

EARLY LIFE HISTORY AND STOCK IDENTITY OF HORSE MACKEREL SPECIES

LMR-PEL-09-09



Trachurus capensis



Trachurus trecae

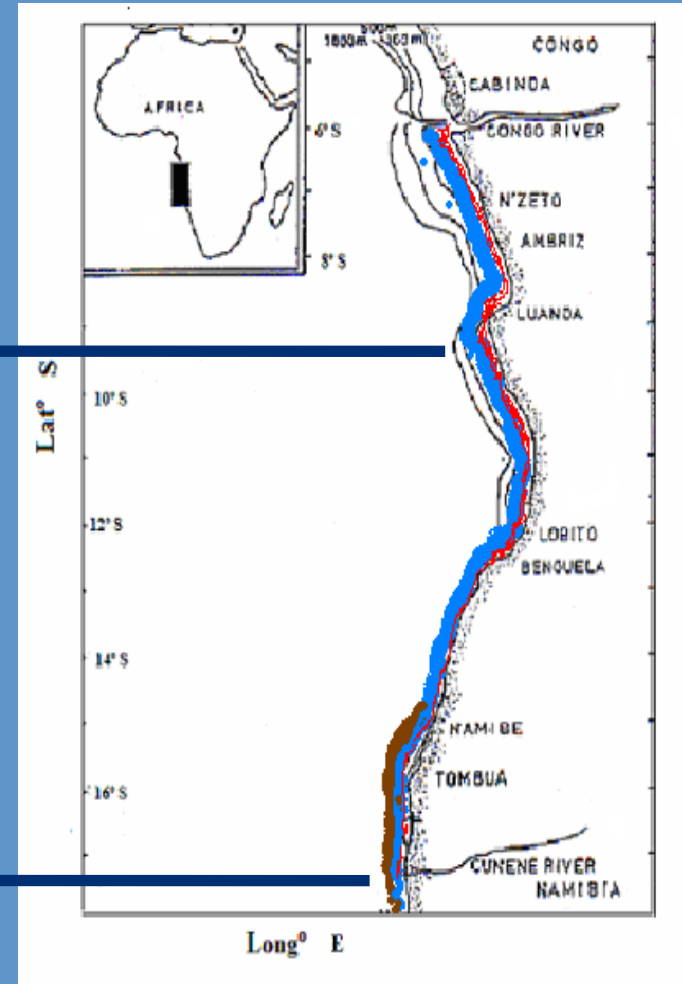


In Angola: in the past Largest fisheries landing in volume; it reached 40% of the total fish catches. Currently < 10% of total catch. High national demand

In Namibia: ~ 60% of total catch

Trachurus trecae ←

Trachurus capensis ←



Objectives

- ✓ Determine the stock identity of Cunene horse mackerel found in northern/central Angola and southern Angola;
- ✓ Determine the stock identity of Cape horse mackerel found in southern Angola and northern Namibia;
- ✓ Identification of the main spawning and nursery areas of the two species of horse mackerel;
- ✓ Recommend on appropriate management strategy for the northern Benguela horse mackerel stocks.

Identification of the main spawning and nursery areas of the two species of horse mackerel

➤ Data types available:

