CHARACTERIZATION OF THE DIVERSITY AND SPATIAL PATTERNS OF THE *PELAGIBACTERACEAE* (SAR11) IN THE SURFACE WATERS OF THE NORTHERN GULF OF MEXICO.

Thays Santos
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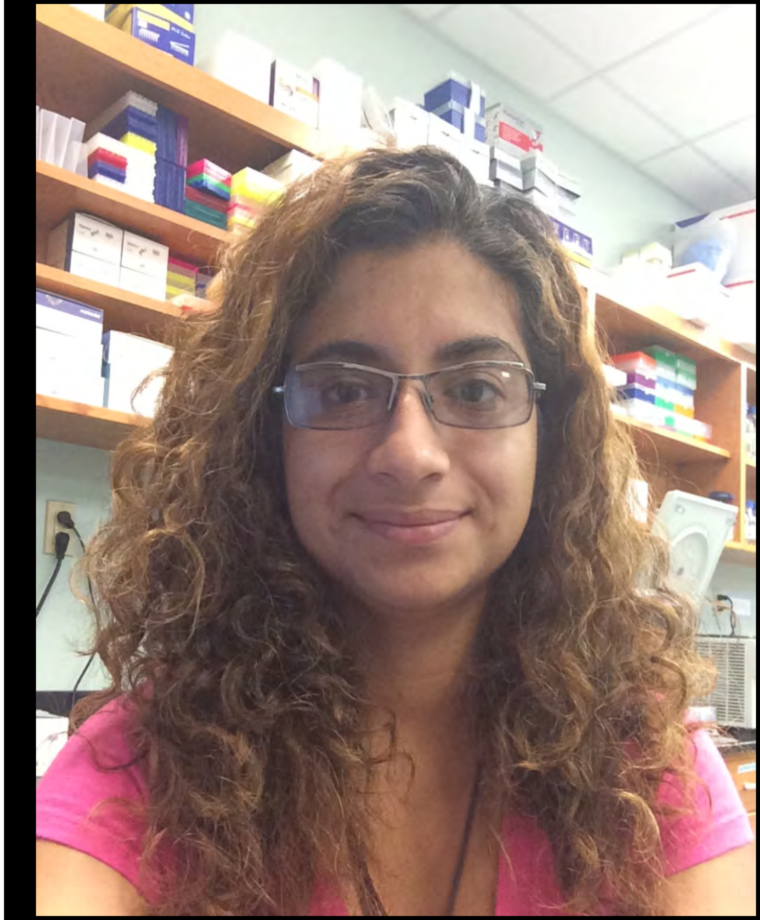
ME



- Exchange Student from Federal University of Maranhao - Brazil;
- Oceanography;
- Funded by: Brazilian Scientific Mobility Program (BSMP);
- University of Maine – United States;

ALICE ORTMANN, Ph.D.
MENTOR

- **Assistant Professor**
  University of South Alabama
  Department of Marine Sciences

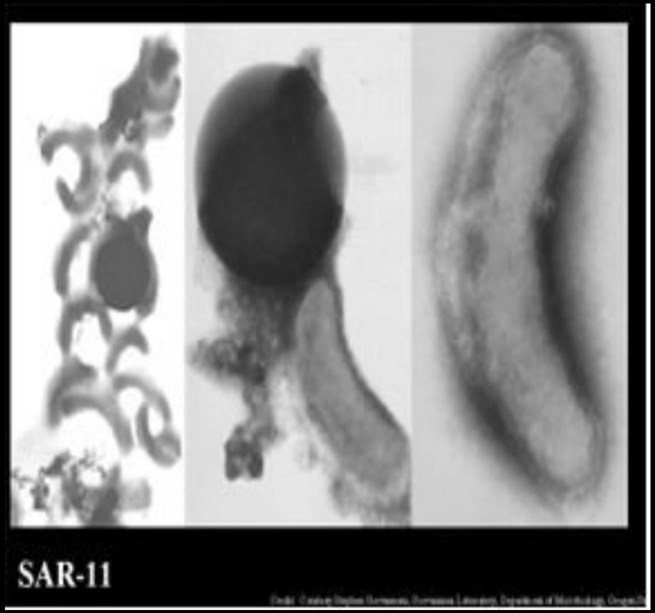
- **Education:**
  Ph.D., University of British Columbia, Vancouver, BC, Canada, 2005;

- **Area of Expertise :**
  Microbiology

- **Projects:**

  Diversity and ecological roles of marine microbes including Bacteria, Archaea and their viruses using both culture-based and molecular biology techniques.

FAMILY
PELAGIBACTERACEAE (SAR11)



