

## Genetic Structure of Brazilian Populations of White Mouth Croaker *Micropogonias furnieri* (Perciformes : Sciaenidae)

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### ABSTRACT

Mitochondrial (mt) DNA population structure was examined by using restriction fragment length polymorphism analysis (RFLP) among 149 white mouth croakers (*Micropogonias furnieri*) sampled from six locations in the Brazilian coast. Heterogeneity tests revealed no differentiation in mtDNA haplotype frequencies within the region between 23°S and 34°S ( $P=0.263$ ), but significant heterogeneity was detected between north and south of 23°S ( $P<0.003$ ). Analysis of molecular variance (AMOVA) indicated a low  $F_{ST}$  value (0.008,  $P=0.180$ ) among south-central localities (23-34°S), but a significant level of population subdivision ( $F_{ST} = 0.322$ ,  $P < 0.003$ ) between north and south-central localities. UPGMA analysis of mtDNA sequence divergence revealed differentiation between white mouth croakers collected from north and south of 23°S. Mantel test found significant association between matrices of genetic distance and geographic distance among samples. Collectively, these data were consistent with a single genetic stock of *Micropogonias furnieri* in the Brazilian coast, with semi-isolated populations occurring in the north and south of 23° S.

**Key words:** Genetic population structure, mitochondrial DNA, RFLP, *Micropogonias furnieri*

### INTRODUCTION

White mouth croaker (*Micropogonias furnieri*) is a euryhaline sublittoral sciaenid fish that uses estuarine and coastal waters as nursery and feeding grounds for larvae and juveniles. The species is distributed from the Yucatan Peninsula, Gulf of Mexico, at 20° N, to the Gulf of San Matias, Argentina, at 41° S (Chao, 1978), but it is particularly abundant on the southeastern shelf of Brazil (south of 23° S) and the shelf of Uruguay.

*M. furnieri* is an important commercial fishery resource along the Southwestern Atlantic shelf. Population dynamics, distribution and abundance vary considerably on both a spatial and temporal

basis, especially in the southern part of the species' range, and appear to be related to environmental factors. In view of their widespread distribution, *M. furnieri* inhabit water masses with different temperature - salinity combinations. This species is found all year in estuaries and brackish waters that vary from 0.1 to 32.8 ‰ and from 11 to 28 °C, and also in waters where winter temperatures and salinities average 9 °C and 20 ‰, respectively. Off the coast it is common in waters of 30 ‰, and 13 to 25° C (Isaac, 1988). Analyses of the catch per unit effort (CPUE) for *M. furnieri* indicate constant levels of abundance throughout the year between 23° S and 28° S, and a systematic variation in abundance with season in waters off southern Brazil between 28° S and 35°

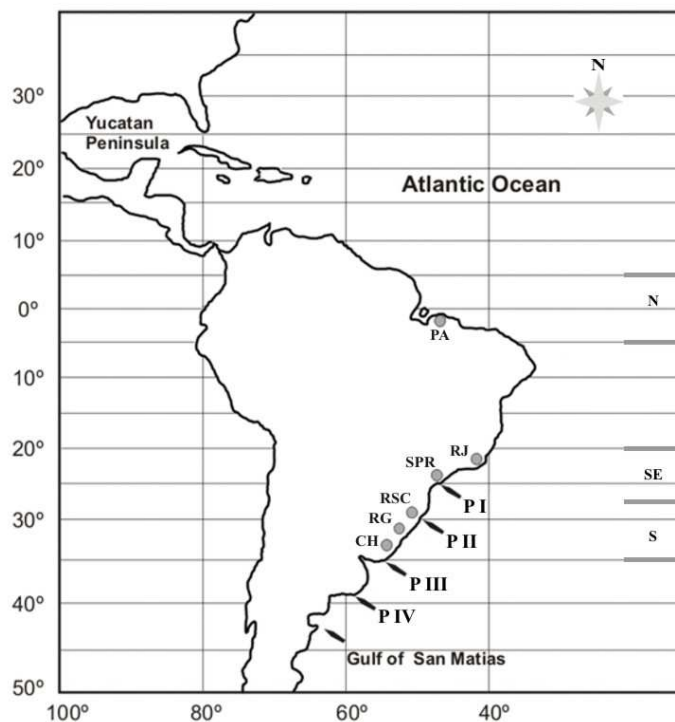
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S (Vazzoler, 1963). Variation in abundance off southern Brazil and Uruguay suggest that fish population migrate southward during summer ( $32^{\circ}$  S -  $35^{\circ}$  S) and northward during winter ( $28^{\circ}$  S -  $31^{\circ}$  S), according to the seasonal displacements of the convergence of subtropical and subantarctic waters (Vazzoler and Santos, 1965; Paiva-Filho, 1977). The subtropical convergence system is situated off the coast of Uruguay ( $35^{\circ}$  S) during summer and north of Santa Catarina ( $27-28^{\circ}$  S) in winter (Emilsson, 1961) and represents a marked transition of temperature and salinity, governing biological production and trophic interactions (Oderbrecht and Castello, 2001).

