

Cytogenetic studies in Brazilian marine Sciaenidae and Sparidae fishes (Perciformes)

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ABSTRACT. Fishes from the families Sciaenidae and Sparidae, the former comprising coastal species associated with shallow waters on the continental shelf and the latter composed of typically marine species, are of significant economic value. Karyotypic data are available for about 20% of the total number of species in these groups. In the present study, cytogenetic analyses were carried out in three Sciaenidae species, Menticirrhus americanus, Ophioscion punctatissimus and Pareques acuminatus, as well as in the sparid fish, Archosargus probatocephalus, using conventional staining (Giemsa) and Ag-nucleolar organizer regions (NORs) and C-banding techniques. The diploid values (2n) and number of chromosome arms were equal to 48 in all species analyzed. NORs were located at pericentromeric positions, equivalent to large heterochromatic blocks, in M. americanus (1st pair), O. punctatissimus (10th pair), P. acuminatus (2nd pair), and A. probatocephalus (3rd pair). Heterochromatin was detected at the centromeric position in most chromosome pairs, being more conspicuous among Scianidae members. The remarkable karyotypic conservativeness detected in these species is similar to that observed in other perciform groups previously studied, regarding both the number of acrocentric chromosomes and NOR location. However, unusual events of heterochromatinization seem to have taken place along the karyotypic evolution of members of the family Sciaenidae. For the family Sparidae, distinct cytotypes between samples of Northeast Brazil and those previously analyzed on the southeastern coast were identified, suggesting that putative biogeographic barriers

Genetics and Molecular Research 7 (2): 358-370 (2008)

Cytogenetic studies in Sciaenidae and Sparidae fishes

could be present throughout both regions on South Atlantic coast.

Key words: Fish cytogenetics; Sciaenidae; Sparidae; Chromosome stasis

INTRODUCTION

Evolutionary stasis has often been referred to as a common phenomenon, whether at a higher or a lower degree, in the karyotypic evolution of Perciformes species (Molina, 2006). Such condition is particularly notorious along the evolution of several fish families that lack a significant relationship between karyotypic changes and time of divergence.

Amongst the examples of marine fishes characterized by chromosomal stasis we can point out the members of the family Scianidae (croakers and drums), whose representatives share several symplesiomorphic cytogenetic features with other Perciformes groups, such as 2n = 48, fundamental number (FN) = 48, single and pericentromeric nucleolar organizer regions (NORs), scarcity of conspicuous heterochromatic blocks and a typical symmetrical karyotype (Galetti Jr. et al., 2006). Such scenario hinders the application of cytogenetic traits as efficient cytotaxonomic and phylogenetic markers within this fish group.

However, other families of Perciformes, such as Sparidae (porgies), show a higher karyotypic diversification (FN = 48-70). Although members of this family have been relatively well studied under a cytogenetic focus in the Indian and Pacific Oceans and Mediterranean Sea (Cataudela et al., 1980; Chakraborty, 1986; Vitturi et al., 1992), there are few available reports about sparids in the Atlantic (Barreto Neto et al., 1998).

The family Sparidae comprises nearly 37 genera and 125 species, and 27 of them were karyotyped. Members of this family are widespread over tropical and temperate waters in the Atlantic, Indian and Pacific Oceans. Most sparids live typically in salt water, with a few freshwater species. They are carnivores, preying mainly on benthonic invertebrates. Cases of synchronic and asynchronic hermaphroditism are frequent in this fish family (Froese and Pauly, 2007).

The scianids represent an important fishery resource and, just like sparids, are found throughout the Atlantic, Indian and Pacific Oceans (Nelson, 2006), comprising about 282 species distributed into 70 genera. They are marine coastal fishes associated with sandy bottoms and reproduce in estuaries, bays or open sea, producing eggs dispersed by tidal currents (Santos et al., 2006). So far, karyotypes are reported for 29 of the total number of Scianidae species (Froese and Pauly, 2007), such as, for instance, the 11 marine species analyzed by LeGrand and Fitzsimons (1988), two South American species (Gomes et al., 1983a,b; Pereira et al., 1988), and three Indian species as well (Chakraborty, 1986; Tripathy and Das, 1988), among others. Most scianids have a diploid number of 2n = 48 chromosomes, nearly all acrocentric (Feldberg et al., 1999).

