



Satellite DNA sites in four species of the genus *Astyanax* (Teleostei, Characiformes)

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Abstract

Cytogenetic data about satellite DNA distribution in four *Astyanax* species (Characidae) from the Paraitinga river, Paraíba do Sul river basin, Brazil, are presented. In order to characterize the constitutive heterochromatin, C-banding, chromomycin A₃ and DAPI fluorescence staining, as well as fluorescence *in situ* hybridization (FISH) with the satellite DNA As-51 probe were performed. *A. scabripinnis* and *A. paraguayana* presented $2n = 50$ and $2n = 48$ chromosomes, respectively. The heterochromatin was located in the pericentromeric and terminal regions of many chromosomes, corresponding to GC-positive regions and to the As-51 satellite DNA in terminal regions. *A. intermedius* and *A. giton*, both with $2n = 50$ chromosomes, showed little heterochromatin, mostly restricted to the terminal and pericentromeric regions of a few chromosomes. No GC-positive regions, neither any correspondence between the scarce heterochromatin of these species and the As-51 satellite DNA was observed. AT-positive blocks were not detected in any of the species studied. Based on these and other available data, the hypothesis that *Astyanax* represents a polyphyletic group is discussed.

Key words: *Astyanax*, fluorescence *in situ* hybridization (FISH), heterochromatin, karyotypic diversity, satellite DNA.

Received: February 3, 2006; Accepted: November 24, 2006.

Introduction

Astyanax, popularly known as lambaris or piabas, comprises around 74 species distributed from southern United States to northern Argentina (Eigenmann, 1921). In a recent review, about 90 valid species were considered *insertae sedis* in Characidae (Reis *et al.*, 2003). Many of these species inhabit stream headwaters, including highly irregular regions (such as mountain ranges) where the headwaters of the Paraitinga river (Paraíba do Sul river basin, Brazil) are located. Morphological analyses led Weitzman and Malabarba (1998) to propose the genus polyphyly, which was corroborated by the study of 5S rDNA sites distribution (Kavalco *et al.*, 2004a).

Chromosome variability in *Astyanax* species reflects their ecological and genetic characteristics. It comprises variations in diploid numbers ($2n = 36$ to $2n = 50$ chromosomes), karyotypical macrostructure, occurrence of natural

polyploidy, presence of B-chromosomes, constitutive heterochromatin polymorphisms, and nucleolar organizer regions (NORs) distribution. Based on these features, at least three “species complexes” can be recognized: *A. scabripinnis* (Moreira-Filho and Bertollo, 1991), *A. altiparanae* (Fernandes and Martins-Santos, 2005) and *A. fasciatus* (Pazza *et al.*, 2006).

Constitutive heterochromatin corresponds to repetitive regions in the genome which are extremely condensed during the cell cycle and have been claimed to have no transcriptional activity. Heterochromatin has played an important role in the study of the diversification of some fish groups, as in the genera *Brycon* (Margarido and Galetti Jr., 1999) and *Leporinus* (Galetti Jr. *et al.*, 1991; Molina *et al.*, 1998; Margarido and Galetti Jr., 2000). In these genera, the karyotypic macrostructure is relatively constant, but the heterochromatin differs between species (Galetti Jr. *et al.*, 1991). In the *Astyanax scabripinnis* species complex (Moreira-Filho and Bertollo, 1991), heterochromatin polymorphisms were useful in the identification of some populations (Mantovani *et al.*, 2000).

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Chromosome banding has been extensively used to study the distribution and nature of constitutive heterochromatin in fishes. The use of base-specific fluorochromes, such as chromomycin A₃ and DAPI, has helped to characterize the composition of the constitutive heterochromatin (GC-, AT-positive or devoid of GC or AT clusters). The occurrence of GC-positive heterochromatin sequences adjacent to or interspersed among NORs has been described for many organisms (Mayr *et al.*, 1985; Schmid and Guttenbach, 1988; Phillips and Hartley, 1988; Sola *et al.*, 1992; Kavalco *et al.*, 2004b). GC-positive heterochromatin not associated with NORs are very rare among fishes (Souza *et al.*, 1996; Artoni *et al.*, 1999; Margarido and Galetti Jr., 2000; Kavalco *et al.*, 2004b). AT-positive regions are also quite uncommon among fishes and have mainly been reported among some Hypostominae species (Artoni and Bertollo, 1999).

