

# Genetic Variability in *Acropora palmata* and *A. cervicornis*

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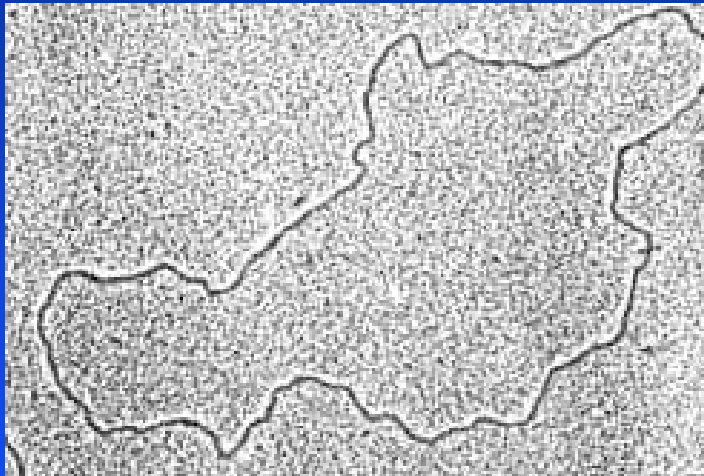
**University of Puerto Rico, Mayagüez**



## Goal of this proposal

- Evaluate the genetic variability of *A. cervicornis* and *A. palmata* at different levels of tissue organization