In order to increase the available cytogenetic reports on both fish families, the goal of the present study was to characterize three marine species of the family Scianidae (*Menticirrhus americanus*, *Ophioscion punctatissimus* and *Pareques acuminatus*) and one species of the family Sparidae (*Archosargus probatocephalus*), through conventional staining, Ag-NOR staining and C-banding, helping to identify the evolutionary processes within these fish groups.

MATERIAL AND METHODS

Specimens of O. punctatissimus, M. americanus, P. acuminatus, and A. probatocephalus

Genetics and Molecular Research 7 (2): 358-370 (2008)

were collected at three sites on the coastline of the State of Rio Grande do Norte, Northeast Brazil: Redinha Beach (5°44'50.50''S, 35°12'10.52''W); Ponta Negra Beach (5°53'1.73''S, 35°9'57.85''W) and Búzios Beach (6°0'28.12''S, 35°6'19.23''W).

Prior to chromosome preparations, the specimens were mitotically stimulated by peritoneal inoculation of yeast suspension (glucose solution with *Saccharomyces cerevisae* at 1 mL/100 g body weight) for 24 h (Lee and Elder, 1980). To reduce the mortality rate in this step, mitotic stimulation was also performed by inoculation of a complex of bacterial and fungal antigens Munolan[®] (Allergan Fruntost) (76 mg suspended in 2.5 mL distilled water), at a proportion of 1 mL/50 g body weight for 24 to 48 h (Molina, 2001). Mitotic chromosomes were obtained by *in vitro* technique according to Gold et al. (1990). NORs and heterochromatic regions were identified by the methods described by Howell and Black (1980) and Sumner (1972), respectively. To establish the number of chromosome arms (FN), acrocentric chromosomes were classified as uni-armed. In order to allow a reliable comparison, the FN in previously reported data was recalculated based on the same criterion.

RESULTS

The chromosomal analyses in the four species showed a common diploid value of 48 chromosomes (Figures 1-4). The chromosomes were classified as acrocentric (FN = 48), with subtle size differences among chromosome pairs. Secondary constrictions related to NORs were observed in all species studied.

A	**							
	88	98	68	8.8	11	08	88	
	1	2	3	4	5	6	7	8
	68		98	41	88	50		00
	9	10	11	12	13	14	15	16
	88	0.8	89		3.6	98	6.0	
	17	18	19	20	21	22	23	24
в	A1	0.0	90	2.5	53	45	50	
	1	2	3	4	5	6	7	8
	6.6	01.	10	6.0	85	81	67	2.5
	9	10	11	12	13	14	15	16
	0.A	10	2.5	6.5	80	5.0	aσ	0.0
	17	18	19	20	21	22	23	24

Figure 1. Karyotype of *Menticirrhus americanus*. **A.** Giemsa staining, 2n = 48a. In detail, the NOR-bearing pair (1st pair). **B.** C-banding. Bar = 5 μ m.

Cytogenetic studies in Sciaenidae and Sparidae fishes

A	0ß	0.6	65	0.0	68	00	8.6	68
	1	2	3	4	5	6	7	8
	9	10 10	40 11	6 8 12	A B 13	AA 14	ቆ በ 15	AA 16
	6.0	ព៨	•					
	17	18	19	20	21	22	23	24
в	69	~ 1	人作	0 n	0.6	A.5.	A.A	80
	1	2	3	4	5	6	7	8
	0.0	6.5		Ŧ٨	6.6		0.0	nn.
	9	10	11	12	13	14	15	16
		45	**	AP			6.0	
	17	18	19	20	21	22	23	24

Figure 2. Karyotype of *Ophioscion punctatissimus*. **A.** Giemsa staining, 2n = 48a. In detail, the NOR-bearing pair (10th pair). **B.** C-banding. Bar = 5 μ m.