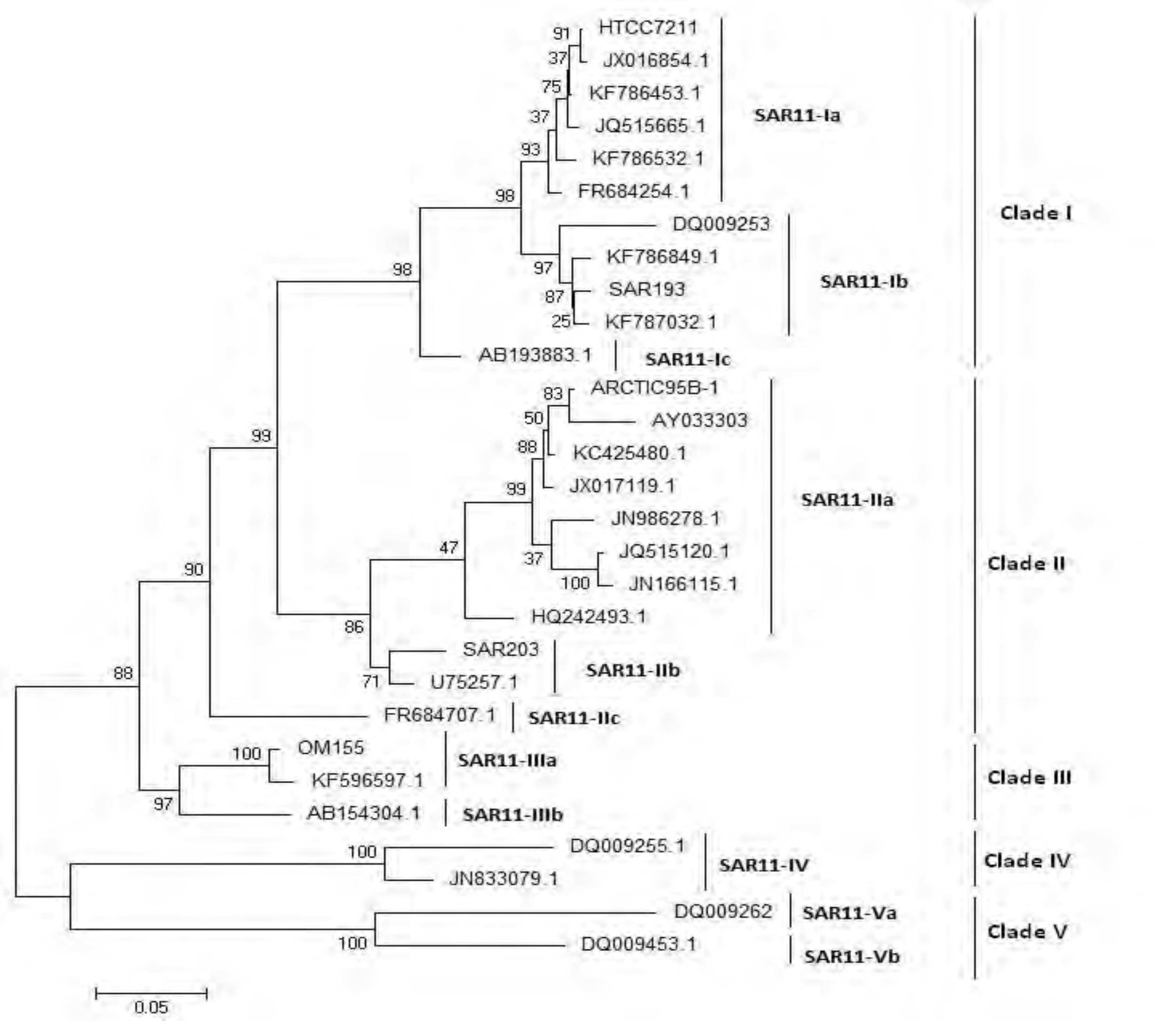
Pelagibacter ubique
Source: The National Science Foundation (www.nsf.gov)

"The ubiquitous SAR11 bacterial clade is the most abundant type of organism in the world's oceans, but the reasons for the its success are not fully elucidated" (Brown et al 2012).

Limited nutrient conditions;

Carbon cycle.

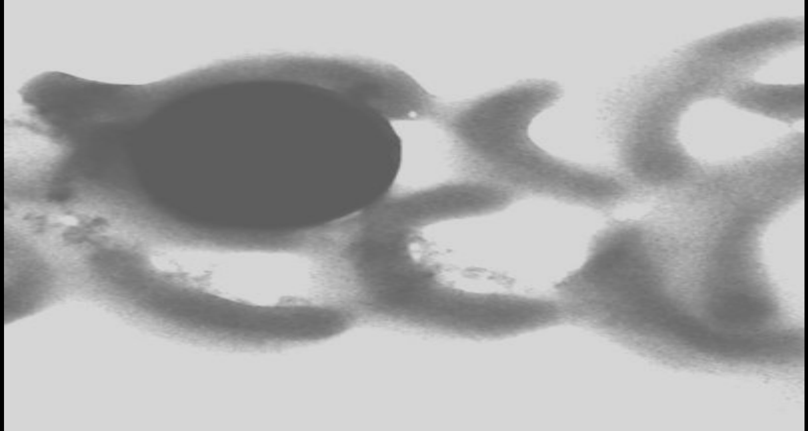
5 SAR11 CLADES



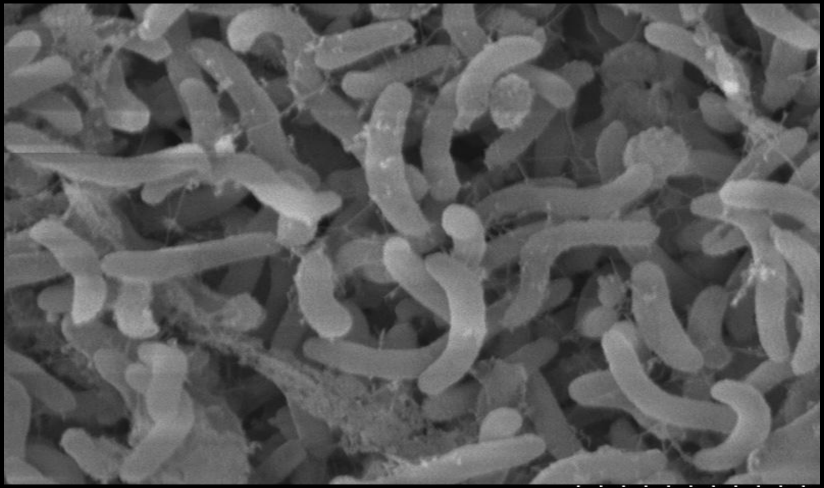
Maximum likelihood 16S rRNA gene phylogenetic tree.

