

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

Joselyd Garcia and Nikolaos Schizas

Department of Marine Sciences

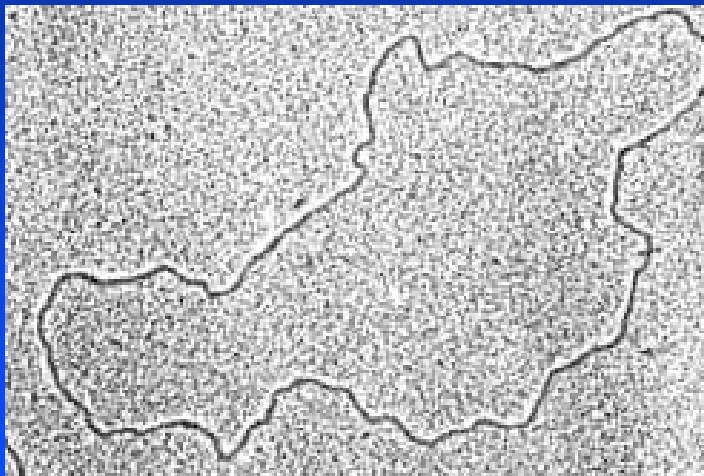
University of Puerto Rico, Mayagüez



Goal of this proposal

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

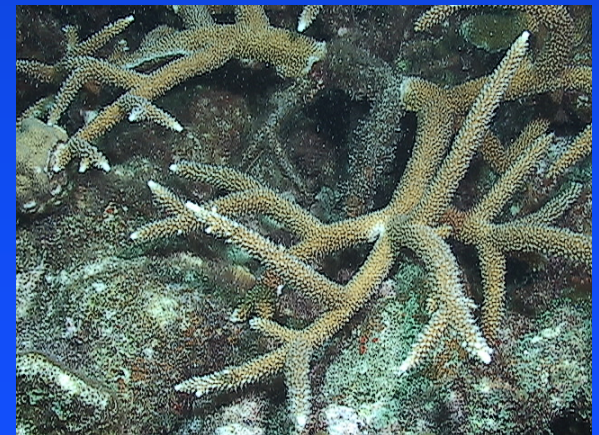
DNA



A. palmata



A. cervicornis



Motivation

- 1) Levels of genetic variation may be used as a proxy for the long term survival of the species
- 2) Identification of distinct populations may aid decisions in management and conservation issues

HOW?