Α	81						
90	00	68	00	۸۸	00	44	nn
1	2	3	4	5	6	7	8
00	pr.	88	nn	02	44	An	00
9	10	11	12	13	14	15	16
00	nn	60	20	00	00	00	~~
17	18	19	20	21	22	23	24
В							
10			88	11			
1	2	3	4	5	6	7	8
20	84	88	88	11		8.0	
9	10	11	12	13	14	15	16
8.9			# A				
17	18	19	20	21	22	23	24

Figure 3. Karyotype of *Pareques acuminatus*. **A.** Giemsa staining, 2n = 48a. In detail, the NOR-bearing pair (2nd pair). **B.** C-banding. Bar = 5 μ m.

Genetics and Molecular Research 7 (2): 358-370 (2008)

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I.V. Accioly and W.F. Molina

A	86	8 8 2		8 A 4	6 6 5	^	80 7	8 8
		88				64		
	9	10	11	12	13	14	15	16
	1 7	8 A 18	N 9 19	2 0	21	8 22	2 3	2 4
В	13	20	11	61	64	6.0	63	14
	1	2	3	4	5	6	7	8
	45	11	12	11	- 9.0	0.1	1.0	11
	9	10	11	12	13	14	15	16
	15	0.1	11	41	01	0.0	0.0	
	17	18	19	20	21	22	23	24

Figure 4. Karyotype of *Archosargus probatocephalus*. **A.** Giemsa staining, 2n = 48a. In detail, the NOR-bearing pair (3rd pair). **B.** C-banding. Bar = 5 μ m.

The Ag-NOR sites in both Scianidae and Sparidae species were single and located at the pericentromeric position on distinct chromosome pairs according to the species. NORs were detected on the 1st pair in *M. americanus*, on the 2nd pair in the reef species *P. acuminatus*, on the 10th pair in *O. punctatissimus*, and on the 3rd pair in the sparid *A. probatocephalus*.

The pattern of heterochromatin distribution was also similar in the karyotype of the species analyzed, which showed heterochromatic blocks mainly located in the centromeric region. However, comparing the C-banded karyotypes, it was possible to observe a higher content of heterochromatin within Sciaenidae than in the Sparidae species. Pericentromeric and somewhat conspicuous blocks were identified on NORs and in some specific chromosomes. In *M. americanus*, a large heterochromatic segment was detected comprising up to two-thirds of the 8th chromosome pair (Figure 1B). A greater variation in heterochromatin content was observed in *O. punctatissimus* which had several chromosome pairs (1, 2, 4, 5, 6, 10, 16, 17) bearing heterochromatic blocks at the pericentromeric position (Figure 2B).

Genetics and Molecular Research 7 (2): 358-370 (2008)

DISCUSSION

Karyotypic stasis is more often detected in marine fish species. The marine realm, due to its high dispersal potential related to transportation of pelagic larvae through tidal flows and less effective biogeographic barriers, favors a higher connectivity among distant populations and, thus, leads to a reduced rate of chromosomal divergence. These characteristics, hypothetically, explain the maintenance of a stable karyotypic structure, resistant to chromosomal diversification processes, in most marine fish species (Molina, 2006).

Several reports have demonstrated that the degree of karyotypic differentiation (number of changes in FN values) in some families of marine reef Perciformes (i.e., Pomacentridae; Labridae) is inversely related to the dispersive potential provided by the extent of pelagic larval duration of each species (Molina and Galetti Jr., 2004; Molina, 2006; Sena and Molina, 2007).

A remarkable example of chromosomal stability within marine perciforms is present in the family Sciaenidae (Table 1). Such trend in chromosomal conservativeness, both numerical and structural, is corroborated by the present results obtained in the scianids M. americanus, O. punctatissimus and P. acuminatus.