➤ Biological commercial sampling

- High temporal coverage

- Daily

- Low spatial resolution

- 3 ports

➤ Survey data

- Low temporal coverage

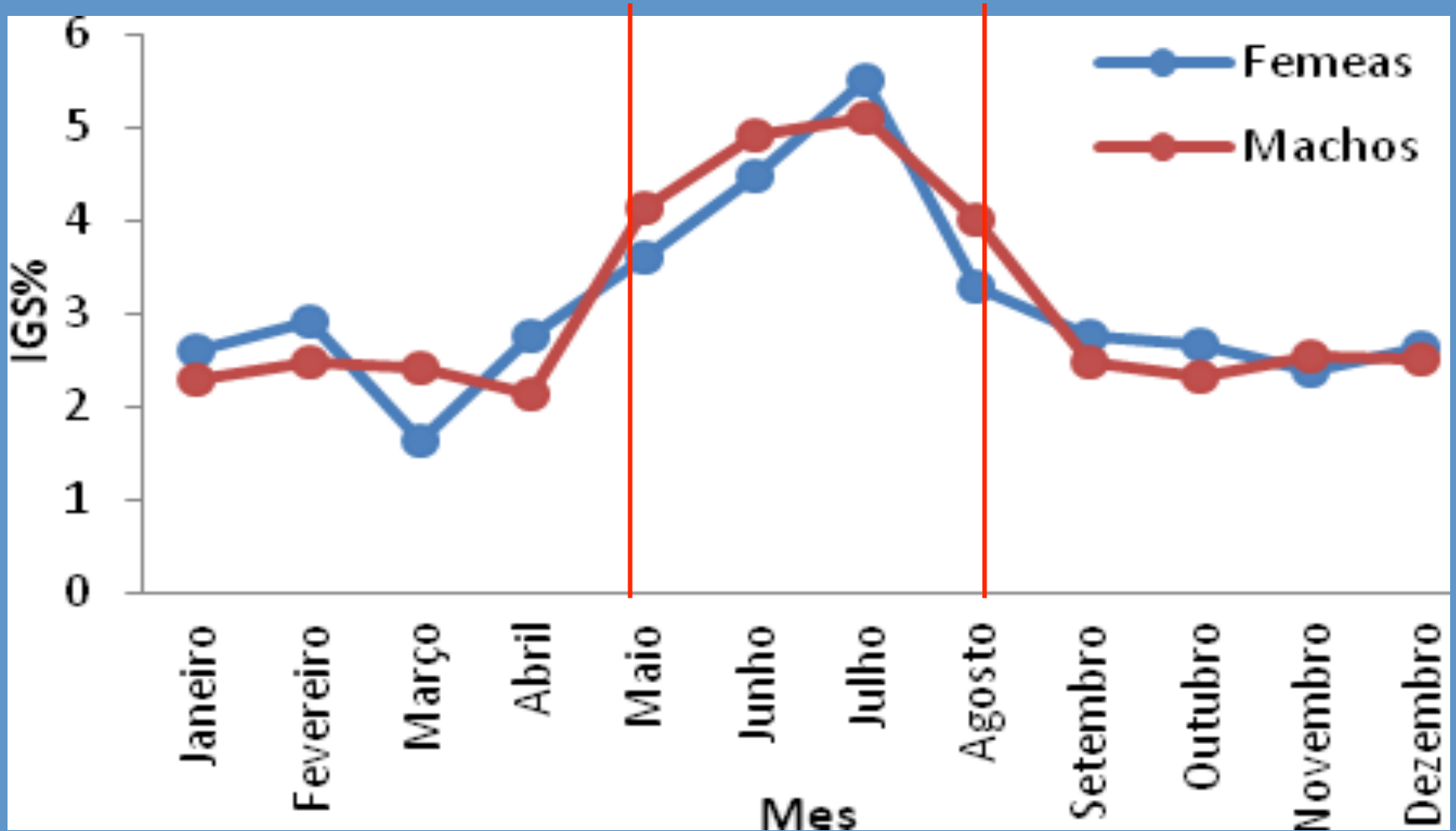
