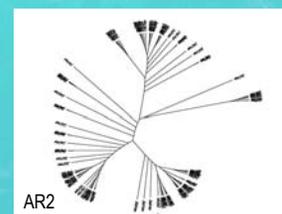
Community composition of four samples being compared.



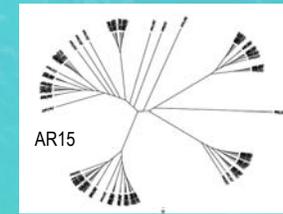
AR1



AR13



AR2



AR15

## Acknowledgements

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