Hierarchical Design

We are evaluating 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*



Collection Sites

■ La Parguera

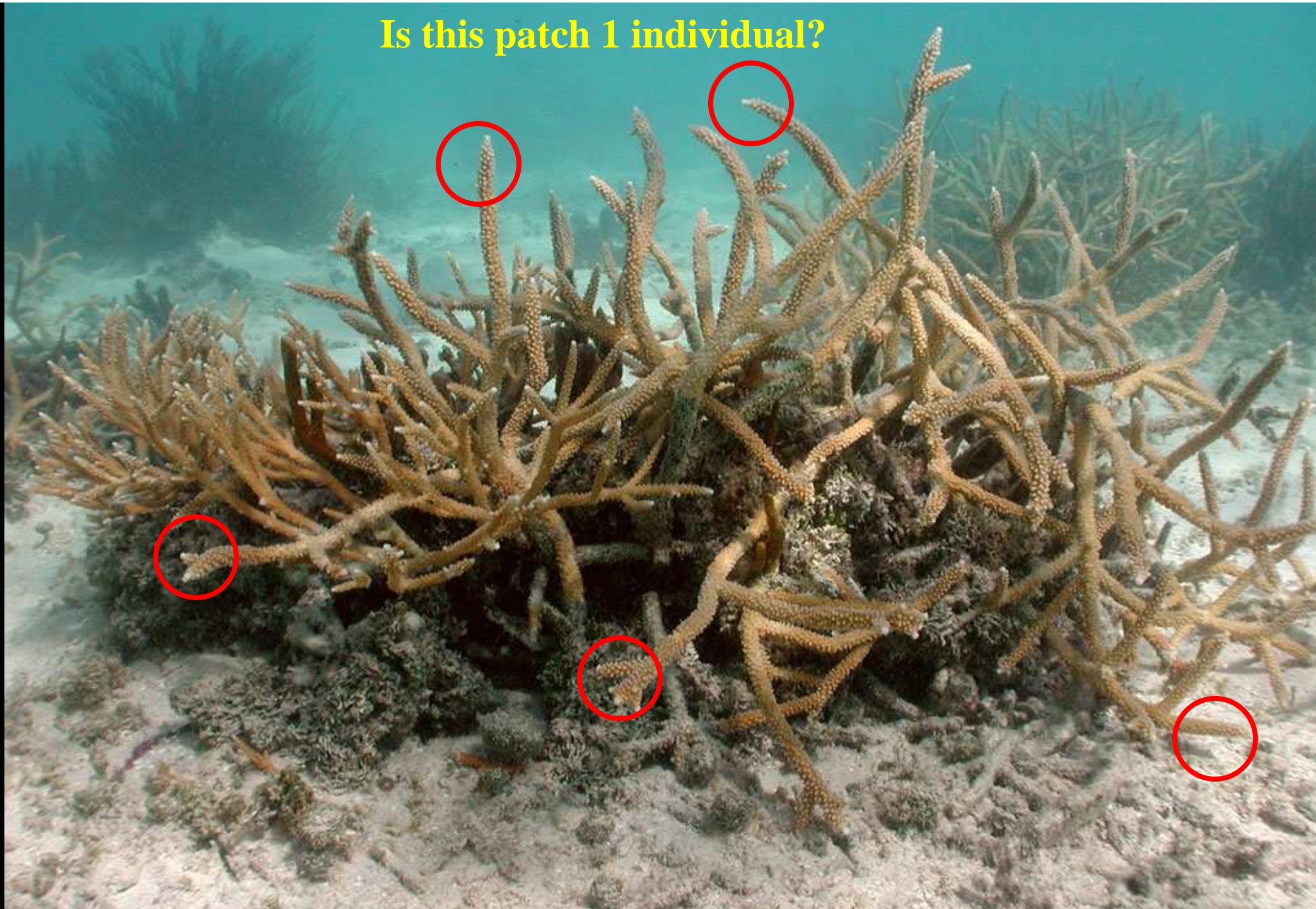
- ◆ Cayo Enrique
- ◆ Cayo Laurel
- ◆ Cayo Media Luna
- ◆ Cayo San Cristobal
- ◆ Cayo Wineberg*
- ◆ Cayo Romero