Recently, concern has been expressed over the apparent decline in the white mouth croaker fishery along the coast of Brazil, Uruguay and

Argentina (Haimovici, 1998). Distinct coastal zone policies and the absence of comparable information on status and trends of the ecosystem have been an obstacle towards an integrated fishery management program among these countries (Oderbrecht and Castello, 2001).

One important question to present and future management is whether discrete breeding units or populations occur within the species range. The status of white mouth croaker populations north of  $23^{\circ}$  S has not been well investigated, although combined data on reproductive features suggest the existence of a population between  $6^{\circ}$  N and  $2^{\circ}$  S (Lowe-McConnell, 1966; Juras, 1984). Available information on population structure south of  $23^{\circ}$  S appears contradictory.



**Figure 1** - Distribution of *M. furnieri* on the Atlantic Ocean (modified from Isaac, 1988). P I, P II, P III, and P IV represent the four hypothesized populations based on biology and morphological studies. N, SE and S are coastal Brazilian regions defined based on environmental characteristics and types of fishing activities. Gray spots (CH, RG, RSC, SPR, RJ and PA) are the six collection sites of the present study.

Geographic variation in meristic characters, body proportions, reproductive and growth features suggest the existence of four partially isolated populations of *M. furnieri* along the southwestern Atlantic (Fig. 1). Vazzoler (1971) described two

different populations in the region between  $23^{\circ}$  S and  $33^{\circ}$  S: population I ( $23-29^{\circ}$  S), with a spawning area in the estuarine lagoon region of Cananéia ( $25-26^{\circ}$  S), and population II that spawned in the Lagoa dos Patos ( $32^{\circ}$  S) and other

coastal waters off Rio Grande do Sul (29-33° S). In the Rio de la Plata region and coastal waters of Uruguay and Argentina, Alamón (1983) reported that *M. furnieri* probably formed one population with spawning and nursery areas in the Rio de la Plata (population III, between 35° S and 38° S), and another population distributed along the oceanic coast of Uruguay and the southern Brazil (population II). Cotrina (1986) suggested the existence of a fourth population with a spawning area in Bahia Blanca (39-40°S).

Genetic studies of *M. furnieri* using starch-gel electrophoresis of allozymes did not support the multiple-stock hypothesis and confirmed the existence of a single population unit along the southwestern Atlantic coast. Maggioni et al. (1994) and Levy et al. (1998) found a high degree of genetic homogeneity in allele frequencies and also high levels of gene flow among white mouth croaker sampled from regions between 23° S and 40° S.