Fluorescence *in situ* hybridization (FISH) used to locate DNA sequences has provided more accurate information on the genomic organization of several organisms. In fish, the hybridization of rDNA probes and of satellite DNAs has provided insights into the relationship among species and their karyotypic diversification (Almeida-Toledo *et al.*, 2002; Ferro *et al.*, 2001; Jesus *et al.*, 2003; Kavalco and Moreira-Filho, 2003; Kavalco *et al.*, 2004a; Kavalco *et al.*, 2005; Martins and Galetti Jr., 1999; Mestriner *et al.*, 2000; Pazza *et al.*, 2005; Vicente *et al.*, 2004).

Satellite DNA consists of many tandem repeats of identical or related short basic repeats. The As-51 satellite DNA is a multimeric fragment of 51pb obtained by *Kpn*I restriction enzyme digestion of *Astyanax scabripinnis* samples. The As-51 satellite DNA seems to have similarities with a portion of the *Anopheles gambiae* RT2 retroposon, suggesting it could have arisen from a mobile element (Mestriner *et al.*, 2000). FISH revealed that the As-51 repetitive DNA family was located in a small portion of the *A. scabripinnis* genome, distributed in all the distal C-bands (Mestriner *et al.*, 2000).

Aiming to compare the nature and distribution of constitutive heterochromatin in four *Astyanax* species (*A. scabripinnis*, *A. parahybae*, *A. intermedius* and *A. giton*) from the Paraíba do Sul river basin, C-banding, chromomycin A₃ and DAPI staining, and FISH with the As-51 satellite DNA probe were performed. This is the first report on the nature and distribution of heterochromatin in *A. intermedius* and *A. giton* of the chromomycin A₃ staining in *A. parahybae* and of As-51 satellite DNA distribution in *A. intermedius*, *A. giton* and *A. parahybae*. Constitutive heterochromatin data for *A. scabripinnis* are compared with previous reports.

Material and Methods

Four *Astyanax* species were analyzed. Six *A. scabripinnis* specimens (all female) were collected from the Macacos river (22°50,050' S, 44°50'940' Wo), nine *A.*

parahybae specimens (6 males and 3 females) and 28 *A. intermedius* specimens (2 males and 26 females) from the Paraitinga river (22°52,225' S, 44°51,041' Wo). A total of 21 *A. giton* specimens were collected in two different sites, three males and ten females in the Paraitinga river (22°52,225' S, 44°51,041' Wo), and three males, four females and a sexually undetermined specimen in the Jacuí stream (23°02,436' S, 44°56,103' Wo), both part of the Paraíba do Sul river basin. The samples were identified and deposited in the ichthyological collection of the National Museum of Rio de Janeiro (Museu Nacional do Rio de Janeiro - Brazil), under the registration OMNRJ REG 20020417.

Mitotic chromosomes were obtained according to Bertollo *et al.* (1978). C-banding, chromomycin A₃ and DAPI staining were performed according to Sumner (1972), Schmid (1980) and Schweizer (1980), respectively. Fluorescent *in situ* hybridization (FISH) with the As-51 satellite DNA probe was performed according to Pinkel *et al.* (1986), with high stringency washes and control experiments. The As-51 probe isolated from *A. scabripinnis* (Mestriner *et al.*, 2000) was labeled with biotinylated uridine (BdUTP) according to the Nick Translation Bionick Labeling System Kit protocol (Invitrogen®). The detection was performed with avidin-FITC and biotin-conjugated-anti-avidin. The slides were mounted with Vectashield Mounting Medium, (Vector®) with propidium iodide (1.5 µg/mL). The preparations were analyzed under a Olympus BX50 epifluorescent microscope and the images were captured (with a 1Mp resolution) with the CoolSnap Pro and the Image Pro Plus softwares (Media Cybernetics). The chromosomes were classified according to their arm ratios, as M-metacentric; SM-submetacentric; ST-subtelocentric; and A-acrocentric (Levan *et al.*, 1964).