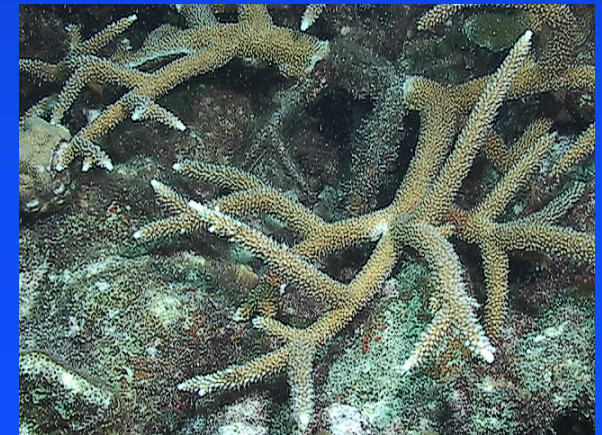
rDNA



*A. palmata*



*A. cervicornis*



# Hierarchical Design

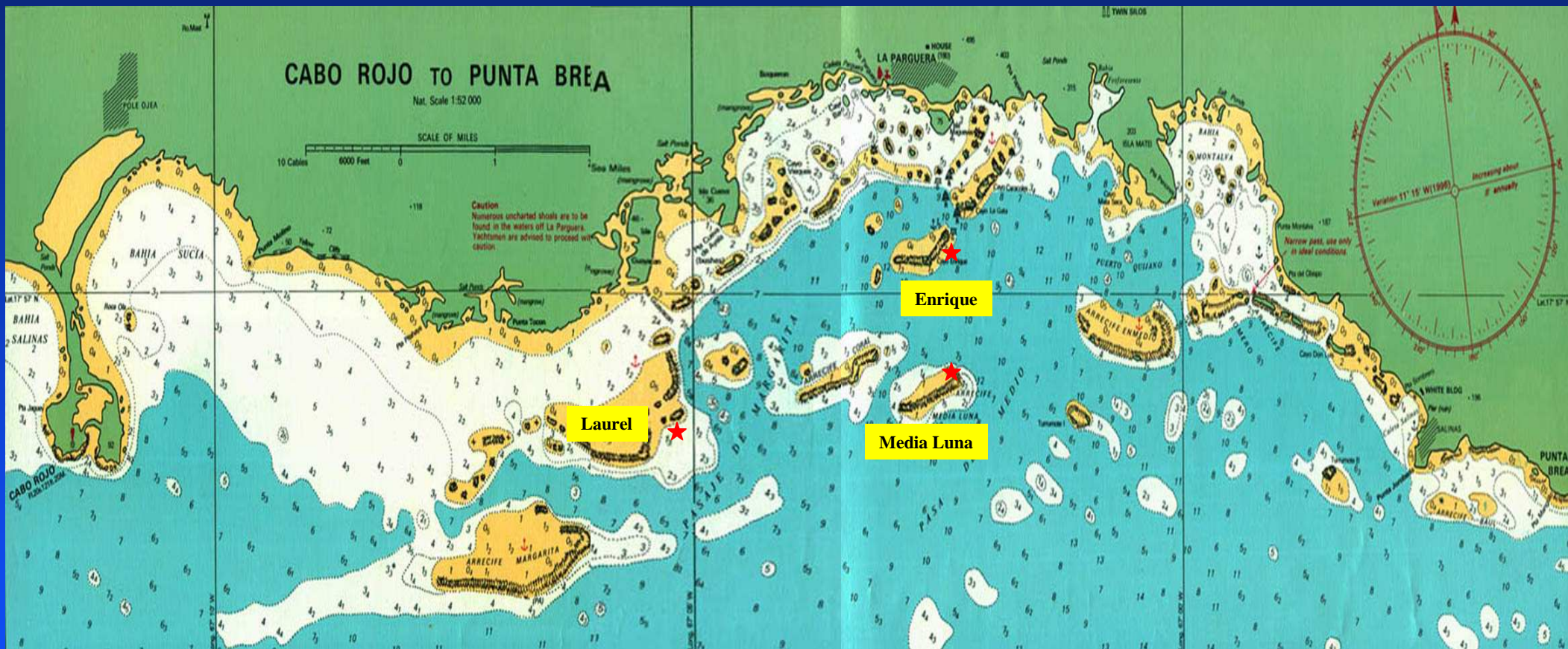
We will evaluate levels of genetic diversity:

- 1) Within discrete patches of *Acropora*
- 2) Among discrete patches of *Acropora* within sampling locations
- 3) Among sampling locations within islands
- 4) Among different islands