Recent studies have shown that restriction fragment length polymorphism analysis (RFLP) of mtDNA is more powerful than protein electrophoresis for differentiating populations within several economically important fish species (Avisé, 1994). MtDNA is a haploid, circular, and non-recombinant molecule that evolves rapidly and provides character states whose phylogenetic relationships can be deduced (Wilson et al., 1985). The geographic distribution of branches in an intraspecific mtDNA phylogeny constitutes the maternal phylogeographic patterns of a species (Avisé et al., 1987). In the present work, we examined mitochondrial DNA (mtDNA) population structure in *M. furnieri* along the Brazilian coast between 1° S and 34° S latitude. Our purposes were to (1) estimate levels of genetic variation within and between localities from Brazilian coast, (2) estimate levels of genetic divergence among localities, and (3) further test the hypothesis that white mouth croaker populations are spatially subdivided, to provide an improved basis for future fishery management.

## MATERIALS AND METHODS

*Micropogonias furnieri* of Brazilian coastal areas were obtained from commercial fishery during late 1999 and early 2000. Freshly caught tissue samples were removed and preserved at 95%

ethanol for genetic analyses. Code names and locations of sample collections are presented in Fig. 1 and Table 1. Sample localities represent the southern (S), southeastern (SE), and northern (N) regions of the species' Brazilian coast range. Regions were defined based on environmental characteristics and types of fishing activities, as suggested by Matsuura (1995). Pooled southeast (SPR and RJ) and southern (CH, RG and RSC) sample localities also represented the geographical distribution of populations I and II, RG and SPR respectively corresponding to the spawning areas of these hypothesized populations.

PA sample was included in analyses to test for population identity in the northern Brazil and was compared to south and southeastern localities for investigating population differentiation among north and south region of 23° S. Collections along the northeastern coast could not be made in this study.

Mitochondrial DNA population structure was examined by using polymerase chain reaction (PCR) and restriction fragment length polymorphism analysis (RFLP). MtDNA extracts were obtained by the procedure of Chow and Inowe (1993). Primers L-THR (5'-3': AGC TCA GCG CCA GAG CGC CGG TCT TGT AAA) and 12 SAR-H (5'-3': ATA GTG GGG TAT CTA ATC CCA GGT) were used in PCR to amplify a 1450 bp product of mtDNA containing the entire D-loop region, tRNA-Pro and tRNA-Phe genes, and portions of the tRNA-Thr and 12S rRNA genes (Lankford Jr. et al., 1999). Amplifications were performed in 50 µl reaction volume containing 1X PCR Buffer, 0.2 mM of dNTP, 2.0 mM of MgCl<sub>2</sub>, 30 pmol of each primer, 1.5 U of *Taq* polymerase, and 20 ng of DNA template. PCR reactions were programmed for 35 cycles at 94° C for 1 min, 65° C for 1 min and 72° C for 2 min, including a final extension at 72° C for 8 min in the last cycle.

PCR products were digested with the following nine restriction endonucleases: Bgl I, EcoR I, EcoR V, Hae III, Hinf I, Hpa II, Pst I, Rsa I, and Sac II. Variant RFLP patterns were separated by gel electrophoresis on 1.5 % agarose gels and visualized after ethidium bromide with UV light illumination (Sambrook et al., 1989). Fragment sizes were estimated by using 1 Kb DNA ladder and Ø 174 - Hae III molecular weight markers, and UVIdoc software program, ver. 98.01.

**Table 1** - White mouth croaker collection data.

Sample	Location	Date	N	Coastal region
CH	Chui (RS) 33° 41' S 53° 27' W	Mar 2000	16	S
RG	Rio Grande (RS) 32° 00' S 52° 20' W	Dec 1999	32	S
RSC	Torres (RS) 29° 20' S 49° 43' W	Dec 1999	25	S
SPR	Paranaguá (PR) Cananéia (SP) 25° 31' S 48° 30' W	Jan 2000	37	SE
RJ	Itaipu (RJ) 22° 54' S 43° 13' W	Feb 2000	28	SE
PA	Ajuruteua (PA) 01°03' S 46° 46' W	Apr 2000	11	N

Distinctive RFLP patterns were identified by letter codes and combined to produce composite mtDNA haplotypes for each individual fish.