- 1 month/year

- High spatial resolution

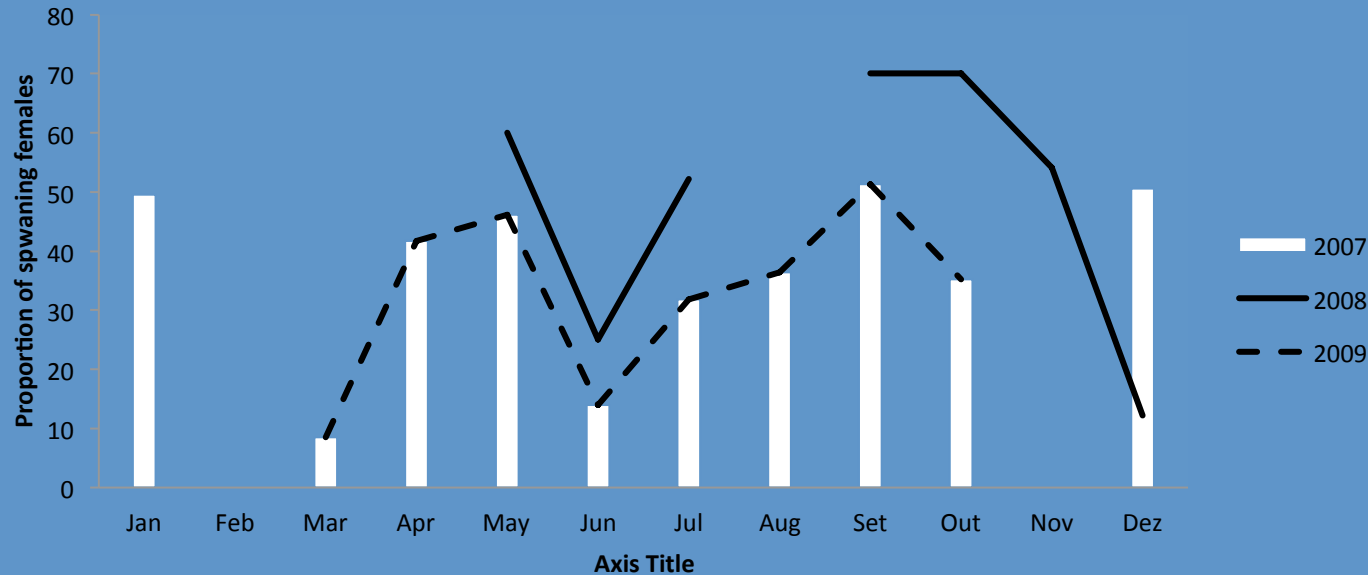
- Whole coast



When do they spawn? -Spawning cycle-