# Proposed Sampling Locations of *Acropora*



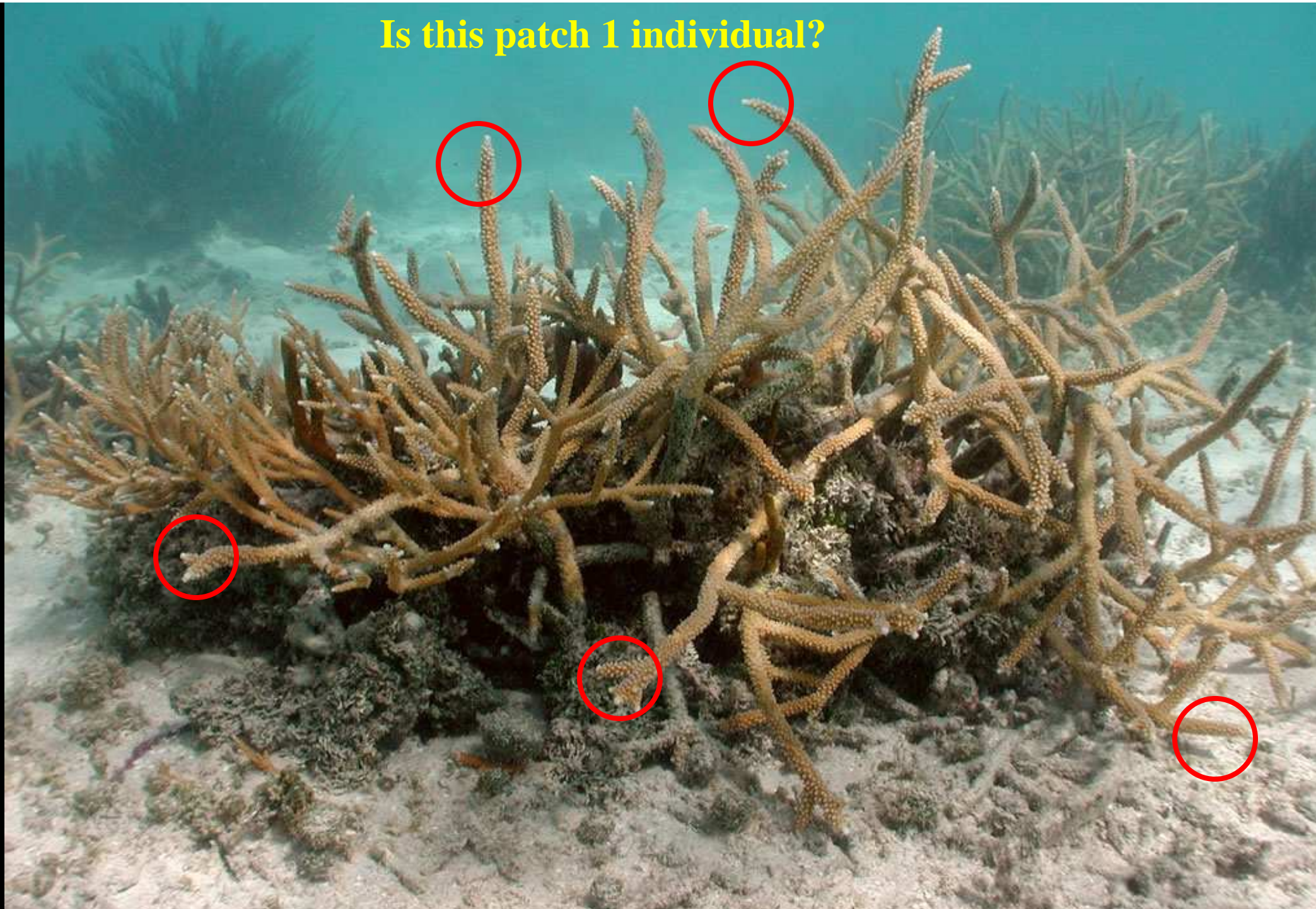