- ❖*Clade;*
- ❖*Subclade;*
- ❖*Operational taxonomic units: OTU.*

OBJECTIVE



Pelagibacter ubique.
Source: Office of Biological & Environmental Research.



Pelagibacter ubique.
Source: Center for microbial oceanography.

- ❖Identify the dominant SAR11 subclade in the surface water population;
- ❖Spatial patterns of the SAR11 clade/subclade.

LOCATIONS:
MOBILE BAY- AL
NORTHERN GULF OF MEXICO;

COLLECTED:
SURFACE SAMPLES;

FOUR SITES SAMPLED:
MB + DI = INSHORE
CP + T35 = OFFSHORE

VARIABLES:
PHYSICAL- CHEMICAL AND BIOLOGICAL.

Image from Google Earth.

METHODS

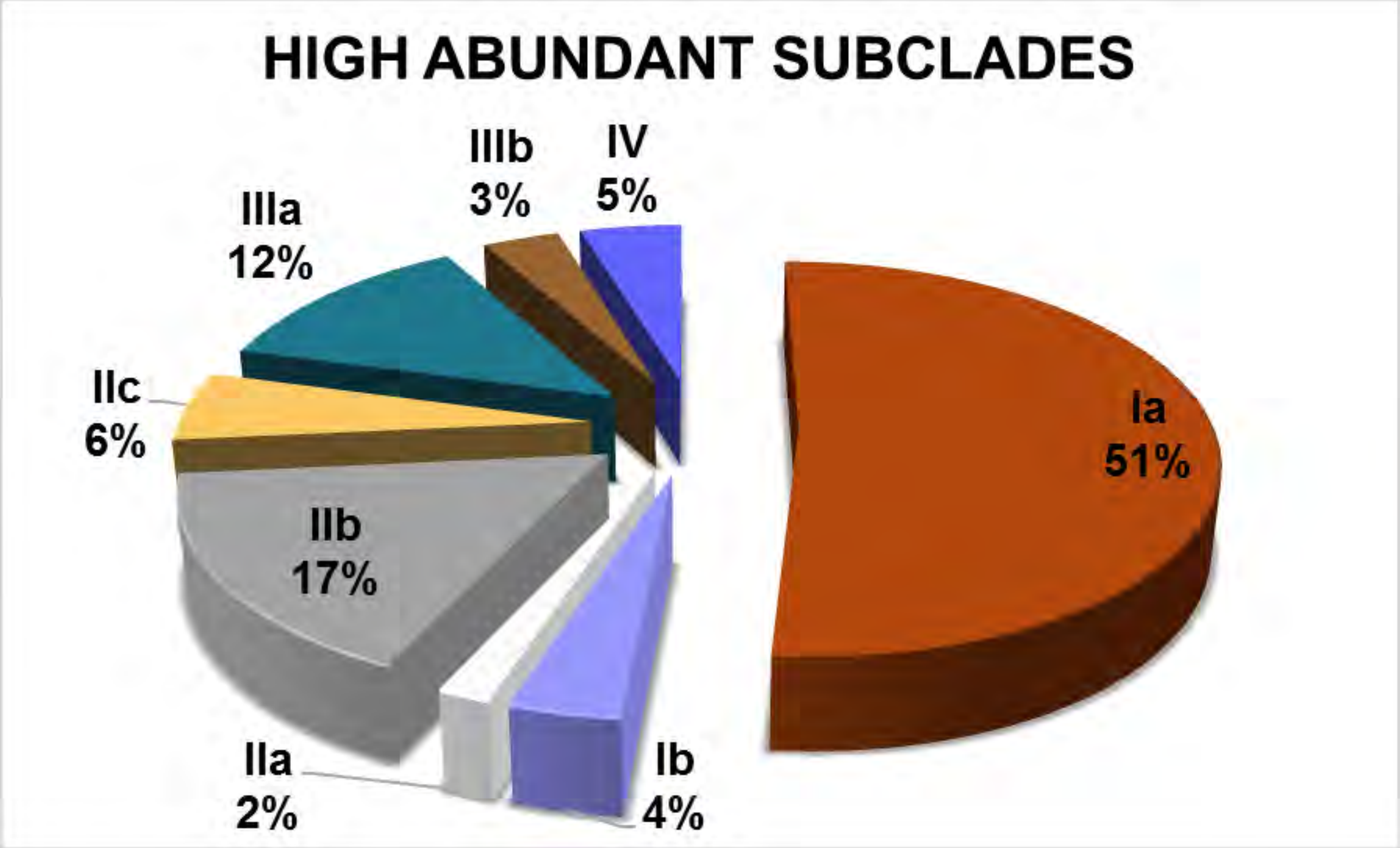
1. DNA extraction sequencing V6 region of 16S rRNA gene;