Species	2n	FN	a/st	m/sm	NORs	C-banding	References
Aplodinotus grunniens	48	48	48a	-	-	-	LeGrande and Fitzsimons, 1988
Bairdiella chrysoura	48	48	48a	-	-	-	LeGrande and Fitzsimons, 1988
B. chrysoura	52	52	52a	-	-	-	Gregory et al., 1980
Cynoscion acoupa	48	48	48a	-	-	-	Brum, 1996
C. arenarius	48	50	46a/2st	-	-	-	Fitzsimons et al., 1985
C. arenarius	48	-	-	-	-	-	Ramirez, 1980
C. nebulosus	48	50	46a/2st	-	-	-	Fitzsimons et al., 1985
C. nebulosus	50	50	50a	-	-	-	Arkhipchuk, 1999
Johnius belangerii	48	48	48a	-	-	-	Chakraborty, 1986
J. borneensis / J. vogleri	48	48	48a	-	-	-	Patro and Prasad, 1979
J. carutta	48	48	48a	-	-	-	Patro and Prasad, 1979
J. dorsalis	48	48	48a	-	-	-	Raghunath and Prasad, 1980; Chanda, 1989
J. dussumieri	48	48	48a	-	-	-	Chanda, 1989
Kathala axillaris	48	48	48a	-	-	-	Tripathy and Das, 1988
Leiostomus xanthurus	48	48	48a	-	-	-	LeGrande and Fitzsimons, 1988
Menticirrhus americanus	48	48	48a	-	-	-	Gomes et al., 1983b
M. americanus	48	48	48a	-	-	-	Arkhipchuk, 1999
M. americanus	48	48	48a	-	s (1st pair); p	c, p	Present study
M. littoralis	48	48	48a	-	S	c, p	Reggi et al., 1986
Micropogonias furnieri	48	48	48a	-	-	-	Gomes et al., 1983a; Pereira et al., 1988
M. furnieri	48	48	42a/6st	-	S	с	Brum, 1996
M. undulates	48	48	48a	-	-	-	LeGrande and Fitzsimons, 1988
Nibea mitsukurii	48	48	48a	-	-	-	Ojima and Kikuno, 1987
Ophioscion punctatissimus	48	48	48a	-	s (10th pair); p	c, p	Present study
Otolithes cuvieri	48	48	48a	-	-	-	Chakraborty and Kagwade, 1989
Otolithoides pama	48	48	48a	-	-	-	Khuda-Bukhsh and Nayak, 1990
Paranibea semiluctuosa	48	48	48a	-	-	-	Chakraborty, 1986
Pareques acuminatus	48	48	48a	-	s (2nd pair); p	р	Present study
Plagioscion sp	48	48-50	48-46	2m	m (1st a/1st m); p	р	Feldberg et al., 1999
P. squamosissimus	48	48	48a	-	s (24th); p	p	Feldberg et al., 1999
Pogonias cromis	48	48	48a	-		-	LeGrande and Fitzsimons, 1988
Protonibea diacanthus	48	48	48a	-	-	-	Chakraborty and Kagwade, 1989
Sciaena umbra	48	48	48a	-	-	-	Vasil'ev, 1978
Sciaenops ocellatus	48	48	48a	-	S	- G	old et al., 1988; LeGrande and Fitzsimons, 1
Umbrina coroides	46	46	46a	-	-	-	Brum, 1996

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FN = fundamental number; a = acrocentric; st = subtelocentric; m = metacentric; sm = submetacentric; p = pericentromeric; c = centromeric; s = single nucleolar organizer region (NOR); m = multiple NORs.

The presence of 48 chromosomes, widespread in karyotypes of Perciformes, including several families and suborders, has been regarded as a primitive condition for this fish group (Galetti Jr. et al., 2000, 2006). Such diploid value, associated with the exclusive presence of acrocentric chromosomes (FN = 48), reflects a synapomorphic condition for modern teleosteans (Brum and Galetti Jr., 1997). Both structural and numerical conservativeness is extensively found within the family Scianidae, although variations related to increase or reduction of diploid number have already been reported, ranging from 2n = 46 in *Umbrina coroides* (Brum, 1996) to 2n = 52 in *Bairdiella chrysura*. The latter is characterized by a chromosomal variation determined by fissions, with cytotypes varying from 2n = 48 to 52 chromosomes (Gregory et al., 1980). Moreover, a few species may show variation in the number of chromosome arms related to pericentric inversions during karyotypic evolution (Takai and Ojima, 1987; Feldberg et al., 1999). However, this variation seems to be insignificant when compared to other Perciformes families, such as Nototheniidae (2n = 22-58; FN = 44-88) or Bathydraconidae (2n = 20-48; FN = 40-58) (Pisano and Ozouf-Costaz, 2000).

