

Genetic diversity of dusky grouper and common snook in Paraty by using microsatellite markers



TEAM

- Alpina Begossi (UNICAMP/ FIFO), researcher
- Tainá Barreto(UNICAMP/ FIFO), biologist
- Vinicius Nora (UNICAMP/CAPESCA), biologist
- Natália Spagnol Stabellini (ESALQ/USP), trainee and graduate student
- Jaqueline Bueno de Campos (ESALQ/USP), trainee and graduate student
- Aluana Gonçalves de Abreu (IAC/APTA), post-doctor
- Regina Helena Geribello Priolli (ESALQ/USP), young-researcher FAPESP

PROJECT GOALS

1. How many populations?
2. Where are their limits?

Dusky Grouper



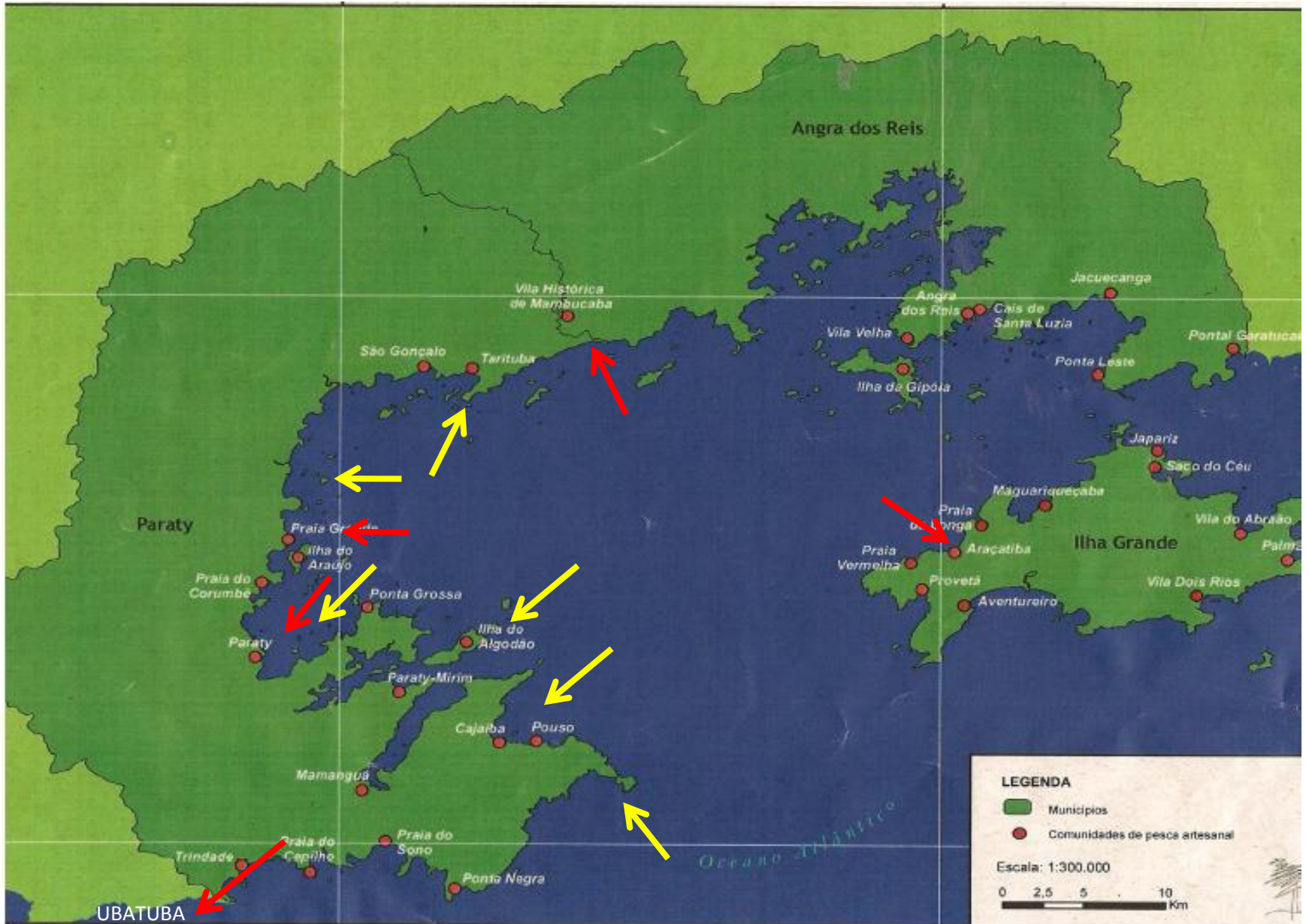
Common Snook



1125 km²

METHODOLOGIES

- Obtaining samples
 - ✓ Points of sale of fish : collection of fish fins
- Define the molecular markers
 - ✓ Microsatellite or Simple Sequence Repeat (SSR) – high polymorphism, co-dominant, specific, neutral
- DNA extraction
 - ✓ Easy and efficient procedure
- Genotype populations of dusky grouper and common snook (94 indiv/specie)
 - ✓ PCR conditions
 - ✓ DNA analyser: 4300 DNA Sequencer (Li-cor Biosciences).
- Allele frequencies and genetic variability parameters
 - ✓ Population differentiation and structure