■ Culebra

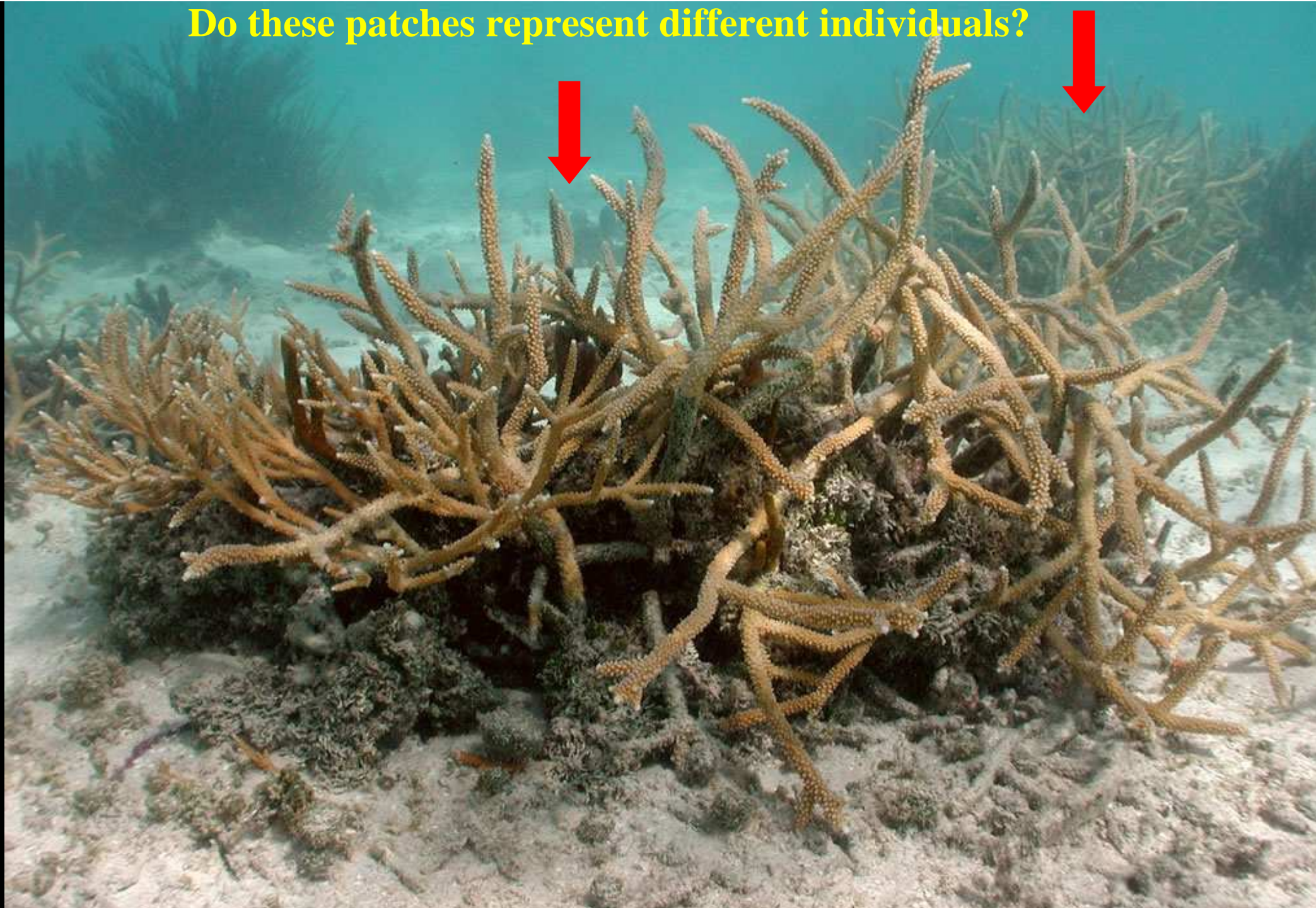
■ Lee Stocking Island, Bahamas (outgroup)

* Samples from the shelf edge

Is this patch 1 individual?



Do these patches represent different individuals?



Joselyd Garcia (MS student) 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

Course of Action

- Develop a reliable DNA extraction technique in *Acropora* ✓
- Optimize PCR amplification conditions for 4-6 genes per specimen ✓
- Expand collection of *Acropora* to other locations ✓
- Analyze data

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



Calmodulin Intron (357 bp)

A. cervicornis

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

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 was heterozygous at 4 nucleotide positions**

PaxC Intron (507bp)

A. palmata

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

Results of *A. palmata* from PaxC

- 1. No genetic variation within colonies**
- 2. No single point mutations detected between colonies**

Calmodulin Intron (357bp)

A. palmata

Sample location	# of sequences	# colonies:
Cayo Enrique	1	1
Cayo Laurel	4	3

Results of *A. palmata* from Calmodulin Intron

- 1. No genetic variation within colonies**
- 2. No single point mutations detected between colonies**

Preliminary Conclusions

- Introns from two nuclear genes indicate that there is no or little genetic variation among our samples
- Identified allelic variants within individuals (i.e. heterozygotes)
- Current data suggest high levels of gene flow
- Sampling is limited, more geographic samples are needed to understand the levels of variability (e.g. Mona, Desecheo)
- Current genes may not be providing well enough resolution