# Locations in La Parguera



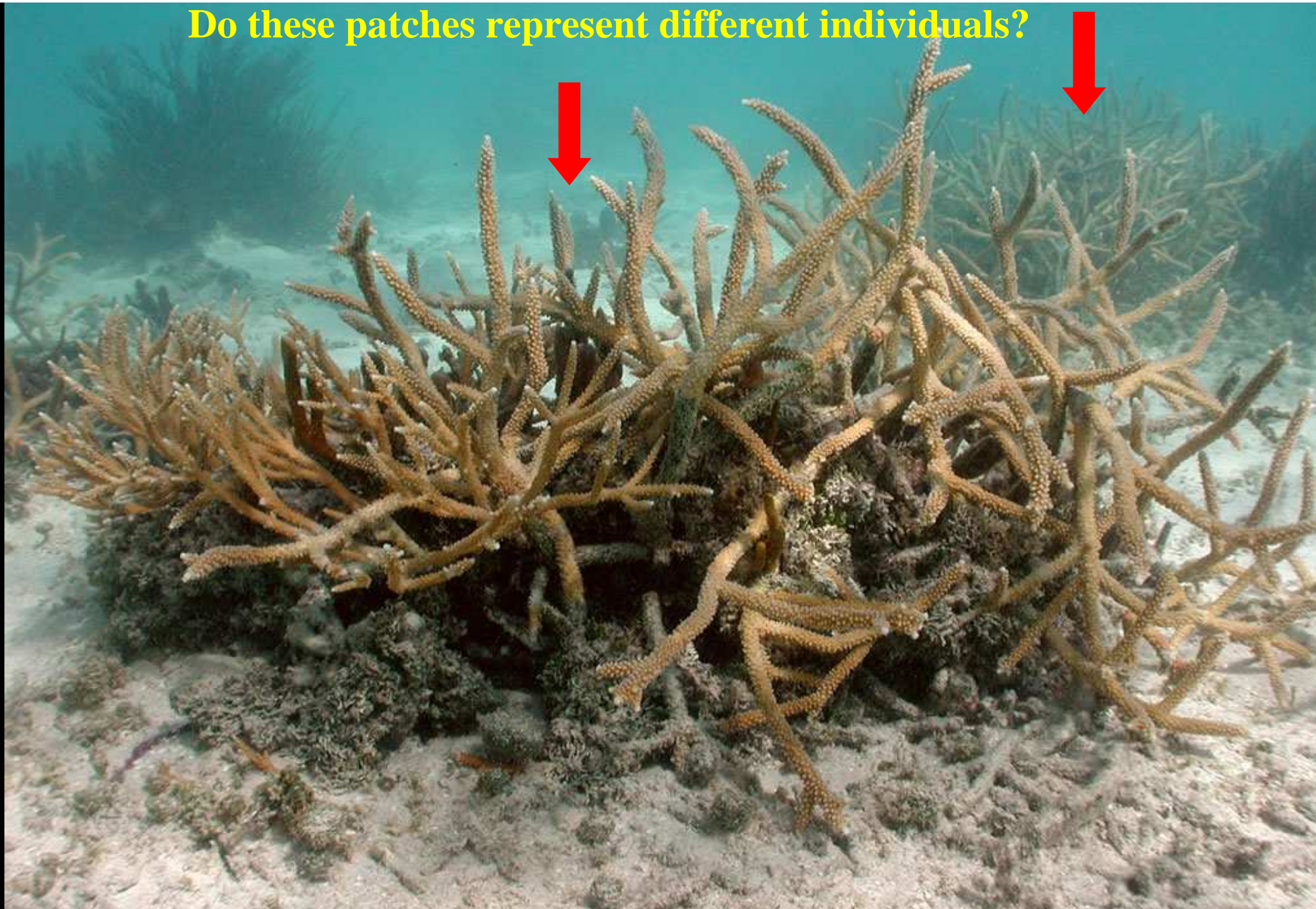
# Sites in Mona



Is this patch 1 individual?