2. Identification of the SAR11 OTUs (79 OTUs);

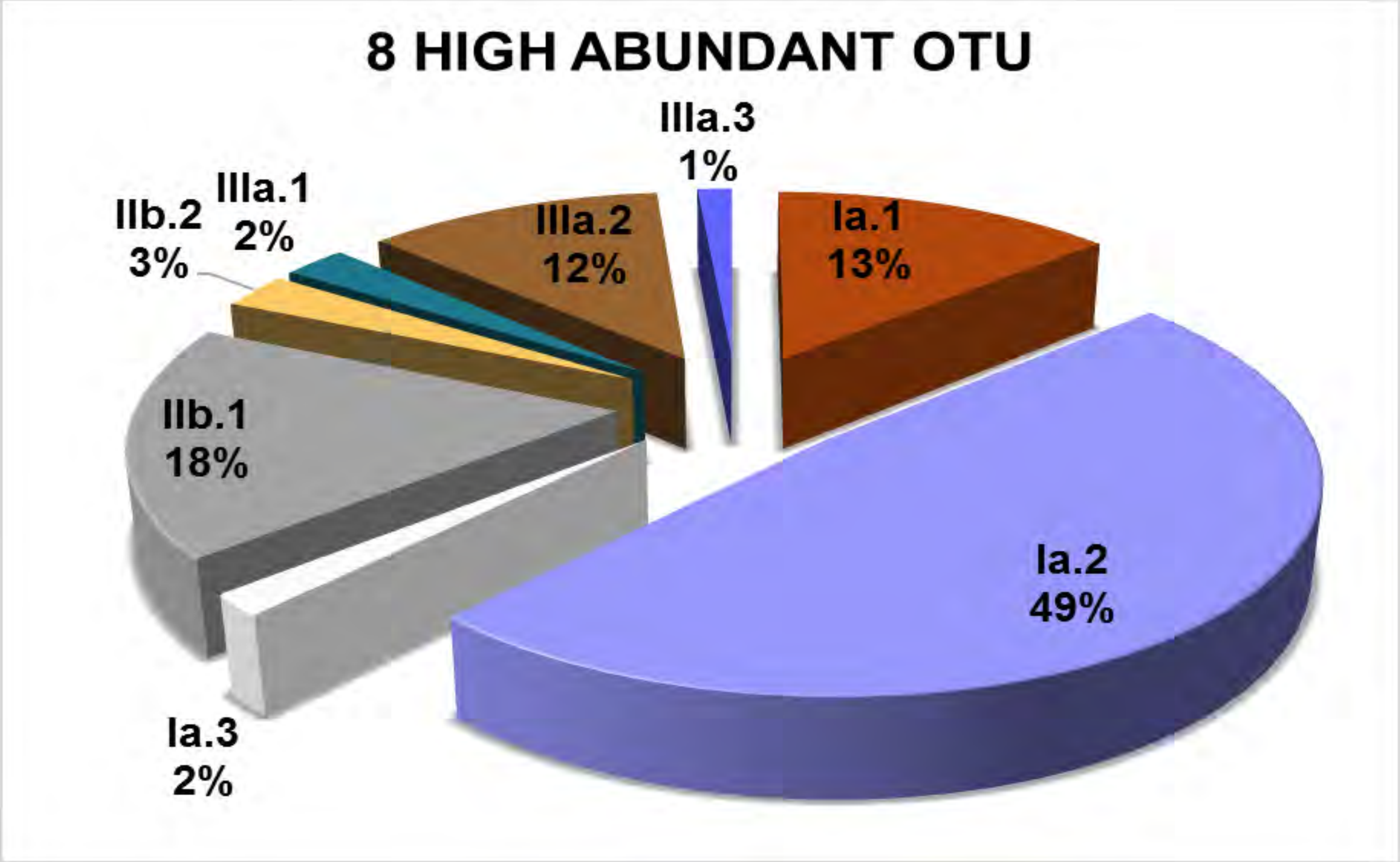
3. Identification of the SAR11 OTUs subclade;

