

Genetic studies on shrimp and groundfish

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Jeremy J. Mendoza

Farfantepenaeus spp

Gusmao 2005. Used allozymes to estimate variability levels and population genetic structure of *F. brasiliensis*, *F. paulensis*, *L. schmitti* and the recently detected species *Farfantepenaeus* sp. along as much as 4,000 km of Brazilian coastline.

No population heterogeneity was detected in *F. brasiliensis* or *L. schmitti* along the studied area. In contrast, F_{st} values found for *Farfantepenaeus* sp. and *F. paulensis* indicate that the populations of those two species are genetically structured, comprising different fishery stocks.

In *Farfantepenaeus* sp., significant differences were detected between the population from Recife and those from Fortaleza and Ilhéus

Gusmao 2005



Table 2 - Pair-wise χ^2 values found between populations of *Farfantepenaeus paulensis* and of *Farfantepenaeus* sp.

Species	Populations	χ^2 F _{ST}	χ^2 contingency
<i>F. paulensis</i>	Santos/Lagoa dos Patos	10.14**	49.69***
	Rio/Lagoa dos Patos	9.26*	42.31***
	Rio/Santos	2.52 ^{NS}	25.71*
<i>Farfantepenaeus</i> sp.	Fortaleza/Recife	5.13 ^{NS}	27.49*
	Fortaleza/Ilhéus	2.59 ^{NS}	20.69 ^{NS}
	Recife/Ilhéus	4.96*	30.57**

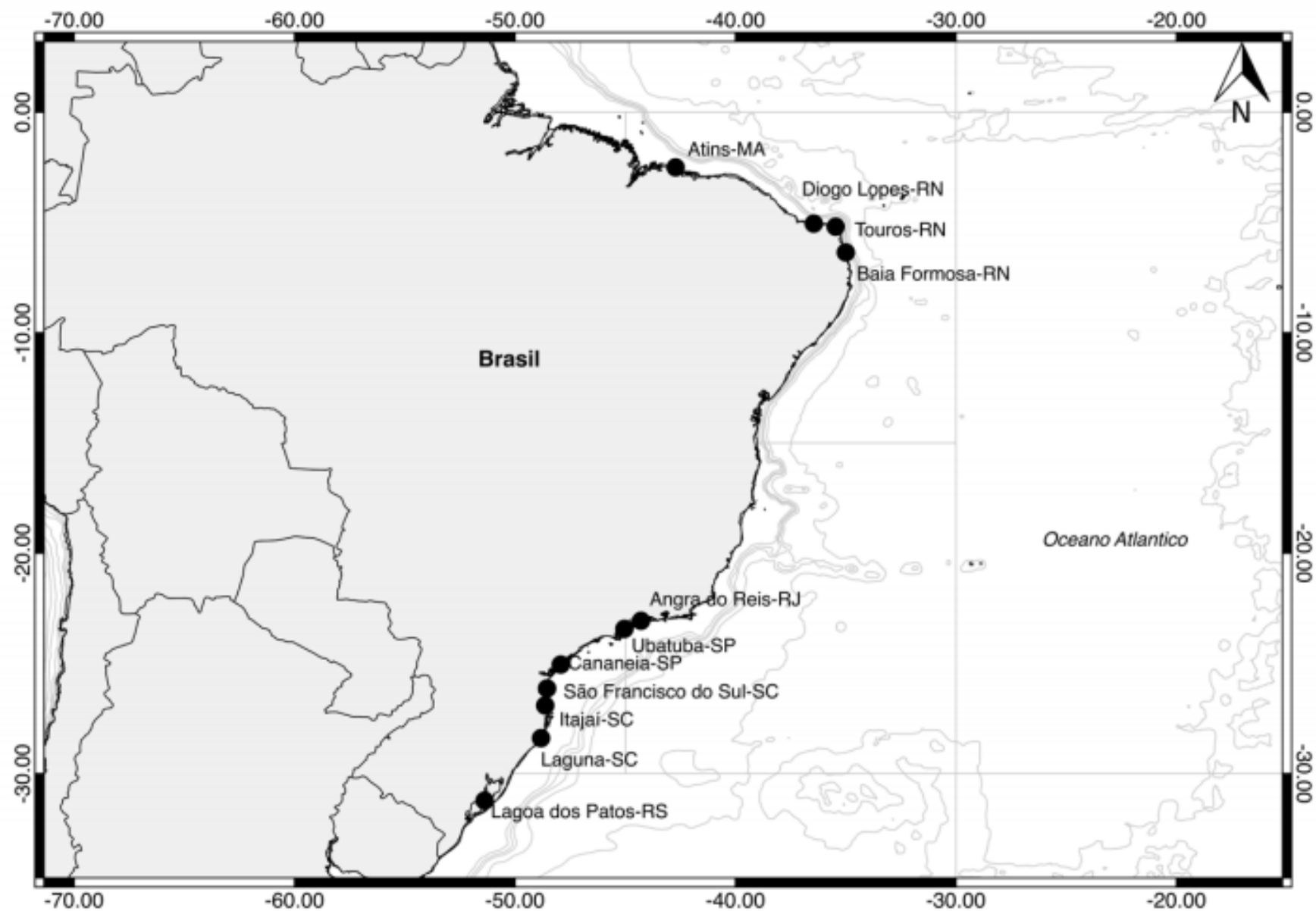
^{NS} - Not significant; $p > 0.05$.