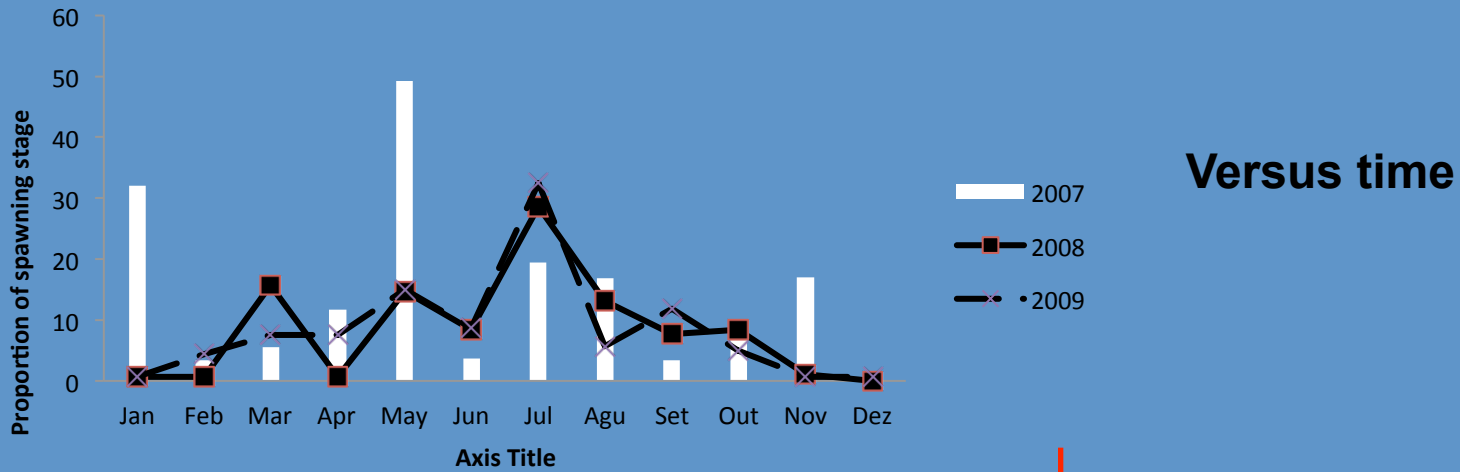


Sampling and fishing among regions -Luanda

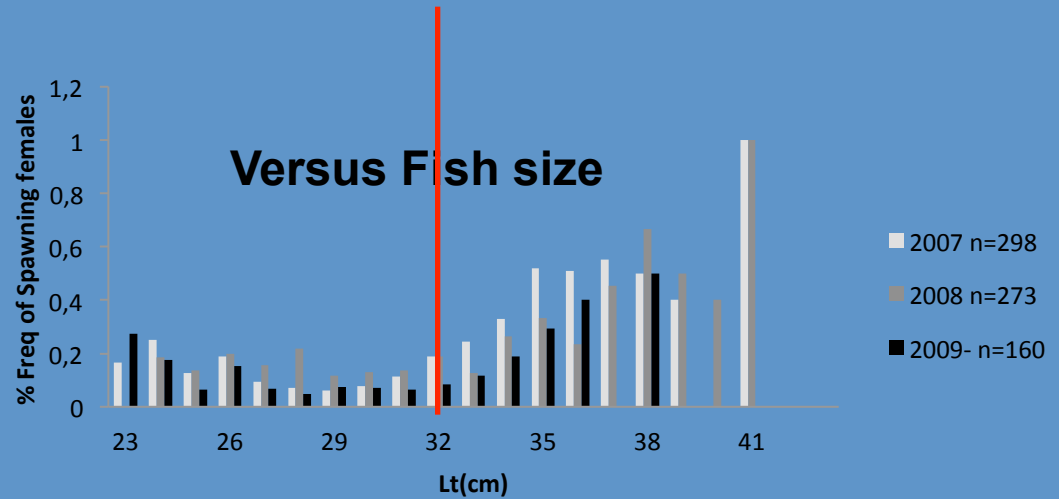


Proportion of macroscopic spawning stage 4 (Spawning)