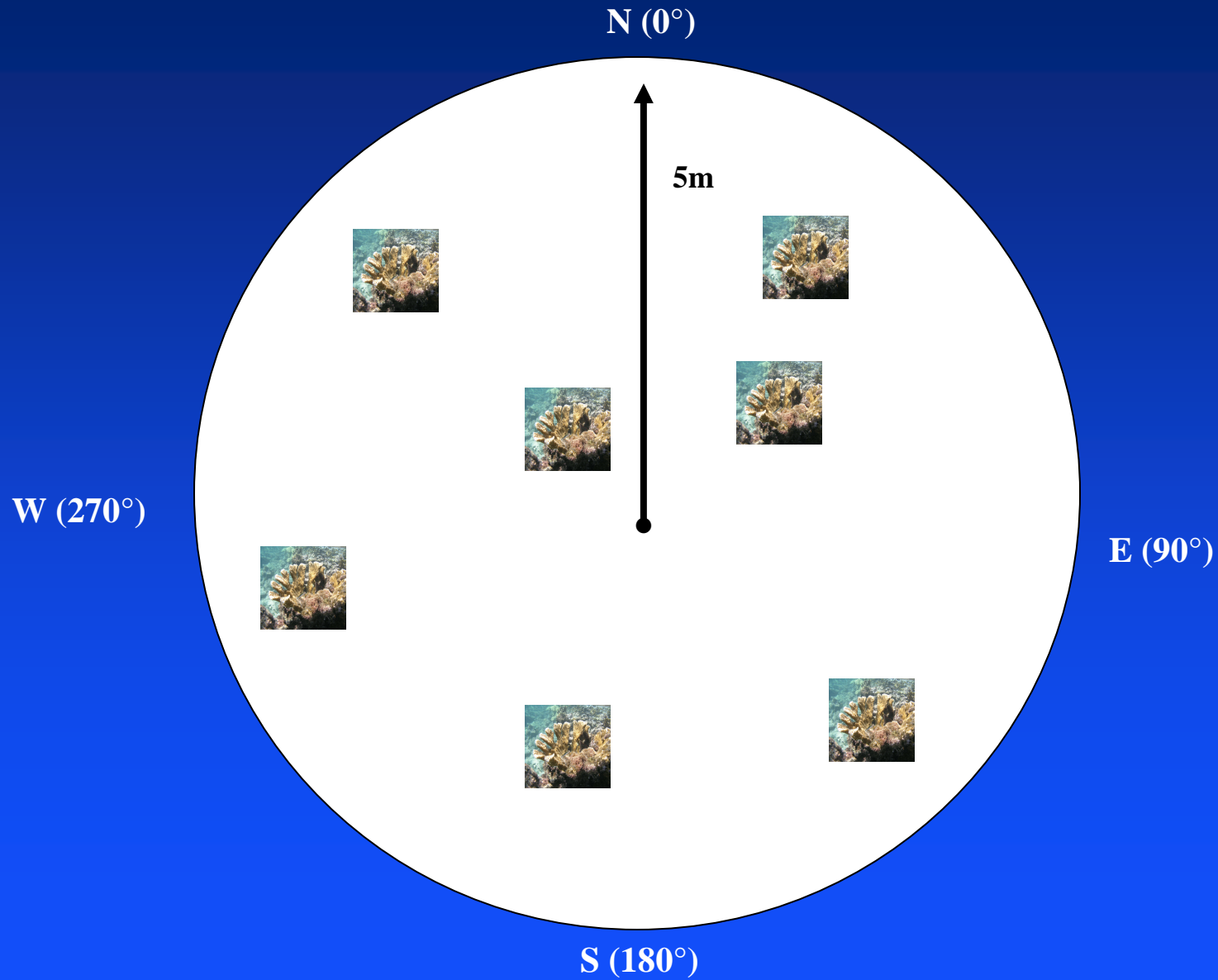


**Do these patches represent different individuals?**





# Collection Method



**Joselyd collecting polyps of *Acropora cervicornis***



# Materials and Methods

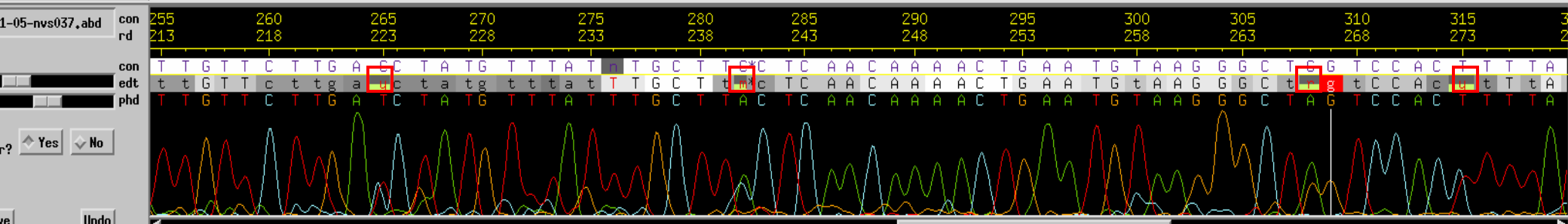
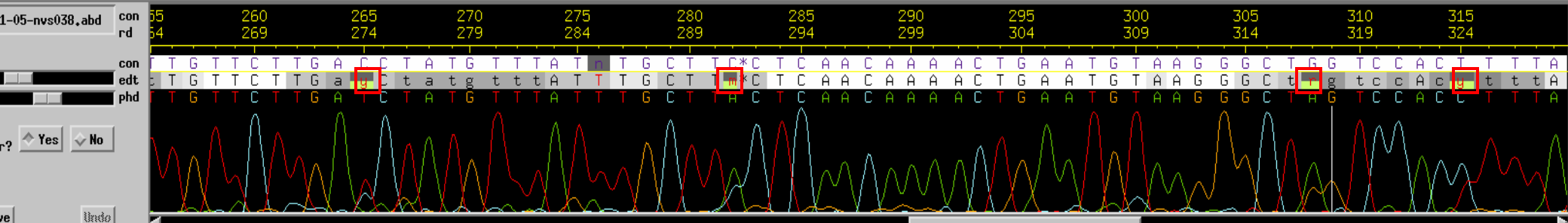
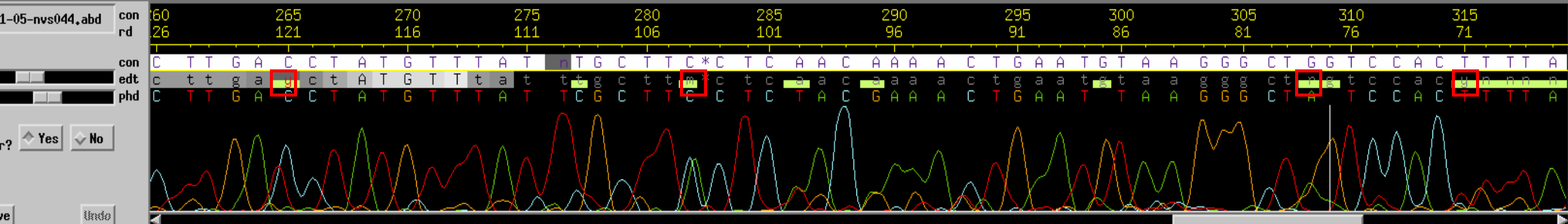
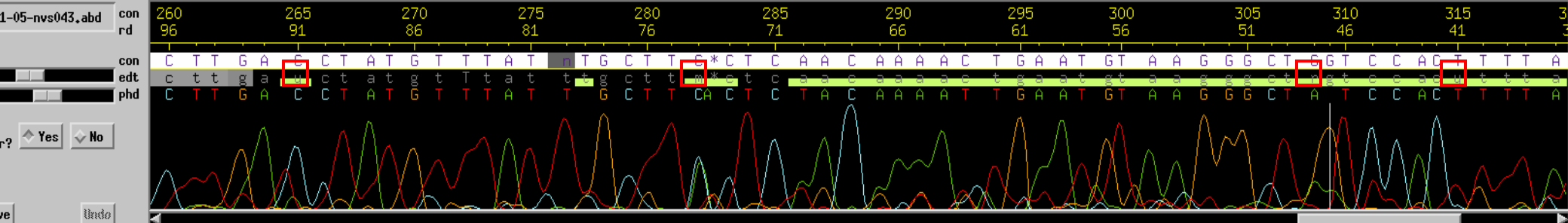
## Candidate Genes:

**MtDNA:** putative control region.

**Nuclear DNA:** ITS-1, and introns from *Pax-C* and calmodulin

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# PaxC Intron (507 bp)

## Polymorphism in *Acropora cervicornis*

Sample location	# of sequences	# colonies:
Culebra	4	2
Cayo Enrique	4	2
Cayo Laurel	3	2

## Results of *A. cervicornis* from Pax-C

1. No genetic variation within colonies
2. No single point mutations detected between colonies
3. 1 colony in Laurel and 1 colony in Culebra were heterozygous at 2 nucleotide positions



Aligned Reads

File Navigate Info Color Bin Misc

caln8\_12.fasta.screen.ace.3

Contigl

Some Tags Pos:

Search for String Compl Cont Compare Cont Find Main Win Err/10kb: 9.44

190 200 210 220 230 240 250 260 270 280 290 300 310 320 330

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8-11-05-nvs042.abd ▶ cccgtacaTctTTA\*TttggTGGGca\*ggttttattgcattgggtgtggatgattttgCTTCCctt\*g\*gttGttcttgacctatgTttatttgccttc\*ctcaacaaaactgaatgtaaggctggTccacttttattgaaattg\*cagtaatt