Results

All species presented heterochromatin distributed in pericentromeric or distal chromosome regions. *Astyanax scabripinnis* presented 2n = 50 and a karyotypic formula composed of 8M+20SM+8ST+14A. In this species, C-banding revealed constitutive heterochromatin in the pericentromeric regions of several chromosomes, and in the terminal regions of the long arms of pairs 1, 2, 7, 14 and 21; a submetacentric pair had an almost entirely heterochromatic short arm (Figure 1-a). Chromomycin A₃ staining showed three GC-positive sites: two in the terminal region of the short arm of a subtelocentric chromosome pair and one in the long arm of a submetacentric chromosome (Figure 2-a). No AT-positive heterochromatin was observed (data not shown). One subtelocentric and two acrocentric chromosome pairs and a single submetacentric chromosome presented conspicuous terminal signals after fluorescence *in situ* hybridization with the pAs-51 probe (Figure 3-a).

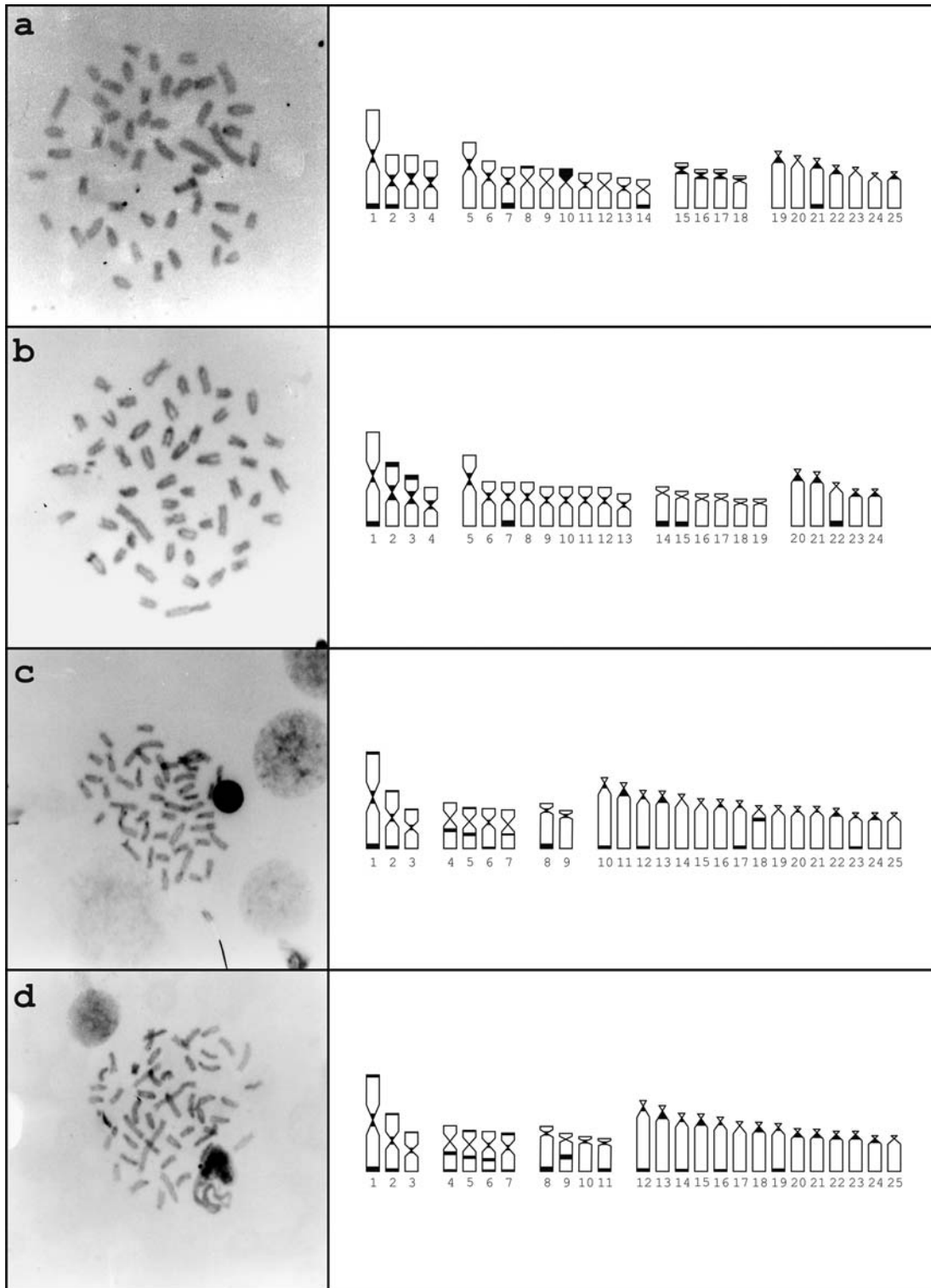


Figure 1 - C-banding metaphases and ideograms of (a) *A. scabripinnis*; (b) *A. parahybae*; (c) *A. intermedius*; and (d) *A. giton*.

Astyanax parahybae showed $2n = 48$ chromosomes, with the karyotypic formula $M+18SM+12ST+10A$. C-banding revealed constitutive heterochromatin in the pericentromeric regions and in the terminal position of the long arms of chromosome pairs 1, 7, 14, 15 and 16, and in

the short arms of chromosomes 2 and 3 (Figure 1-b). GC-positive regions were detected in the terminal region of the short arm of a single large metacentric chromosome and of a medium-sized metacentric pair (Figure 2-b). No AT-positive heterochromatin was observed (data not shown).

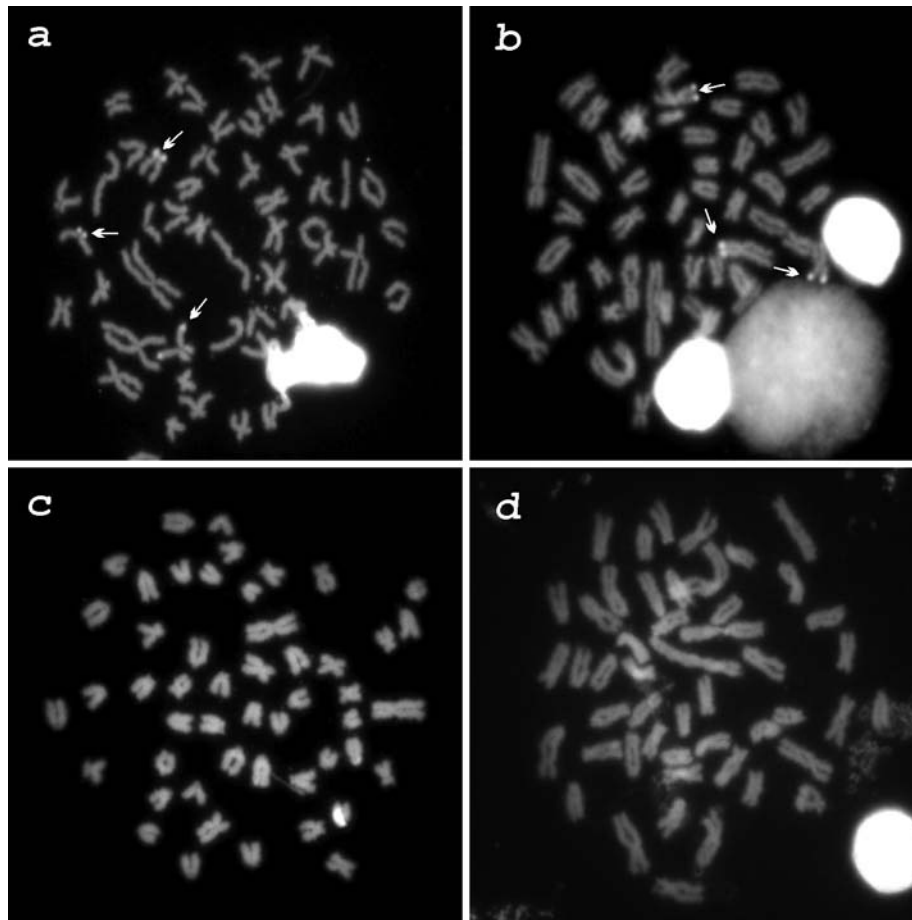


Figure 2 - Chromomycin A₃ stained metaphases evidencing GC-positive regions in (a) *A. scabripinnis*; and (b) *A. parahybae*, and the absence of these sites in (c) *A. intermedius*; and (d) *A. giton*.