Statistical analyses were performed with the Arlequin Package, ver. 2000 (Schneider et al., 2000). Gene diversity and nucleotide diversity were calculated for each sample and for the pooled samples, according to Nei (1987). The distribution of mtDNA haplotype frequencies was evaluated for homogeneity between samples using P-exact test of population differentiation (Raymond and Rousset, 1995) and a total of 10,000 steps in Markov chain. *P*-values < 0.003 were considered as significantly different, after Bonferroni sequential procedure. Population structure in *M. furnieri* was also calculated by using a hierarchical analysis of molecular variance (AMOVA, Excoffier et al., 1992). Samples were stratified by locality (PA, RJ, SPR, RSC, RG, and CH) and nested within region (N, SE, and S). Total genetic variation was partitioned into covariance components “within geographic localities”, “among geographic localities”, and “between regions”. Covariance components were used to compute fixation indices in terms of inbreeding coefficients. The significance of fixation indices was tested using 1,000 random permutations to generate null distributions for each variance component. An Euclidian distance matrix between

pairs of haplotypes was used for the computation of a minimum spanning tree between haplotypes, and also for the calculation of pairwise  $F_{ST}$  values as short-term distances between populations. The null distribution of pairwise  $F_{ST}$ s under the hypothesis of no difference between populations was obtained by permuting haplotypes between populations. *P*-values < 0.003 were considered as significantly different. Percent mean nucleotide sequence divergences within and among samples were estimated by the average number of pairwise differences within and between populations (Nei and Li, 1979). The sample genetic distance matrix was clustered using unweighed pair-group method with arithmetic means (UPGMA) in Inference Phylogeny Package (PHYLIP), version 3.5 (Felsenstein, 2000). A matrix correlation (Mantel) test was carried out between the sample genetic distance matrix and a matrix of geographic distances (in miles) between all pairs of sample localities. A total of 1,000 permutations were employed to test the significance level of the Mantel correlation.

## RESULTS AND DISCUSSION

RFLP analysis of the D-loop regions revealed a total of 23 unique fragments, 16 restriction sites

and five composite mtDNA haplotypes in *M. furnieri* collected from the Brazilian coast (Table 2). Only two of the nine enzymes employed (Hinf I and Rsa I) produced variant patterns. The digestion profiles of variants were consistent with the hypothesis of single gains or losses of restriction sites.

Of the 149 individuals surveyed, 116 (78%) shared the same haplotype. Haplotype 1 (h1) was numerically dominant (> 0.70% frequency) at all localities, except northern sample (PA, 0.45% frequency). The haplotype 4 occurred at 0.55% frequency in PA, at low (< 0.18%) frequencies in the other samples, and it was absent in CH sample. The haplotype 3 was present at 25% frequency in CH, at very low (< 0.08%) frequencies in the other samples and it was absent in PA. The haplotype 2 occurred at low (< 0.12%) frequencies in RG and RSC samples and the haplotype 5 at 0.04% frequency only in RSC sample. The minimum

spanning tree between all pairs of haplotypes showed that geographically segregated haplotypes were closely related (1-2 restriction site changes) to the common haplotype (h1).

Gene diversity averaged  $0.388 \pm 0.097$  (mean  $\pm$  SE) for the pooled sample and ranged from  $0.203 \pm 0.084$  in SPR to  $0.546 \pm 0.072$  in PA. Nucleotide diversity also varied geographically, ranging from  $\pi = 0.086 \pm 0.071$  in SPR to  $\pi = 0.216 \pm 0.141$  in RSC (Table 3). Estimates of gene and nucleotide sequence diversities indicated that mtDNA variation in *M. furnieri* was lower than that in most other marine fish species surveyed to date (Gold and Richardson, 1991; Avise, 1994; Lankford Jr. et al. 1999). Mean values were only larger than those reported for the weakfish *Cynoscion regalis* (Graves et al., 1992) and the Atlantic black sea bass *Centropomus striata* (Bowen and Avise, 1990).