4. Comparison of SAR11 OTUs structure and environmental data (8 most abundant OTUs).

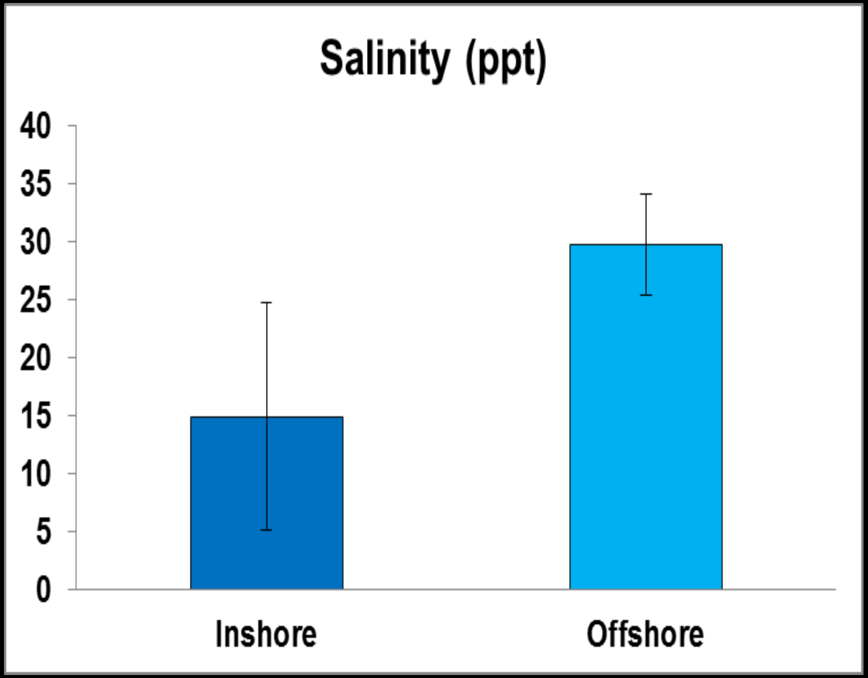
3 SUBCLADES DOMINANT: Ia, IIb AND IIIa

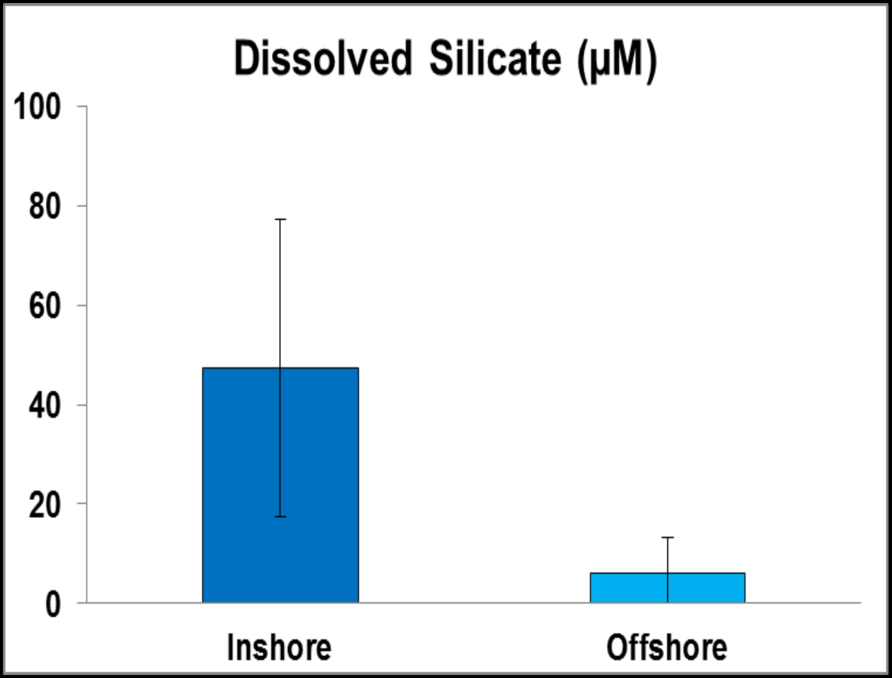


1 DOMINANT OTU

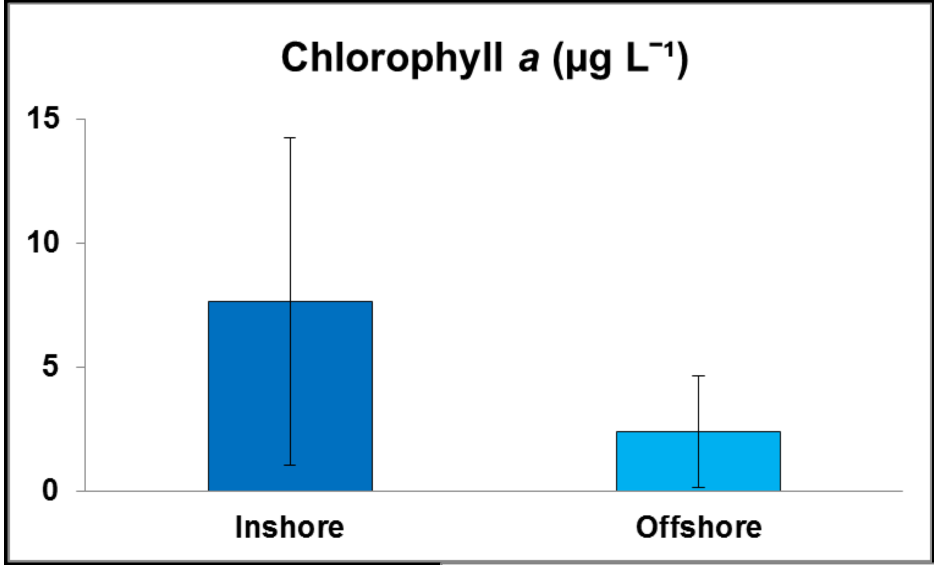


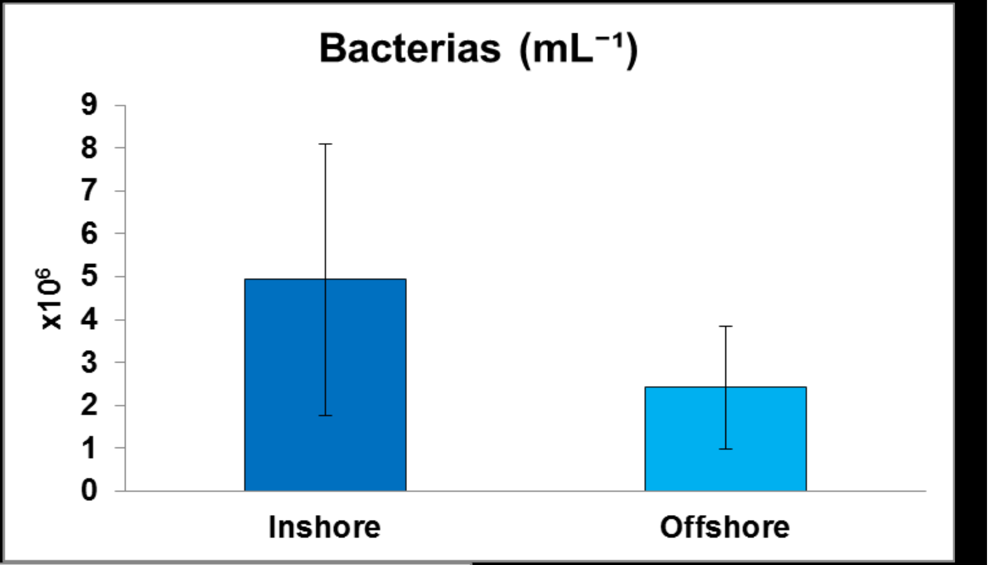
PHYSICAL-CHEMICAL VARIABLES: DIFFERENT VARIABILITY