The As-51 satellite DNA was terminally located in two small chromosome pairs, one metacentric and one subtelocentric-acrocentric. In a few cells, an additional signal was observed in the interstitial region of the long arm of a single acrocentric chromosome (Figure 3-b).

Astyanax intermedius presented $2n = 50$ and a $6M+8SM+4ST+32A$ karyotypic formula. The heterochromatin was located in the pericentromeric region of many chromosomes and in the terminal region of chromosome pairs 1, 2, 8, 10, 12, 17 and 23 (Figure 1-c). Interstitial positive C-bands were observed in chromosomes 4, 5 and 18. No GC (Figure 2-c), AT- (data not shown) or As-51 satellite DNA sites were observed (Figure 3-c).

Astyanax giton showed $2n = 50$ and a karyotype composed of $6M+8SM+8ST+28A$ in both populations studied. C-banding revealed heterochromatin in the pericentromeric regions of many chromosomes and in interstitial regions of chromosomes 4, 5, 6 and 9 (Figure 1-d). The interstitial band in the ninth pair is more conspicuous than the corresponding band in the *A. intermedius* karyotype. As in *A. intermedius*, no GC- (Figure 2-d), AT (data not shown) or As-51 satellite DNA sites were observed (Figure 3-d).

Discussion

Astyanax is an interesting group for cytogenetic studies, as it comprises species with distinct evolutionary trends leading towards either karyotypic conservation or diversification. The macrokaryotypic diversification that occurs in species from the “*A. scabripinnis*” and “*A. fasciatus*” complexes extends to heterochromatin variation, with frequent heteromorphisms on the nature and location of C-bands among populations, individuals and homologues (Moreira-Filho and Bertollo, 1991; Souza *et al.*, 1996; Mantovani *et al.*, 2000; Fernandes and Martins-Santos, 2005; Abel *et al.*, 2006; among others). No heteromorphisms were observed in the *A. scabripinnis* population herein studied (Figure 1-a), possibly due to the small sample. Its GC-positive heterochromatin distribution was similar to the one reported for other populations from the Tietê river basin (Souza *et al.*, 1996). The exceptions were the single chromosome with a fluorescence signal, an exclusive trait of the population herein analyzed (Figure 2-a), and the distribution of the As-51 satellite DNA (Figure 3-a), less abundant than in the populations from the upper Paraná river basin (Mantovani *et al.*, 2004; Abel *et al.*, 2006).