**Table 2** - Distribution of *Micropogonias furnieri* mtDNA haplotypes based on restriction endonucleases among different collections. The order of restriction enzyme morphs, represented from left to right, is HinfI and RsaI.

Haplotype	Sample						Total
	CH	RG	RSC	SPR	RJ	PA	
h1 (AA)	12	27	17	33	22	5	116
h2 (AB)	0	1	3	0	0	0	4
h3 (AC)	4	2	1	3	1	0	11
h4 (BA)	0	2	3	1	5	6	17
h5 (BB)	0	0	1	0	0	0	1
Total	16	32	25	37	28	11	149

**Table 3** - Gene and nucleotide diversity (mean  $\pm$  SE) in *M. furnieri* collected from the Brazilian coast.

Sample Locality	Gene	Nucleotide Diversity
	Diversity	
CH	$0.400 \pm 0.114$	$0.178 \pm 0.125$
RG	$0.288 \pm 0.102$	$0.113 \pm 0.087$
RSC	$0.527 \pm 0.110$	$0.216 \pm 0.141$
SPR	$0.203 \pm 0.084$	$0.086 \pm 0.071$
RJ	$0.362 \pm 0.100$	$0.133 \pm 0.098$
PA	$0.546 \pm 0.072$	$0.182 \pm 0.131$

Average nucleotide divergence within (1.362%) and among (0.248%) pooled samples indicated that most of observed mtDNA variation occurred within geographic localities. There were no significant levels of mtDNA divergence between

southeast and southern localities (except between RJ and CH samples), but significant differences occurred between northern (PA) and all others samples (Table 4).

UPGMA clustering-analysis of mtDNA genetic distances (Table 4) indicated that white mouth croaker from the north and the south of 23° S were genetically distinguishable from one another (Fig. 2). The correlation (Mantel) test between matrices of sample genetic distances and geographic distances was significantly different from zero (0.883,  $P < 0.003$ ), and revealed a geographic component to the distribution of mtDNA haplotypes in *M. furnieri*.

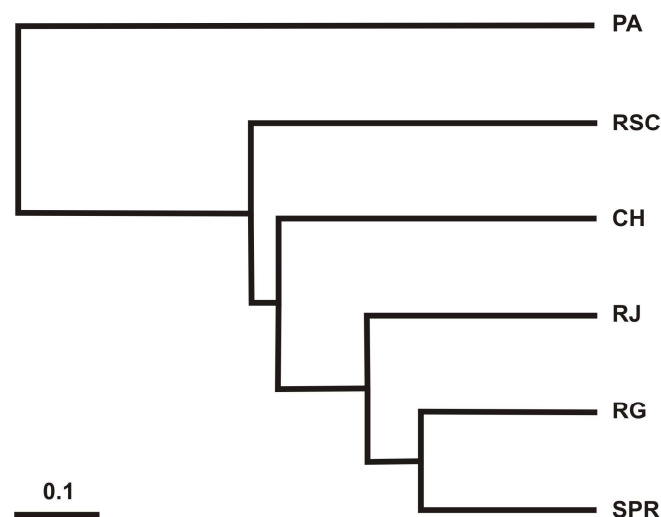
AMOVA also revealed that the majority (87.24%) of mtDNA variation in *M. furnieri* occurred within sample localities ( $P < 0.002$ ). A significant portion (3.72%) was attributable to differences among localities ( $P = 0.047$ ), but variation between regions (9.04%) was not significantly structured ( $P = 0.112$ ). Pairwise  $F_{ST}$  values ranged from -

0.023 to 0.446 and averaged 0.134 (Table 5). The  $F_{ST}$  value found in *M. furnieri* was higher than those reported in other sciaenid: 0.046 for *Micropogonias undulates* (Lankford Jr. et al. 1999), and 0.057 for *Sciaenops ocellatus* (Gold and Richardson, 1991).