Within the family Sparidae, 22% of the species were karyotyped, revealing a higher degree of chromosomal variation regarding FN values when compared to Scianidae. The number of chromosome arms in this family may range from 48 to 70, with the presence of acrocentric, subtelocentric and submetacentric chromosomes. Most of the species karyotyped have been studied by different authors, sometimes showing discordant FN values for a single species (e.g., *Acanthopagrus latus*) (Table 2). Despite such variation in the chromosome formulae, the diploid number is still conserved among sparids (2n = 48), like the majority of marine Perciformes families studied so far (Sola et al., 1981; Galetti Jr. et al., 2000).

Comparative analyses about the frequency of chromosomal rearrangements in Atlantic Perciformes species have revealed some evolutionary trends within distinct groups (Galetti Jr. et al., 2006). The families Chaetodontidae, Haemulidae, Serranidae, and Sciaenidae were characterized by a low frequency, or even absence, of apparent structural chromosomal rearrangements (inversions, fusions and fissions). Such karyotypic conservativeness may be related to an evolutionary process based on chromosomal microdiversification driven by nondetectable changes in the karyotype.

The conserved pattern of karyotypic evolution in marine Perciformes has been associated with the interaction of distinct aspects, such as lack of well-defined geographic barriers, high inter-populational gene flow, dispersal potential of adults and/or larvae, and the common presence of large populations in marine ecosystems (Molina, 2006). The combined action of these features would restrain the fixation of polymorphic chromosomal rearrangements and lead to a reduced karyotypic diversification. This hypothesis is corroborated by the identification of some marine species bearing derived karyotypes that lack one or more of such features (Molina and Galetti Jr., 2004).

However, even freshwater Scianidae species, such as *Plagioscion squamosissimus* and *Plagioscion* sp, inhabiting inland waters and, therefore, more propitious to karyotypic diversification by the presence of more effective geographic barriers, share a similar karyotype structure (2n = 48 acrocentric) also found in their related marine representatives (Feldberg et al., 1999). These data, coupled with the present results, reinforce that, besides environmental partitions, whether related to physical or biological features, there should be an intrinsic condition for the maintenance of stable karyotypes in some groups.

Genetics and Molecular Research 7 (2): 358-370 (2008)