Benguela

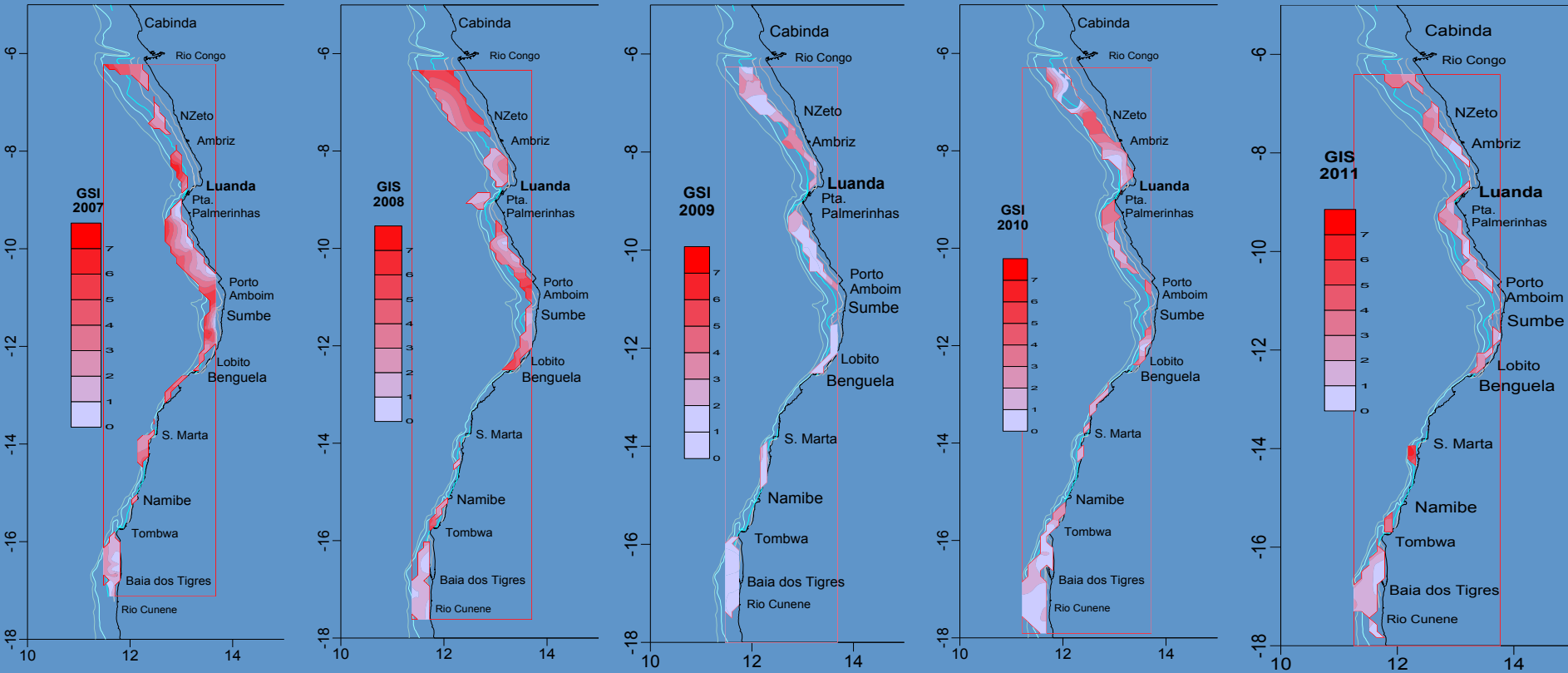


Proportion of macroscopic spawning stage 4 (Spawning)