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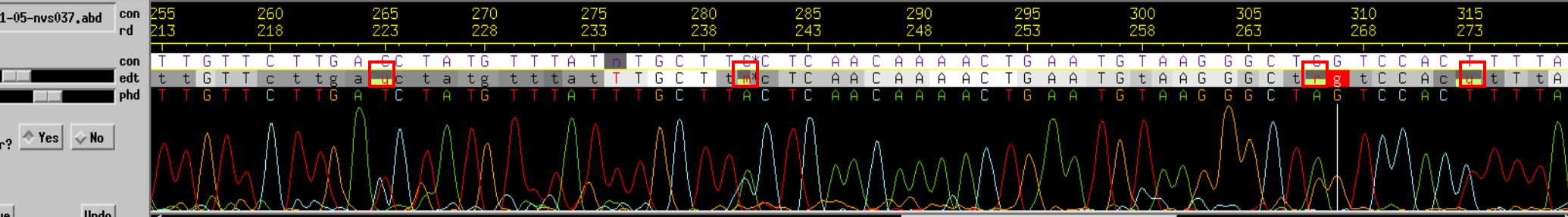
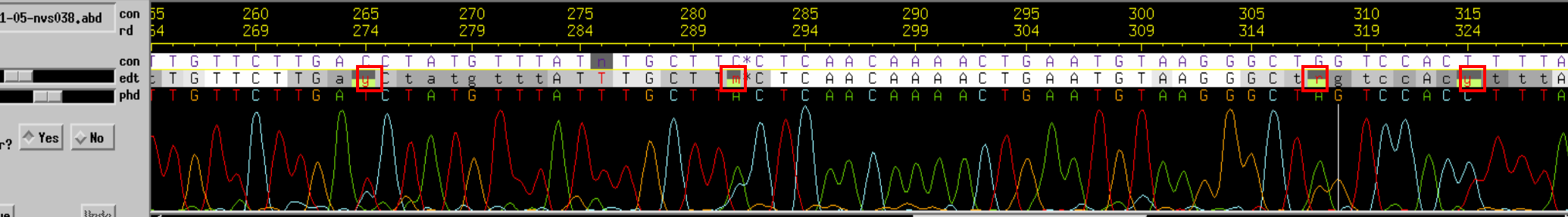
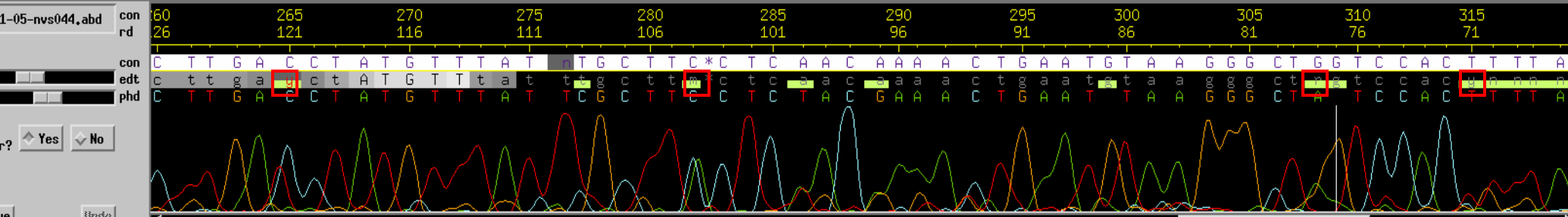
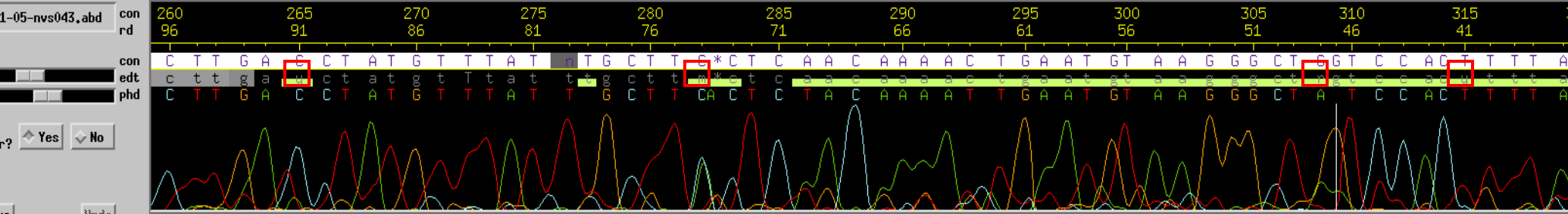
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Trace Window: Contig1