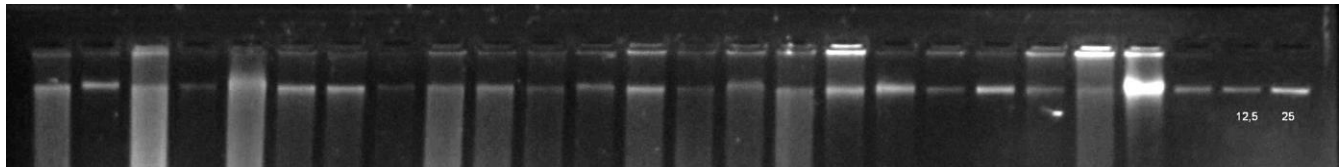


INITIAL RESULTS

- Local catch, period and fish traits
 - ✓ Dusky grouper
 - ✓ Eight sites fishing (5 analysed), 67 samples genotyped
 - ✓ May/2010 – Sept/2010
 - ✓ Length: mean 35 cm; weight 600 g; Gonad development: not visible; female juvenile stages
 - ✓ Common snook
 - ✓ Eight sites fishing (5 analysed), 46 samples genotyped
 - ✓ Feb/2010 – Aug/2010
 - ✓ Length: mean 75 cm; weight 4 kg; Esperm visible in half of samples; male in juvenile and adult stages

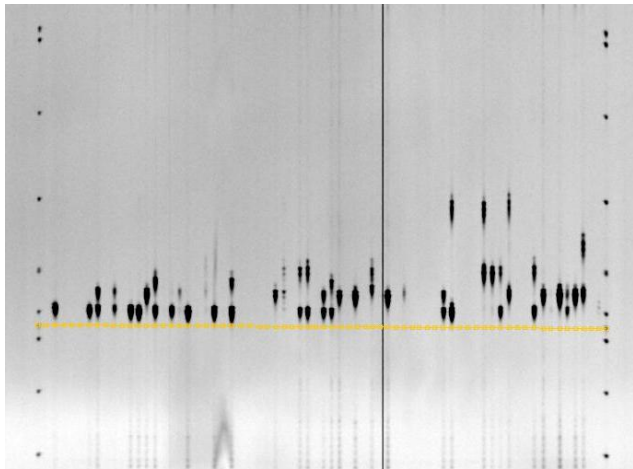
MOLECULAR ANALYSIS

- DNA extraction
- ✓ lyophilized tissue of the each individual by procedure with salt and without fenol (toxic) according Almeida (2010)
- ✓ Dusky grouper: 67 individuals (mean 5 ng/uL)
- ✓ Common snook: 46 individuals (25 ng/uL)

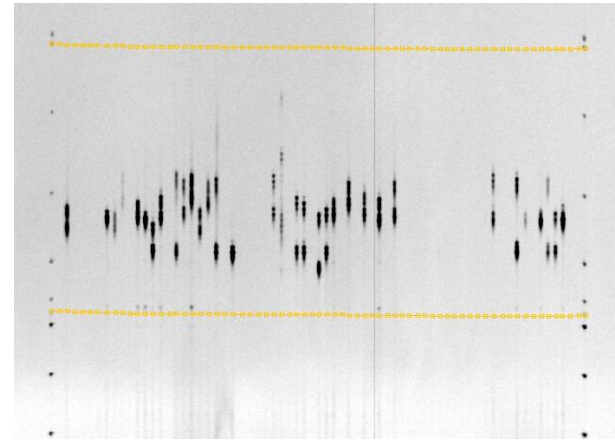


- SSR markers
- ✓ Dusky grouper: 11 SSR loci-markers heterologous developed for *Mycoteroperca micropelis* (Chapman et al 1999) e *Epinephelus quernus* (Rivera et al 2003); **8 SSR amplified in *E. marginatus***
- ✓ Common snook: 15 SSR loci-markers specific for the *Centropomus undecimalis*: **15 SSR amplified**
- PCR amplifications were performed in touchdown program
- Amplicons were detected using an 4300 DNA Sequencer (Li-cor Biosciences). Marker data were analyzed with SAGA v.3.3 software from Li-cor Biosciences.
- Data analysis: genetic structure was inferred using Structure v.2.2 and Statistic F in Genetix