* $p < 0.05$. ** $p < 0.01$. *** $p < 0.001$.

Farfantepenaeus spp

- Mitochondrial and nuclear markers were used in order to clarify aspects related to the geographic distribution and genetic relationships among the studied penaeid species (*Xiphopenaeus kroyeri*, *Farfantepenaeus paulensis*, *F. subtilis* and *F. brasiliensis*)
- The existence of species complex was investigated for both *X. kroyeri* and *F. subtilis*.
- Phylogeographical signs and population structure were not observed for *F. subtilis* along the Brazilian coast
- All tests performed to investigate population structuring in *F. subtilis* morphotype II point to the existence of a unique population along the Brazilian coastline. Similar results were obtained for *F. brasiliensis*. The author cautioned, however, on the low sample size for both species.

Marques, 2015



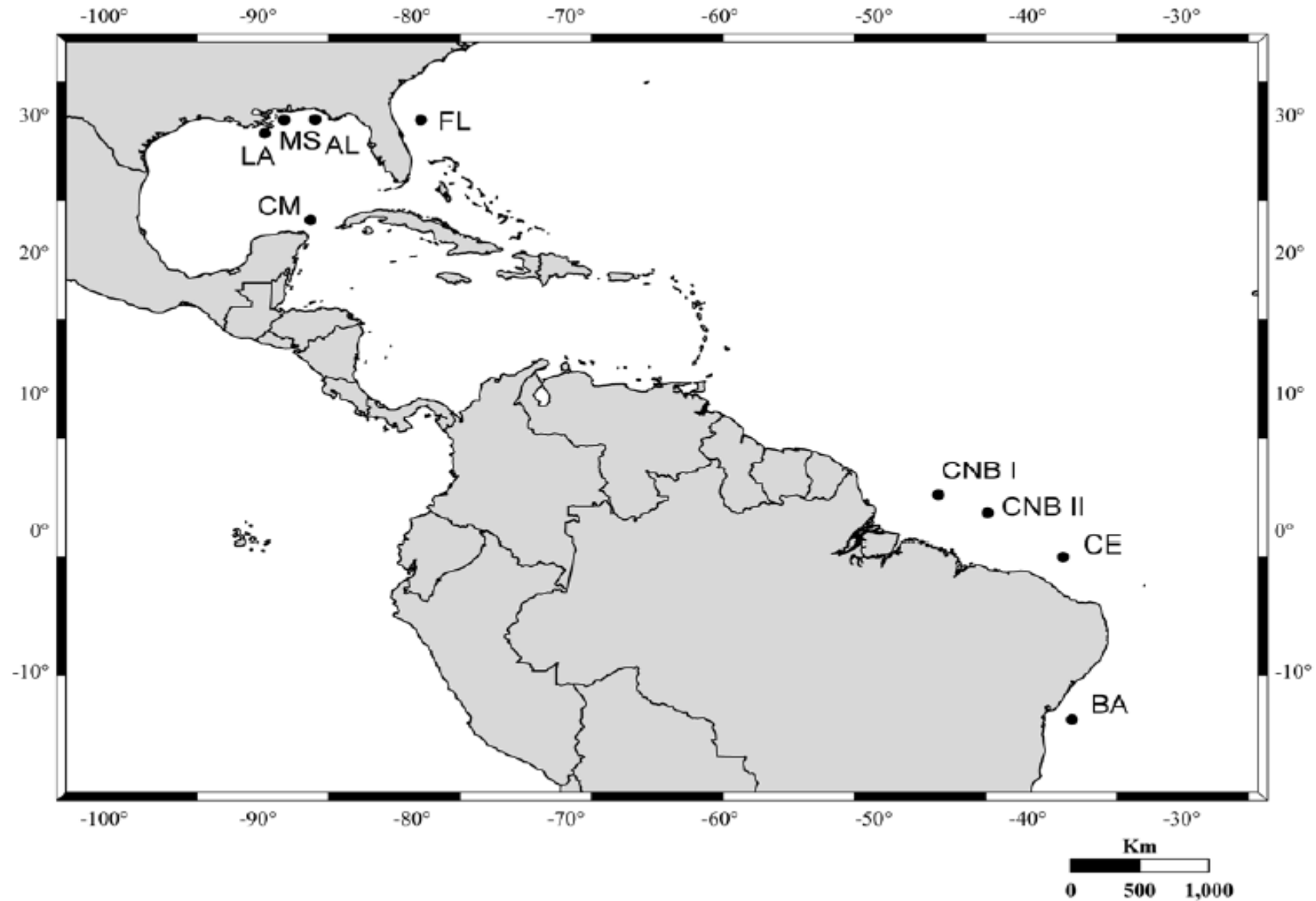
Lutjanus purpureus

Gomes et al. 2008. found that morphological and the present mitochondrial data were not able to discriminate between the two Atlantic red snappers species (*L. campechanus* and *L. purpureus*), the most plausible and parsimonious hypothesis would be that *Lutjanus* from the North and South Atlantic Ocean represent slightly different populations of a single species with a large geographical distribution

Gomes et al. 2012. This study focused on the mitochondrial control region to investigate phylogeographic patterns and population structure in *Lutjanus purpureus*, and to evaluate the genetic similarity between *L. purpureus* and *L. campechanus*.

A total of 810 base pairs sequence from control region were obtained from 239 specimens of *L. purpureus* collected from four localities off the Brazilian coast. The results revealed the presence of a single panmictic population characterized by high values of genetic diversity.

L. purpureus Gomes et al. 2012



Lutjanus purpureus

Da Silva et al. 2016 used a multilocus approach (12 segments of mitochondrial and nuclear DNA) to elucidate the levels of genetic diversity and genetic connectivity of *L. purpureus* populations and their demographic history.

L. purpureus had high levels of genetic diversity, which probably implies high effective population sizes values for the species.

The data show that this species is genetically homogeneous throughout the geographic region analyzed, most likely as a result of dispersal during larval phase.