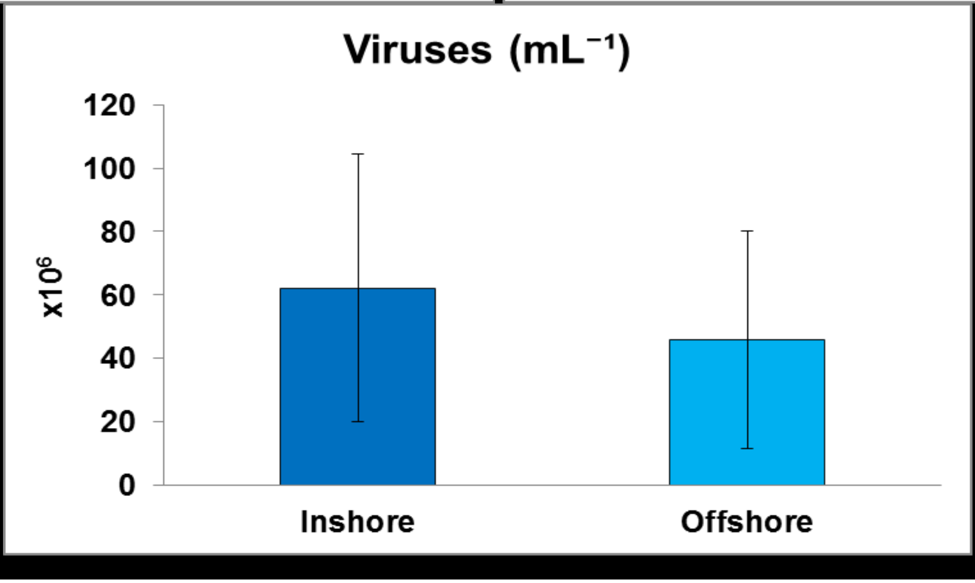




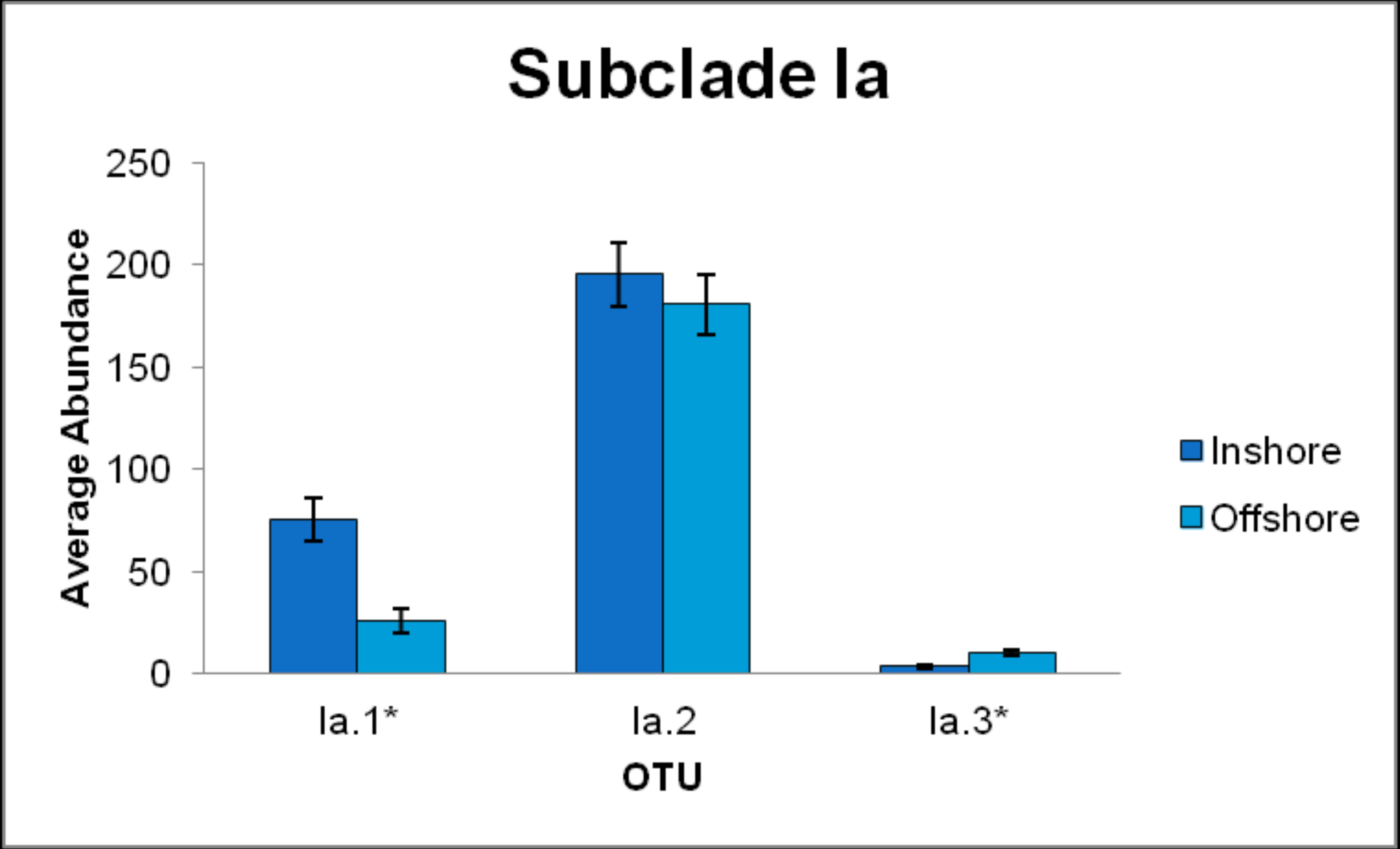
BIOLOGICAL VARIABLES HIGHER INSHORE







DOMINANT SUBCLADE IN SURFACE WATER: IN-OFFSHORE

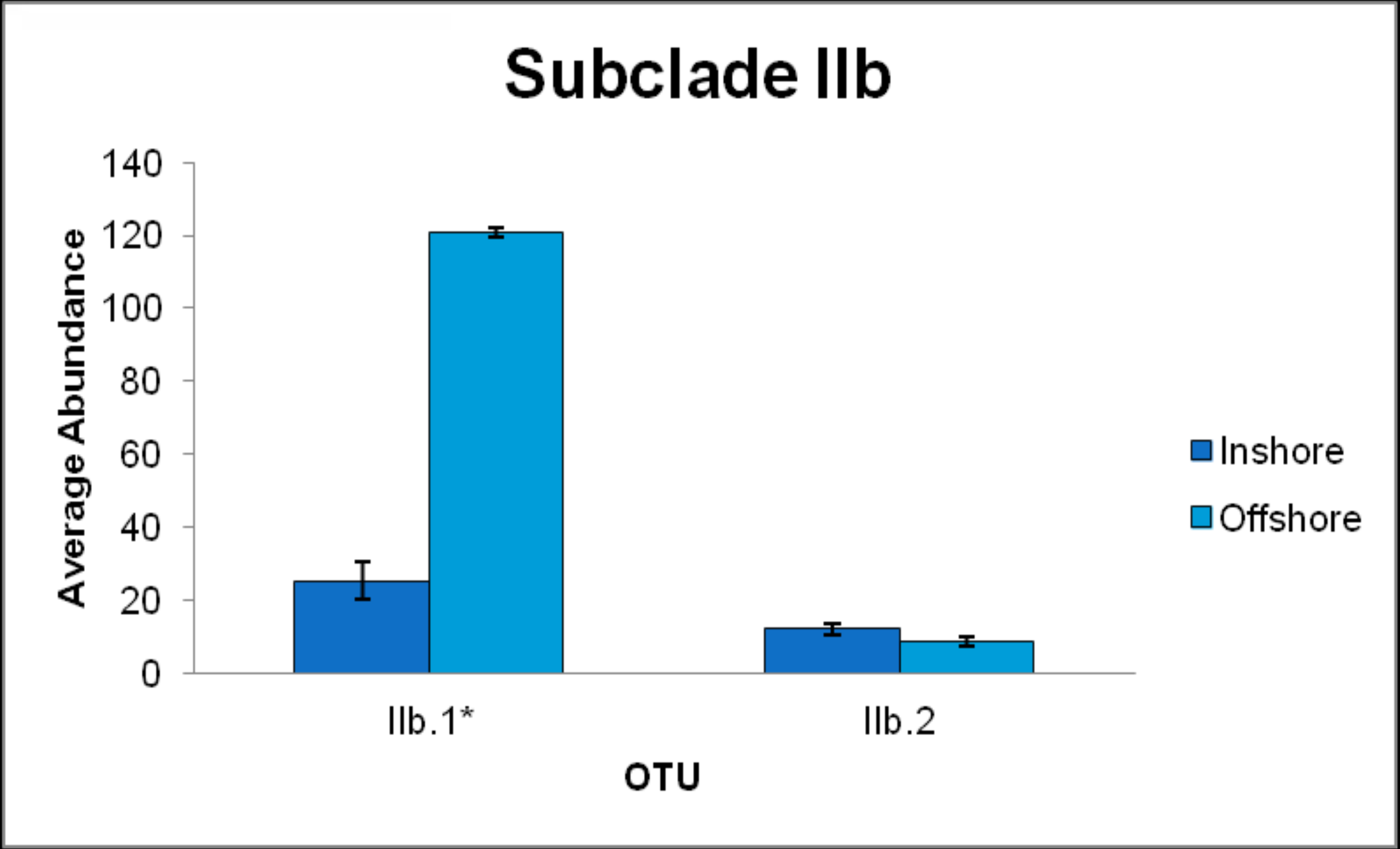


DIFFERENT CORRELATIONS: IN – OFFSHORE VARIABLES

OTU	Salinity	DSi	chl *a*	Bacterias	Viruses
Ia.1	**-0.53**	0.46	**0.51**	**0.62**	**0.54**
Ia.2	0.19	-0.08	0.04	0.02	-0.11
Ia.3	0.46	-0.40	**-0.62**	-0.42	-0.11

Spearman correlation.

DEEP WATER SUBCLADE: DIFFERENT PATTERNS.