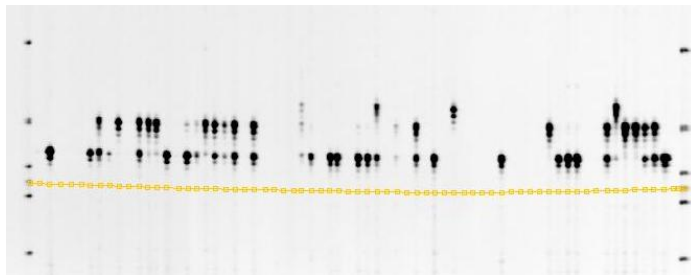
SSR loci in dusky grouper



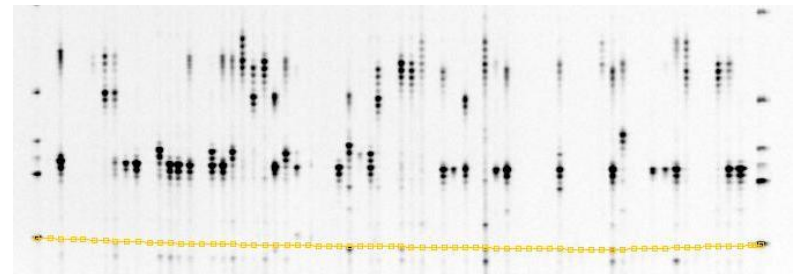
GAG049



CA 3

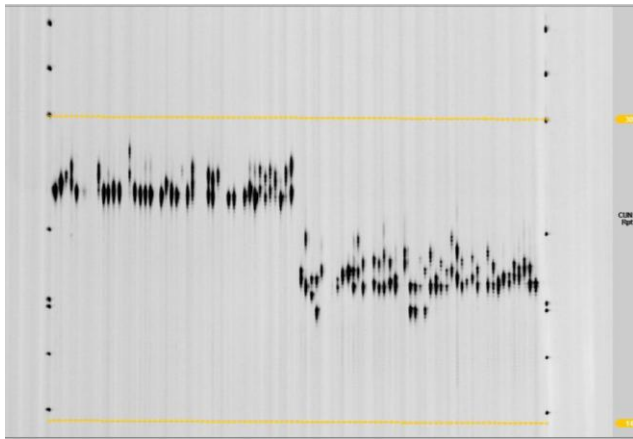


GAG023



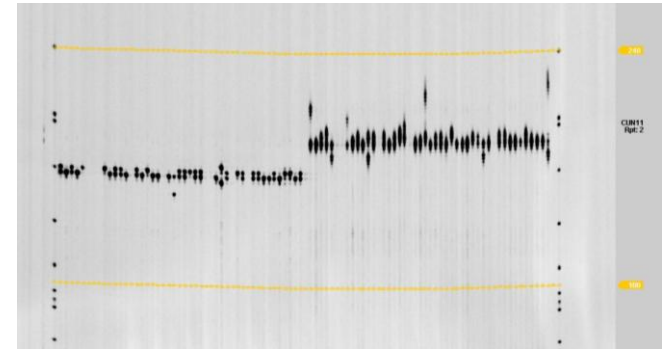
GAG045

SSR loci in common snook



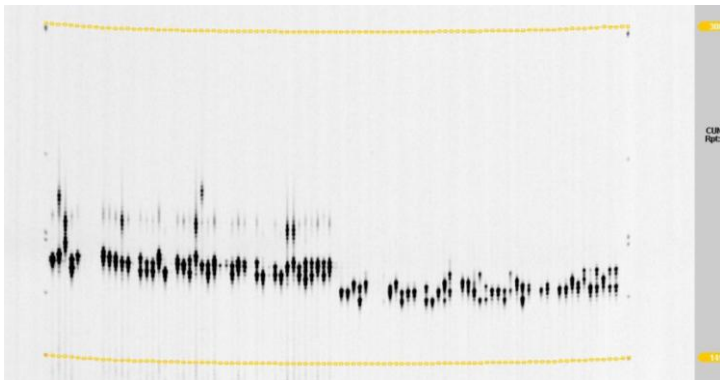
CUN09

CUN14



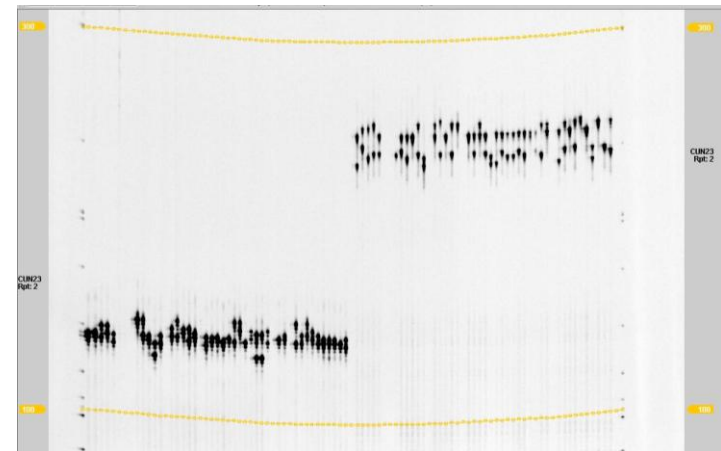
CUN05

CUN11



CUN12

CUN08



CUN18

CUN23

STRUCTURE OF DURSKY GROUPER

✓ No genetic

differentiation among
five sites

✓ Panmitic population

✓ Strategies of

conservation: choose
random sites of Paraty
Bay

- **F -statistics**

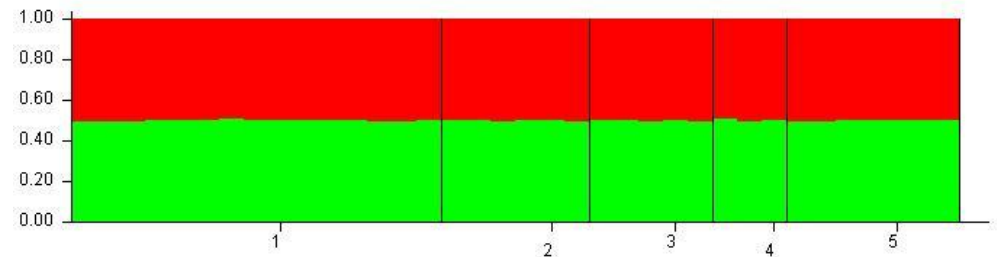
✓ $F_{st} = 0.0004$ (ns)

✓ $F_{is} = 0.0000$ (ns)

✓ $H_o = H_e$

- **Bayesian analyzes**

✓ $K = 1$