Fig 1. Map of the spatial distribution of *L. purpureus* specimen collection points used in this study. CNB1- North Coast of Brazil 1 (Pará and Amapá). CNB2- North Coast of Brazil 2 (Maranhão). Map created in GMT 5.1.2 [14].

Cynoscion acoupa.

Rodrigues et al. 2008 In this study, DNA sequences were determined from the entire control region (D-loop) of the mitochondrial genome of 297 individuals collected during seven different months between December 2003 and August 2005 on the northern coast of Brazil (Amapá and Pará states). Samples were obtained from the fish market at Braganca.

Genetic variability expressed by haplotype ($h = 0,892$) and nucleotide ($\pi = 0,003$) diversities were low compared to other heavily exploited marine fish species from the western Atlantic and eastern Asia.

AMOVA depicted a lack of genetic structuring among the samples from different years, indicating the presence of a single stock of *C. acoupa* within the sample area.

Macrodon ancylodon

Santos et al. 2003 studied differences between king weakfish populations using cytochrome b and 16S rRNA genes to characterize *M. ancylodon* specimens caught throughout its South American range from Venezuela to Argentina.

Results clearly distinguished two genetically different groups which show nucleotide divergence and genetic structuring patterns that strongly suggest they may be different species.

The data indicated the existence of two panmictic and genetically isolated *Macrodon* populations, one, the tropical group, being distributed from Venezuela to Pernambuco and the other, the subtropical group, occurring from São Paulo to Argentina.



Macrodon ancylodon

Santos et al. 2006 studied phylogeographic patterns in *Macrodon ancylodon* sampled from 12 locations across all its range were investigated using mitochondrial DNA cytochrome b sequences, and analysed together with patterns of morphometric differentiation.

Populations of the North Brazil and the Brazil currents, with warmer waters, form a clade (tropical clade) separated by 23 fixed mutations from the populations that inhabit regions of colder waters influenced by the Brazil and Malvinas currents (subtropical clade).

No gene flow exists between the tropical and subtropical clades, and most likely also between the two groups of the tropical clade.

Distribution of these clades and groups is correlated with flow of currents and their temperatures, and is facilitated by larval retention and low adult migration. Despite differentiation at the molecular level, fishes analysed from all these current-influenced regions are morphometrically homogeneous.