Proposed Schedule

- **Fall 2005-Summer 2006**
 - **Collection of *Acropora* from all locations**
 - **Culebra, Mona, 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

A_palmata2ITS

A_cerv1ITS

TGATCACACATCTTTGTTACTTAGTCAGTCGGACCTCGGCT

TGATCACACATCTTTGTTACTTAGTCAGTCGGACCTCGGCT

T-----TTG--AATCAGTCAGTCGGACCTCGGTT

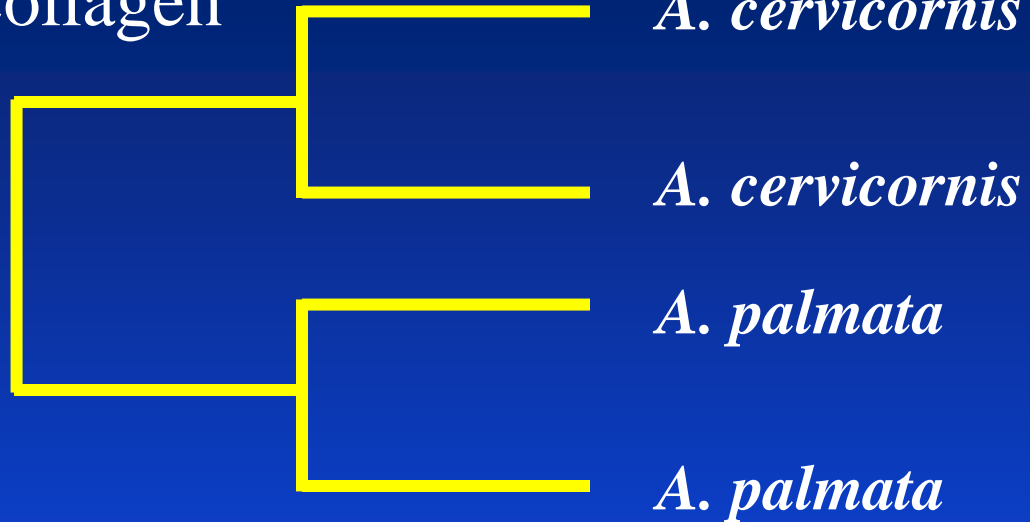
*

*

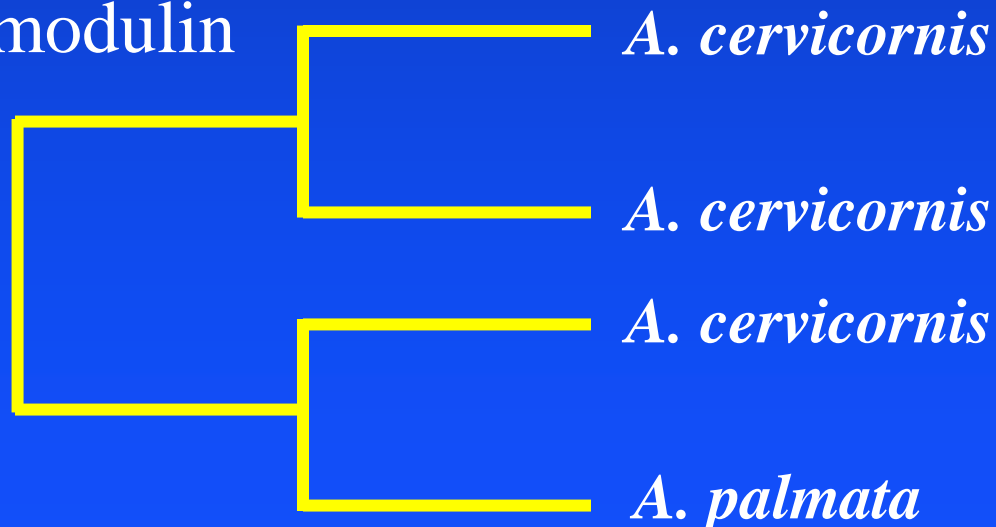
*

*

Minicollagen



Calmodulin



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