STRUCTURE OF COMMON SNOOK

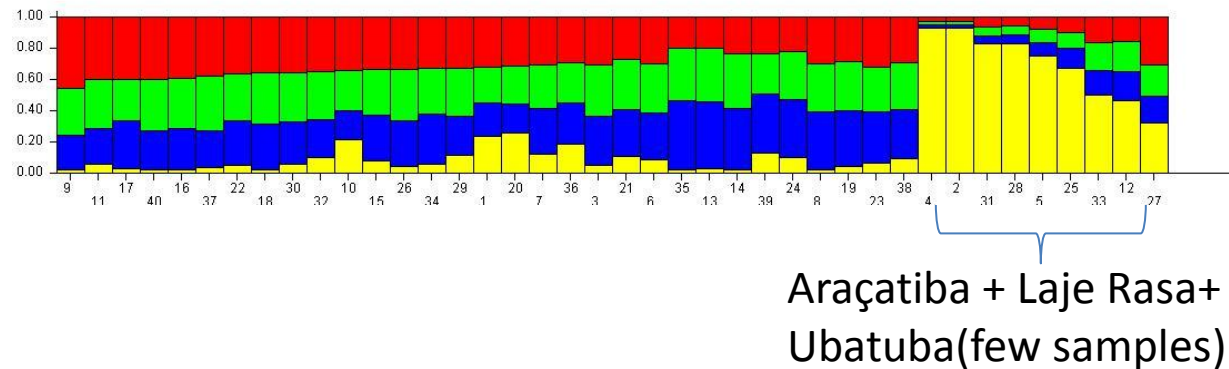
- ✓ There was genetic differentiation among of five sites
- ✓ No panmitic population, restriction of genic flow
- ✓ Strategies of conservation: sampling at least the two different sites of Paraty Bay

- **F -statistics**

- ✓ $F_{st} = 0,018$ (ns)
- ✓ $F_{is} = 0.18$ *(Pop Araçatiba)

- **Bayesian analyzes**

- ✓ $K = 2$



CONCLUSIONS

- SSR loci provided sufficient variability to study genetic population of dursky group and common snook
- Dursky group: one population, but should be confirmed with an external sample of Paraty Bay
- Common snook: no panmictic population: two populations at least. Would be different sites of reproduction?

THANKS!