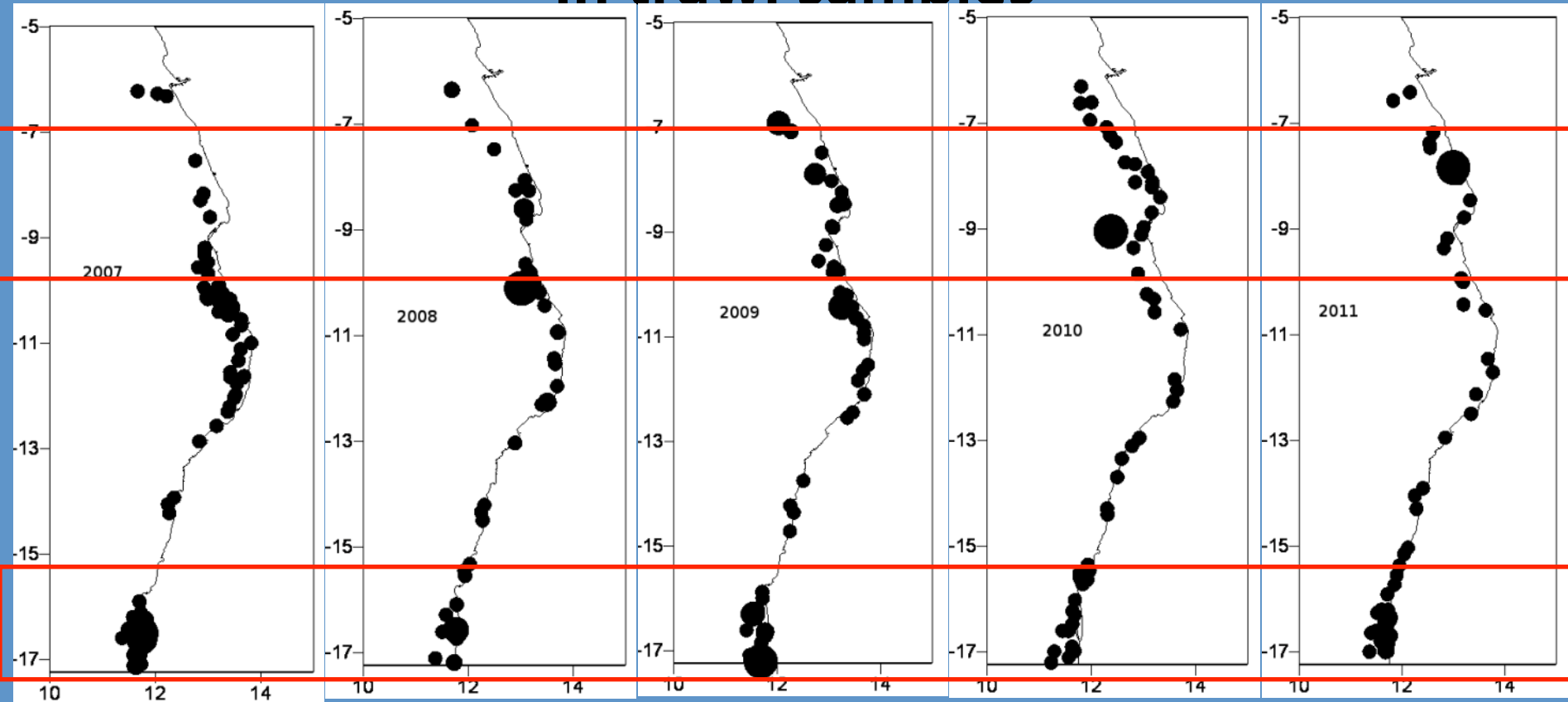


Spatial distribution – Spawning

Evolution with time (Last 5 years)



Distribution of recruits In trawl samples



Spawning and recruitment seem to be concentrated in a few areas

Does this mean they are different populations?

Stock identity of horse mackerel in northern BCLME region

- ✓ A total of 63 individuals from the whole *T. trecae* distribution and 82 of *T. capensis* were used for DNA isolation, purification and sequencing;
- ✓ The total DNA isolation and was performed using kit GE (GE Healthcare, Brazil);
- ✓ Cytochrome *b* from mitochondrial DNA was amplified using the primers:
L-14841
5'AAAAAGCTTCCATCCAACATCTCAGCATGATGAAA 3'
H-15149
3'AAACTGCAGCCCCTCAGAATGATATTTGTCCTCA 3'

Molecular Methodologies

- ✓ Genetic variability was estimated using the following parameters:
Nucleotide and haplotype diversities using DnaSP package.
- ✓ Inter population variability was in silico evaluated using AMOVA implemented by Arlenquin version 3.5.1.2.

Results: *Trachurus trecae* Genetic Variability



Characteristic	North	Center	South	Total
Sequence Number	25	22	16	63
Total sites	350	350	350	
Total number of mutation	10	12	9	22
Diversity nucleotide (\pm SD)	0,00448 (\pm 0,001)	0,00549 (\pm 0,0010)	0,00557 (\pm 0,001)	0,00501 (\pm 0,009)
Number of haplotype	10	10	8	23
Diversity haplotype (\pm SD)	0,690 (\pm 0,102)	0,662 (\pm 0,116)	0,800 (\pm 0,0920)	0,707 (\pm 0,065)
D Tajima	-1.70678*	-1.82659*	-1.50615 ^{NS}	2,16013*

The observed values of diversity nucleotide are below of variation reviewed for marine fish that varies 0,8-3,20%.



Diversity haplotype for northern and central region are below of the variation demonstrated for marine fish ($h=0,7-1,0$). For the southern region is within the variation.



* significant values ($p < 0,05$); NS no significant value ($p > 0,05$)

Results: *Trachurus trecae* Genetic Variability



- ✓ According to the classification Grant e Bowen, 1998 *Trachurus trecae* seems to be a population with high diversity haplotypes and low diversity nucleotide is characteristic for population over exploited. For stable population both diversity haplotypes and nucleotide are high.
- ✓ The effective number of inbreeding females (N_{ef}) calculated from the Θ_S indicates 371.000 female. The effective population size is always considerably smaller than census size.