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# Calmodulin Intron (357 bp)

*A. cervicornis*

Sample location	# of sequences	# colonies:
Cayo Enrique	3	2
Cayo Laurel	3	2
Other PR*	6	6

\*Genebank from (Vollmer and Palumbi) 2002

# Results of *A. cervicornis* from Calmodulin

1. No genetic variation within colonies
2. No single point mutations detected between colonies
3. 1 colony in Laurel and 2 other PR were heterozygous at 4 nucleotide positions
  - 4 out of 10 patches of *A. cervicornis* were heterozygotes at the calmodulin locus in Puerto Rico
    - ◆ Heterozygosity ( $H$ ) = 0.4

# PaxC Intron (507bp)

*A. palmata*

Sample location	# of sequences	# colonies:
Cayo Enrique	2	1
Cayo Laurel	7	5
Culebra	8	4

# Calmodulin Intron (357bp)

*A. palmata*

Sample location	# of sequences	# colonies:
Cayo Enrique	1	1
Cayo Laurel	4	3
Other PR*	7	7

\*GeneBank (Vollmer and Palumbi 2002)

## Results of *A. palmata* from Calmodulin Intron

1. No genetic variation within colonies
2. No single point mutations detected between colonies
3. 4 out of 11 patches are heterozygotes
  1. Heterozygosity ( $H$ ) = 0.36

## Preliminary Conclusions

- *A. cervicornis* calmodulin Heterozygosity ( $H$ ) = 0.4
- *A. palmata* Heterozygosity ( $H$ ) = 0.36
- The presence of heterozygosity in *Acropora* indicate occurrence of sexual reproduction (so it's not just asexual repro through fragmentation)
- Sampling is limited, more sampling localities are needed to characterize genetic variability (e.g. Desecheo, Mona)
- In the process of developing alternative molecular markers

- 4 out of 10 patches of *A. cervicornis* in the calmodulin intron in Puerto Rico were heterozygotes (say some samples are mine and others are from genebank)

Heterozygosity ( $H$ ) = 0.4

- Cannot determine allelic diversity (we need more individuals)

# Proposed Schedule

- **Fall 2005-Summer 2006**
  - **Collection of *Acropora* from all locations**
  - **Culebra, Desecheo, North Coast of PR**
  - **Collection of data**
  - **Data Analysis**
  
- **Fall 2006**
  - **Manuscript Preparation**



## Sequenced Regions from both *Acropora* species

Gene	Sequence Length
*Control Region	673 bp
ITS region	239 bp ( <i>A. palmata</i> ); 188 bp ( <i>A. cervicornis</i> )
<i>Calmodulin</i> intron	357bp
<i>PaxC</i> intron	507 bp
In Total	1776 bp

\* Mitochondrial DNA

## Control Region (673 bp)

**Polymorphism (*A. palmata*, n=3)**

**0**

**Divergence**

**15.76% (106 mutations)**

# ITS region (239 bp)

Polymorphism (*A. palmata*, n=2)

Divergence

1

5.9% (11 mutations out of 188)

4 putative sequence gaps in the ITS alignment

```
A_palmata1ITS      TGATCACACATCTTTGTTACTTAGTCAGTCGGACCTCGGCT
A_palmata2ITS      TGATCACACATCTTTGTTACTTAGTCAGTCGGACCTCGGCT
A_cerv1ITS         T-----TTG--AATCAGTCAGTCGGACCTCGGTT
*                   ***  * *  **** * * * * * * * * * * * * *
```

Sequence divergence in minicollagen, calmodulin, and PaxC (0.6%-2.1%). In ITS-1 is up to 13.2%.