Population structure in *M. furnieri* was indicated by genetic differentiation between PA and CH sample localities ( $F_{ST} = 0.387$ ,  $P < 0.003$ ), which represented both limits of the species' range in this study (1° S - 34° S). Differentiation was also observed between PA and RG, and PA and SPR localities. PA, SPR, and RG respectively represented spawning areas of *M. furnieri* on the north, southeast and southern Brazilian shelf.

**Table 4** - Average number of pairwise differences (Nei and Li, 1979) within population (diagonal elements) and between populations (above diagonal). Below diagonal: corrected average pairwise difference. Bolded elements were estimated as significantly different ( $P < 0.05$ ).

	CH	RG	RSC	SPR	RJ	PA
CH	1.600	1.375	1.880	1.243	1.607	2.636
RG	0.066	1.018	1.496	0.876	1.121	1.963
RSC	0.107	0.014	1.947	1.422	1.593	2.233
SPR	0.056	-0.021	0.061	0.775	1.032	1.953
RJ	<b>0.208</b>	0.012	0.020	0.045	1.198	1.731
PA	<b>1.018</b>	<b>0.636</b>	<b>0.441</b>	<b>0.748</b>	<b>0.313</b>	<b>1.636</b>



**Figure 2** - UPGMA phenogram showing genetic distances (Nei and Li, 1979) among white mouth croaker sample localities.

**Table 5** -  $F_{ST}$  values of population differentiation in *M. furnieri* along the Brazilian coast. Bolded values were significantly different ( $P < 0.003$ ).

	CH	RG	RSC	SPR	RJ
CH	0.000				
RG	0.058	0.000			
RSC	0.054	0.012	0.000		
SPR	0.065	-0.023	0.052	0.000	
RJ	0.137	0.011	0.014	0.047	0.000
PA	<b>0.387</b>	<b>0.359</b>	0.189	<b>0.446</b>	0.198

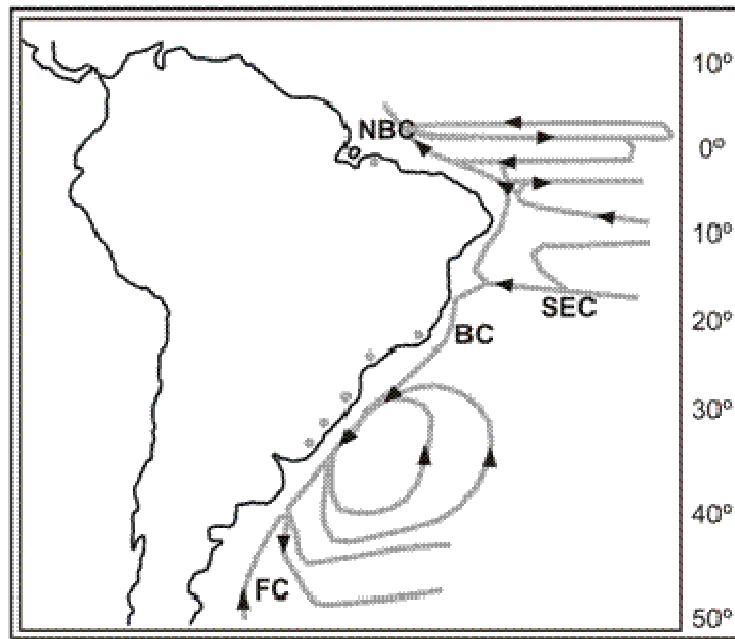
The P-exact test of population differentiation revealed significant differences ( $P < 0.003$ ) in mtDNA haplotype frequencies between PA and CH, and between PA and SPR samples. Given the lack of heterogeneity between pooled south (CH, RG and RSC) and southeastern (SPR and RJ) sample localities ( $P = 0,263 \pm 0,009$ ), composite haplotype frequencies were pooled across south-central localities (23-34° S) and compared with the northern sample. Significant heterogeneity in mtDNA frequencies was found in the north versus south region of 23° S. AMOVA also indicated no significant mtDNA population subdivision between pooled southeast and southern sample localities ( $F_{ST} = 0.008$ ,  $P = 0.180$ ), but significant genetic differentiation was found between north and south-central Brazilian coast ( $F_{ST} = 0.322$ ,  $P < 0.003$ ).