Spagios	22	EN	e/st	m/cm	NOP	C handing	Pafaranaas
Species	2n	FN	a/st	m/sm	NOKS	C-banding	Keterences
Acanthopagrus latus	48	58	38a/6st	4sm	-	-	Murofushi et al., 1983
"	48	58	38a/4st	4m/2sm	-	-	Lin and Liu, 1989; Jiahan
							and Lisha, 1989
Archosargus	48	48	48a	-	s (1a)	с	Present study
probatocephalus							
"	48	53	43a	1m/4sm	-	-	Law et al., 1978
"	48	50	46a	2m	-	-	Arkhipchuk, 1999
"	48	60	36a	4m/8sm	-	-	Fitzsimons et al., 1985
Acanthopagrus	48	58	38st	6m/4sm	-	-	Liu and Tian, 1991
schlegelii czerskii							
A. schlegelii schlegelii	48	58	38a/4st	6sm	-	-	Murofushi et al., 1983
"	48	56	40a	8sm	-	-	Kim et al., 1989
Boops boops	48	54	42a	4m/2sm	-	-	Cano et al., 1981
Chrysophrys auratus	48	50	46a/2st	-	-	-	Nishikawa and Karasawa, 1972;
	10						Liu and Tian, 1991
Dentex tumifrons	48	52	44a/4st	-	-	-	Arkhipchuk, 1999
	48	48	46a/2st	-	-	-	Murofushi et al., 1983
Diplodus annularis	48	54	42a/st	2m/4sm	-	-	Arkhipchuk, 1999
	48	56	40a/2st	6m/sm	-	-	Cataudella et al., 1980
	48	54	42a/st	6m/sm	-	-	Vitturi et al., 1996
	48	56	40a/2st	6m	-	-	Sola and Cataudella, 1978
"	48	54	42a	2m/4sm	-	-	Vasil'ev, 1978
D. argenteus argenteus	48	48	48a	-	-	-	Brum, 1996
D. bellottii	46	54	38a/st	2m/6sm	m (1a, 1sm)	-	Amores et al., 1993
D. cervinus cervinus	48	54	-	-	-	-	Amores et al., 1993
D. puntazzo	48	54	-	-	m (6 pairs)	-	Vitturi et al., 1996
D. sargus sargus	48	56	40a/2st	6m/sm	-	-	Cataudella et al., 1980
"	48	54	42a/2st	2m/2sm	-	-	Cano et al., 1981
"	48	54	42a/st	6m/sm	-	-	Vitturi et al., 1996
"	48	56	40a/2st	6m	-	-	Sola and Cataudella, 1978
D. vulgaris	48	54	42a/2st	2m/2sm	-	-	Cano et al., 1981
"	48	54	-	-	-	-	Vitturi et al., 1996
Evynnis japonica	48	50	46a	2sm	-	-	Murofushi et al., 1983;
							Manna, 1989
Lagodon rhomboids	48	54	42a	6m	-	-	Fitzsimons and Parker, 1985
Lithognathus mormyrus	48	70	26a/16st	6m/sm	-	-	Cataudella et al., 1980;
							Sola et al., 1981
"	48	70	26a/16st	6m	-	-	Sola and Cataudella, 1978
"	48	52	44a	2m/2sm	-	-	Cano et al., 1981
Oblada melanura	46	58	34a/6st	6m/sm	-	-	Cataudella et al., 1980;
"	16	50	24 16 1	6			Sola et al., 1981
	46	58	34a/6st	6m	-	-	Sola and Cataudella, 1978
Pagellus acarne	48	56	40a	2m/6sm	-	-	Arknipchuk, 1999
	48	52	44a	4m	-	-	Cano et al., 1981
	48	56	40a/6st	2m	-	-	Sola et al., 1981
"	48	56	40a/6st	2m	-	-	Sola and Cataudella, 1978;
	40	40	10				Cataudella et al., 1980
P. erythrinus	48	48	48a	-	-	-	Sola and Cataudella, 1978;
							Cataudella et al., 1980;
D .	40	40	40				Sola et al., 1981;
Pagrus auriga	48	48	48a	-	S	-	Vitturi et al., 1992
P. caeruleostictus	48	50	-	-	S	-	Vitturi et al., 1992
P. major	48	50	46a/2st	-	-	-	Nishikawa and Karasawa, 1972;
							Murofushi et al., 1983;
							Yu et al. 1993

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Genetics and Molecular Research 7 (2): 358-370 (2008)

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I.V. Accioly and W.F. Molina

Table 2 Continued

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Species	2n	FN	a/st	m/sm	NORs	C-banding	References		
P. major	48	48	48a	-	-	-	Kim et al., 1989		
P. pagrus	48	50	-	-	S	-	Vitturi et al., 1992		
"	48	50	46a	2sm	-	-	Barreto Neto et al., 1998		
Rhabdosargus sarba	48	60	36a/6st	6sm	-	-	Murofushi et al., 1983		
Sarpa salpa	48	64	32a/10st	6m	-	-	Sola and Cataudella, 1978;		
							Cataudella et al., 1980;		
							Sola et al., 1981		
"	48	58	38a	2m/8sm	-	-	Arkhipchuk, 1999		
"	48	54	42a/2st	2m/2sm	-	-	Cano et al., 1981		
Sparus aurata	48	66	30a/10st	8m/sm	S	-	Sola and Cataudella, 1978;		
-							Vitturi et al., 1992;		
							Cataudella et al., 1980		

FN = fundamental number; a = acrocentric; st = subtelocentric; m = metacentric; sm = submetacentric; c = centromeric; s = single nucleolar organizer region (NOR); m = multiple NORs.

Population studies based on mtDNA sequences in the scianid *Macrodon ancylodon* along the Brazilian coast identified genetic differences between populations from north-north-eastern shore, under influence of warm waters (tropical clade), and populations on south-south-eastern coast, inhabiting cold waters from the Malvinas current (subtropical clade) (Santos et al., 2006). The distribution of both clades, presenting a high level of genetic differentiation, was related to differences in water temperature and tidal flow (physical barrier), and reinforced by a putative larval retention and low migration rate of adult individuals. Inversely, no apparent karyotypic differences were found after cytogenetic analyses in samples of *Menticirrhus americanus* (Scianidae) from Northeastern Brazil in relation to previous studies carried out in populations from the southeastern shore (Gomes et al., 1983b), albeit both collection sites are more than 2000 km apart. However, the lack of karyotypic variation between these samples needs to be confirmed through refined techniques of chromosomal mapping using hybridization with specific DNA probes or replication banding.