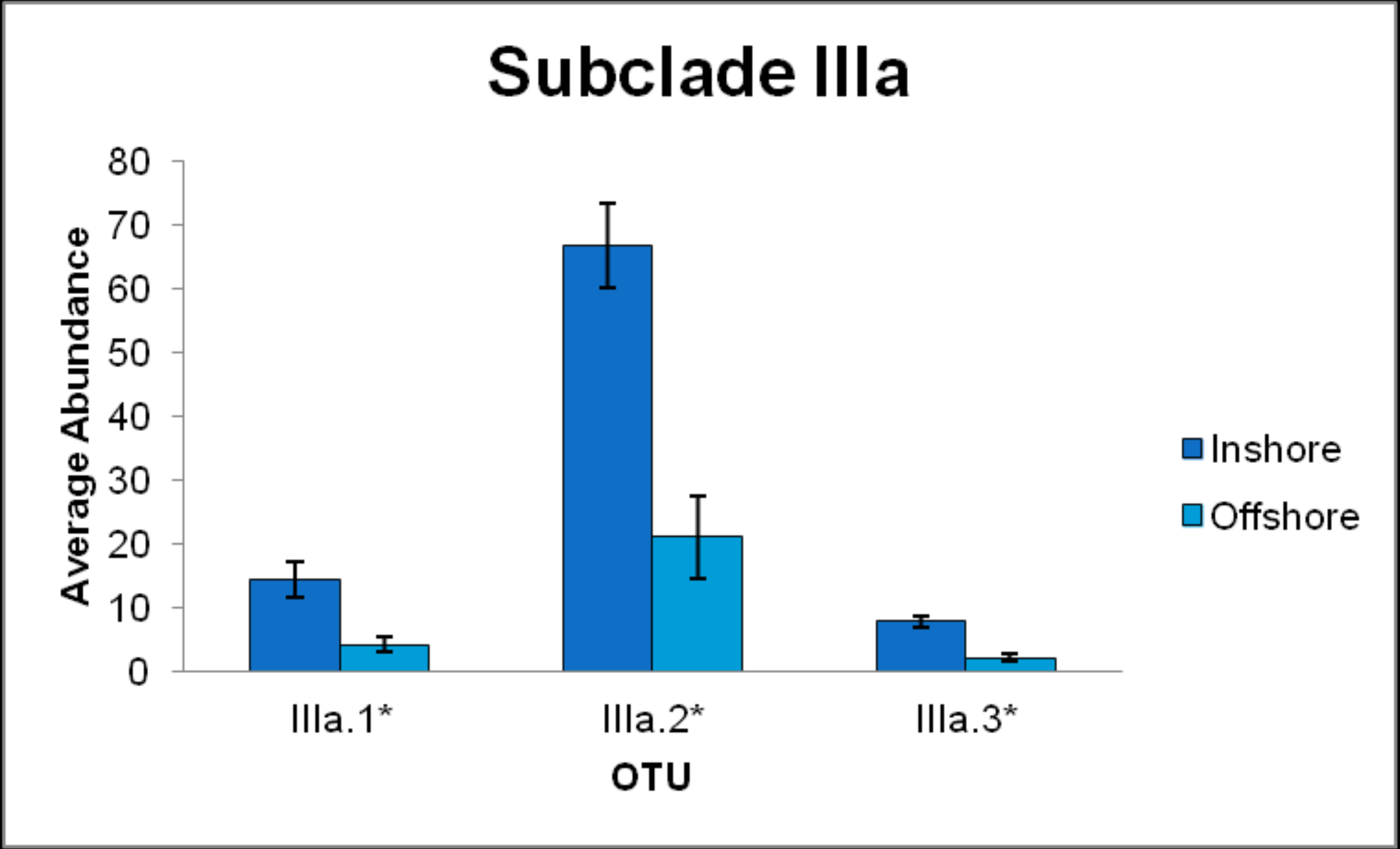


POSITIVE CORRELATION: OFFSHORE VARIABLE

OTU	Salinity	DSi	chl *a*	Bacterias	Viruses
IIb.1	**0.66**	-0.48	**-0.70**	**-0.59**	**-0.57**
IIb.2	0.01	0.17	0.18	0.10	-0.02

Spearman correlation

FRESHWATER SUBCLADE HIGHER INSHORE.



POSITIVE CORRELATION: INSHORE VARIABLES

OTU	Salinity	DSi	chl a	Bacterias	Viruses
IIIa.1	**-0.65**	**0.54**	**0.58**	0.25	0.02
IIIa.2	**-0.64**	**0.64**	**0.65**	0.45	0.11
IIIa.3	-0.48	**0.50**	**0.60**	0.45	0.09

Spearman correlation

SUMMARY OF DOMINANT SUBCLADES

Subclade	OTU	In/Out	Positive correlation	Negative correlation
Ia	Ia.1	Inshore	chl a/ Bacterias/ Viruses	Salinity
	Ia.2	Inshore/Offshore	-	-
	Ia.3	Offshore	-	chl *a*
IIb	IIb.1	Offshore	Salinity	Dsi/ chl *a*/ Bacterias
	IIb.2	Inshore/Offshore	-	-
IIIa	IIIa.1	Inshore	DSi/ chl *a*	Salinity
	IIIa.2	Inshore	DSi/ chl *a*	Salinity
	IIIa.3	Inshore	DSi/ chl *a*	-

NOAA- NGI INTERNSHIP PROGRAM

- Challenge;
- Value of my internship experience;
- Collaborations;
- NOAA as a career.

ACKNOWLEDGMENTS

National Oceanic and Atmospheric Administration -NOAA

Northern Gulf Institute- NGI

Marine Microbial Ecology Lab Members- DISL
Alice Ortmann, Ph.D.
Natalie Ortell.
Lei Wang.

Brazilian Scientific Mobility Program- BSMP