The geographic structure of any species is a product of both historical and contemporary gene flow and is likely to have been affected by such factors as geographic or ecologic impediments to movement and dispersal capability (Bowen and Avise, 1990). In the case of *M. furnieri*, dispersal capability on the north and south region of 23° S may be affected by geographic variation in environmental factors between the tropical and subtropical circulation of water masses within the Southwestern Atlantic. Stramma and England (1999) demonstrated that subtropical South Atlantic was governed by the subtropical gyre, while the tropical circulation showed several depth-dependent zonal current bands (Fig. 3).

The observed genetic heterogeneity between *M. furnieri* in the north and south of 23° S suggested that migration rate was not high enough to preclude genetic divergence of populations by random drift (Slatkin, 1987). Spatial autocorrelation analysis of the distribution of mtDNA divergence over all Brazilian localities

indicated that geographically proximate localities were more similar genetically than were more geographically distant localities. The observed autocorrelation was consistent with isolation-by-distance patterns, whereby migration of individuals within the Brazilian shelf was inversely related to geographic distance from sample localities. Although genetic divergence in *M. furnieri* occurred between north (PA) and all other sample localities, population subdivision was only statistically significant between PA and CH, PA and RG, and PA and SPR. Particularly when the migration rate was small, selection could easily be strong enough to dominate the pattern of genetic differentiation, and either increased or decreased  $F_{ST}$  relative to the neutral case. However, significant assumption of allele neutrality could be an important source of error in the interpretation of population structure statistics and it must be considered with caution (Whitlock and McCauley, 1999). These observations indicated that white mouth croaker population was weakly subdivided, with semi-isolated populations occurring in the north and south region of 23° S.

In the south of 23° S, mtDNA analysis provided no evidence that *M. furnieri* is subdivided into discrete genetic stocks between south and southeastern Brazil (23° S - 34° S). Frequency- and distance- based analyses both suggested a single, panmictic population. Dispersal capability influenced genetic diversity of south and southeastern populations, but it was not able to cause significant divergence. Low levels of mtDNA divergence between southeast and southern localities (0.011%), although not statistically significant, were more consistent with a pattern of semi-isolation by distance rather than marked subdivision by the oceanographic patterns of the subtropical convergence system.



**Figure 3** - Circulation of water masses within the South Atlantic Ocean (modified from Stramma and England, 1999). In the northeastern Brazil, the South Equatorial Current (SEC) in the near-surface layer reaches the shelf of Brazil (near 16° S) and separates into the northward and southward flow of Brazil Current (NBC and BC). The southern Brazil shelf is influenced by the Subtropical Convergence system, made up of the confluence zone of southward flow of BC with the Falkland Current (FC).

MtDNA results supported the hypothesis of contemporary gene flow among south-central Brazilian coast and were in agreement with previous allozyme data reported by Levy et al. (1998), suggesting that migration rate among white mouth croaker populations was high enough to maintain the homogeneity in gene frequencies and therefore, avoided differentiation by genetic drift. The lack of genetic heterogeneity found within *M. furnieri* in both mtDNA and nuclear gene frequencies was supported by several aspects of the physical environment and white mouth croaker life history, which should facilitate dispersal and minimize geographic subdivision within the south-central Brazil. Lima et al. (1996) showed that the general form of the circulation of water masses in the southern Brazilian shelf could be characterized by a combination of different processes that presented high levels of gene flow in this area. *M. furnieri* are long-lived pelagic spawners (Vazzoler, 1971), meaning that individuals could spawn at multiple localities throughout their life-times. Since adult spawn near the mouths of bays or estuaries (Isaac, 1988), pelagic eggs and larvae could be transported to

adjacent bay or estuarine localities by oceanic currents. Some adults in the southern Brazil also may spawn offshore and that larvae and juveniles could enter various bays or estuaries at a later time (Barbieri, 1986). Although larvae and juveniles appear to remain in the bays and estuaries, some adults move into deeper waters and are capable of forming offshore schools that can migrate extensively (Paiva-Filho, 1977).