On the other hand, the cytogenetic data in Sparidae show a remarkable diversification regarding karyotype formulae among species or populations of a single species, such as *Lithognathus mormyrus* (FN = 52, 54, 70) (Sola and Cataudella, 1978; Cataudella et al., 1980; Sola et al., 1981; Cano et al., 1981). This feature was also verified in *A. probatocephalus*, since the individuals analyzed in the present study showed a distinct karyotype formula (FN = 48) in relation to previous reports in populations of the North America coast (FN = 53 and 60) (Fitzsimons et al., 1985). Such remarkable karyotypic diversification in allopatric samples of *A. probatocephalus* indicates a level of chromosomal modification suggesting that both populations actually refer to different species lacking a proper denomination.

Few cytogenetic reports in the families Sciaenidae and Sparidae refer to structural karyotype aspects, constraining their application as cytotaxonomic markers. A single NOR in the pericentromeric region has been considered a basal condition within Perciformes (Affonso et al., 2001), and they are widespread within Scianidae. However, the NOR-bearing chromosome pair can differ among species, such as in *Plagioscion* sp (1st pair) and *P. squamosissimus* (24th pair) (Feldberg et al., 1999) or in *M. americanus* (1st pair), *P. acuminatus* (2nd pair) and *O. punctatissimus* (10th pair), presently studied.

NORs within the family Sparidae present a more diversified pattern of karyotypic evolution. Therefore, species bearing a single NOR (e.g., *A. probatocephalus*) or multiple

NORs (*Diplodus bellottii*; Amores et al., 1993; *D. puntazzo*; Vitturi et al., 1996) have been identified (Table 2).

There are several reports in marine species showing the co-location of NORs and heterochromatin (Galetti Jr. et al., 2000; Affonso and Galetti Jr., 2005; Molina and Bacurau, 2006; Sena and Molina, 2007; among others), similar to what was observed in the karyotype of the species analyzed herein (*M. americanus*, *O. punctatissimus*, *P. acuminatus*, and *A. probatocephalus*).

In general, the distribution of heterochromatic segments at the centromeric and pericentromeric position identified in Atlantic scianids follows the pattern previously reported in other species of this family (Reggi et al., 1986; Feldberg et al., 1999). A similar heterochromatin distribution pattern was also observed in the sparid *A. probatocephalus*.

Phylogenetic studies based on internal body structures (swim bladder and otoliths) placed Sciaenidae as a closely related phylogenetic group to Haemulidae (Trewavas, 1977; Chao, 1978, 1986; Schwarzhans, 1993). Yet, the cytogenetic data available for Scianidae and Haemulidae are not reliable enough to corroborate such phylogenetic affinity since they share symplesiomorphic karyotypic features also present in several other families of Perciformes (Molina, 2006).

As for the phylogeny of Sparidae, morphological comparisons suggest that this family would be closely related to Caesionidae, Haemulidae, Lethrinidae, Lutjanidae, and Nemipteridae (Schultz, 1953; Jordan and Fesler, 1983). Analyses based on mtDNA sequences have corroborated such relationship (Orrell and Carpenter, 2004), and further indicate that the six Sparidae subfamilies (Boopsinae, Denticinae, Diplodinae, Pagellinae, Pagrinae, and Sparinae) are not monophyletic, suggesting that the characteristic dentition and feeding behavior of each subfamily have both arisen independently at different evolutionary stages. The occurrence of within-family divergent cytogenetic features seems to support the polyphyletism proposed for this group.

The shared karyotypic organization observed within Scianidae places it as one of the most cytogenetically conserved Perciformes group. However, the presence of a higher mean heterochromatin content seems to represent a particular trend of this family. This feature indicates an evolutionary pathway dissociated from either chromosomal rearrangements, such as pericentric inversion (the most common rearrangement related to karyotypic diversification within Perciformes), or mechanisms of decrease/increase in diploid number.

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