Frequency of haplotype of Cytochrome b

Trachurus trecae



haplotype	N	North (%)	Center (%)	South(%)	
Hap_1		34	41	38	21
Hap_2	1	100	0	0	0
Hap_3	4	25	0	75	0
Hap_4	1	100	0	0	0
Hap_5	2	100	0	0	0
Hap_6	3	66	34	0	0
Hap_7	1	100	0	0	0
Hap_8	1	100	0	0	0
Hap_9	2	50	50	0	0
Hap_10	1	100	0	0	0
Hap_11	1	0	100	0	0
Hap_12	1	0	100	0	0
Hap_13	1	0	100	0	0
Hap_14	1	0	100	0	0
Hap_15	1	0	100	0	0
Hap_16	1	0	100	0	0
Hap_17	1	0	100	0	0
Hap_18	1	0	0	100	0
Hap_19	1	0	0	100	0
Hap_20	1	0	0	100	0
Hap_21	1	0	0	100	0
Hap_22	1	0	0	100	0
Hap_23	1	0	0	100	0

- ✓ Only the haplotype number one is present in the three populations;
- ✓ Haplotype 3 is present in the north and south population;
- ✓ haplotype 6 and 9 are present in the north e center;
- ✓ The presence of several unique haplotype can be an indication that the abundance of population is fluctuating leading probably the accumulation of new mutation.

Genetic structure of populations

Trachurus trecae



Source variation	Variance components	% variance	Φ Statistics	P-value
Inter-populations	0.00069	0.10	0.00096	>0,05
Intra-population	0.71613	99.90		>0,05

- ✓ High genetic variability is found within each population;
- ✓ No genetic differentiation is found between population.

The lack of genetic differentiation can be attributed to high level of genetic flow characteristic for species with high capacity of dispersion as horse mackerel.

Results: *Trachurus capensis*

Genetic Variability



Characteristic	Angola	Namíbia	Total
Sequence Number	29	53	82
Total sites	350	350	350
Total number of mutation	14	23	30
Diversity nucleotide	0,00872	0,00838	0,00067
Number of haplotype	8	21	27
Diversity haplotype	0,8867	0,96807	0,94640
D Tajima	-1,27328 *	1,33640 *	1,9906 *

The observed values of haplotype and nucleotide diversity are within the variation demonstrated in reviews of the mitochondrial DNA of marine teleost fish ($h=0,7-1,0$ and $\pi = 0.8$ to 3.20%).

Frequency of haplotype of Cytochrome b

Trachurus capensis



✓ Only two haplotypes are present in the two populations the others are unique to each the population;

✓ The presence of several unique haplotype can be an indication that the abundance of population is fluctuating leading probably the accumulation of new mutations.

haplotype	N	Angola	Namibia
Hap_1		19	48
Hap_2		38	37
Hap_3		1	0
Hap_4		1	0
Hap_5		1	0
Hap_6		1	0
Hap_7		1	0
Hap_8		1	0
Hap_9		1	0
Hap_10		1	0
Hap_11		1	0
Hap_12		1	0
Hap_13		1	100
Hap_14		1	100
Hap_15		1	100
Hap_16		1	100
Hap_17		1	100
Hap_18		1	100
Hap_19		1	0
Hap_20		1	0
Hap_21		1	0
Hap_22		1	0
Hap_23		1	0
Hap_24		1	0
Hap_25		1	0
Hap_26		1	0
Hap_27		1	0

Genetic structure of populations

Trachurus capensis



Source variation	Variance components	% variance	Φ Statistics	P-value
Inter-populations	-0,00246	-0,67	-0,0067	>0,05
Intra- populations	0,36955		100,67	>0,05

- ✓ A large genetic variation is found within each population, in this case, Angola and Namibia ;
- ✓ No genetic differentiation was found among populations.

Final Remarks

- ✓ According to Sardinha and Naeval (2002) studies with using isozymes was suggested the existence of two genetic groups on the Angola coast, one in tropical waters and another group in the south. However, the present study based on a different molecular marker did not show genetic differentiation among populations of *T. trecae*;
- ✓ The genetic variability is within the range for fish marine species, there was no signal for decrease due to fisheries activity , at least using the Cytochrome b;
- ✓ For *T. capensis*, the analysis showed no difference among populations caught in Angola and Namibia, suggesting that no oceanographic barriers exist that prevent gene flow between stocks captured in Angola and Namibia;
- ✓ Due to the economic importance of *T. tracea* and *T. capensis* for fisheries along the Angola and Namibia coast, it is pivotal to develop other more polymorphic molecular markers, such as Microsatellites, specific for the species to further genetic monitoring of *Trachurus* populations for their sustainable use.