Combined with white mouth croaker life history patterns and nuclear data, the present mtDNA analysis supported the idea that species dispersal capability resulted from the interaction between physical environment conditions and species ecological requirements, and that life history variation when present, showed an ecophenotypic basis.

In other marine fishes with similar life histories and/or the capability for long-distance dispersal, genetic divergence is also typically small, and most of the genetic variation occurs within localities (Avice, 1994). Hierarchical analysis of variance presented here showed that a similar large component of mtDNA variance was found within populations. The low "among group" variance



component was likely to be the result of the narrow geographical range covered in this study and the part of the variance distributed among populations within groups could be attributed to the limited populations within each group. Thus, at the level of genetic resolution employed in this study, the null hypothesis that *M. furnieri* shared a common gene pool could not be refuted. RFLP technique proved sufficiently powerful to detect genetic heterogeneity within the north versus south region of 23° S, but did not reveal structured genetic stocks within the Brazilian coast between 23° S and 34° S. It would be interesting to apply this method on a larger geographical scale, with a sampling design that included more populations to investigate possible additional groupings. The hypothesized genetic stock boundary between south and southeastern Brazil could be tested further by using fine-scale markers such as microsatellites, or direct sequencing of the mitochondrial D-loop region to provide better resolution of geographic structure.

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## RESUMO

No presente estudo, a estrutura genético - populacional da corvina, *M. furnieri*, foi determinada ao longo da costa do Brasil entre as latitudes 1° S e 34° S, por meio da análise de fragmentos polimórficos de DNA mitocondrial (mtDNA) obtidos por enzimas de restrição (RFLP). Os objetivos foram: (1) documentar a magnitude da variação e a distribuição geográfica do mtDNA em *M. furnieri*, (2) testar a hipótese de subdivisão populacional em *M. furnieri* ao longo da costa do Brasil e (3) estimar níveis de diferenciação genética entre regiões, como base para o manejo pesqueiro e a conservação da espécie. A análise RFLP revelou um total de cinco haplótipos de mtDNA que apresentaram

freqüências de distribuição geográfica diferentes. Os testes de distribuição das freqüências haplotípicas não revelaram heterogeneidade genética entre as costas sudeste e sul do Brasil, entre 23° S e 34° S ( $P = 0,263$ ), mas houve diferenças significativas entre as regiões ao norte e ao sul de 23° S ( $P < 0,003$ ). Os resultados da análise de variância molecular (AMOVA) detectaram subdivisão populacional entre as localidades ao norte e ao sul de 23° S ( $F_{ST} = 0,322$ ,  $p < 0,03$ ), mas não indicaram diferenciação genética de 23° S a 34° S ( $F_{ST} = 0,008$ ,  $p = 0,180$ ). Os valores de distâncias genéticas foram estatisticamente significativos entre as amostras de *M. furnieri* nas regiões ao norte e ao sul de 23° S ( $p < 0,05$ ). O teste de correlação entre as matrizes de distâncias genéticas e distâncias geográficas (em milhas) revelou um componente geográfico significativo na distribuição do mtDNA ao longo da costa do Brasil. Estes dados confirmam a hipótese de uma única população de *M. furnieri* na costa centro-sul do Brasil, entre as latitudes de 23° S e 34° S, e indicam a existência de populações parcialmente isoladas ao norte e ao sul de 23° S.

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