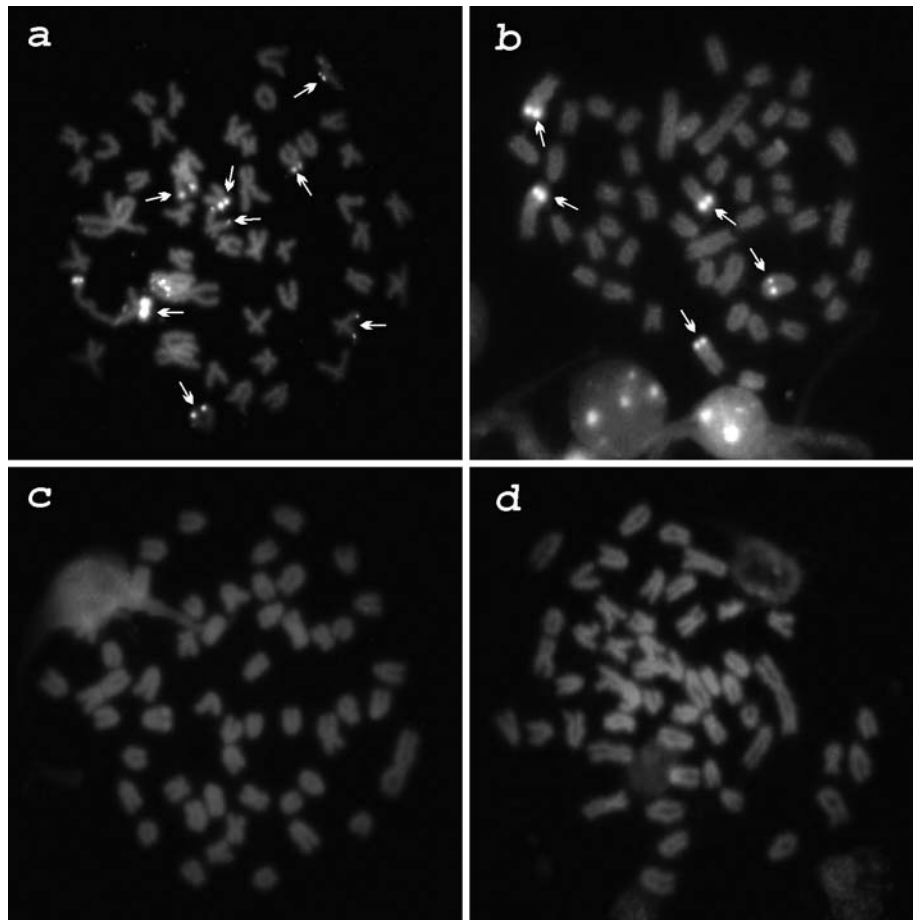


Figure 3 - Fluorescence *in situ* hybridization with As-51 satellite DNA probe. The arrows indicate these sites in: (a) *A. scabripinnis*; (b) *A. parahybae*. In (c) and (d) it is showed lack of signals of the satellite DNA correspondence in *A. intermedius* and *A. giton*, respectively.

In *A. parahybae*, the heterochromatin was distributed in the pericentromeric regions of almost all chromosomes and in the terminal regions of a few ones (Figure 1-b). GC-positive sites were identified in a chromosome pair and in a single homologue of another chromosome pair (Figure 2-b), as in *A. scabripinnis*. This differences between homologues may be due to uneven exchanges during meiosis. The As-51 satellite DNA probe hybridized to the terminal regions of a few chromosomes (Figure 3-b) and to one interstitial site with an apparent size heteromorphism between the homologues. *A. parahybae* has been grouped as a subspecies inside the “*A. fasciatus*” complex until recently. Its taxonomic status was defined by Melo (2001) in a revision of *Astyanax* species from the Serra dos Órgãos, Paraíba do Sul river basin. It is relevant that other *A. fasciatus* populations, from the Piracicaba river (Abel *et al.*, 2006) and from the Mogi-Guaçu river basin (Pazza, 2005) also presented such satellite DNA. Thus, its detection in *A. parahybae* could indicate a closer relationship between both species.

Besides very similar karyotypic formulas and scarce heterochromatin distribution, *A. giton* and *A. intermedius* presented other chromosomal features which indicate a

close cytotaxonomical relationship: both of them did not show any GC-positive (Figure 2-c,d) or AT-positive heterochromatin, neither hybridization with the As-51 satellite DNA probe (Figure 3-c,d). Heterochromatin without GC- or AT-positive clusters is uncommon in fish, but has been observed in *Harttia loricariformis* (Kavalco *et al.*, 2004b). Besides the macrokaryotypic differentiation, the presence or absence of the As-51 satellite DNA could corroborate the polyphyletism of the genus *Astyanax*, suggested by Weitzman and Malabarba (1998). Although phylogenetic relationships between these species should be assessed by molecular analyses including several *Astyanax* species, cytogenetic data could support the hypothesis that *A. giton* and *A. intermedius* belong to a clade different from the *A. scabripinnis* and *A. parahybae* clade.

Although cytogenetic data are only available for a small number of *Astyanax* species, the heterochromatin data indicate that at least two distinct *Astyanax* groups occur in the Paraíba do Sul river basin: one group with few acrocentric chromosomes, As-51 satellite DNA and GC-positive sites, and another group with many acrocentric chromosomes, no GC-positive heterochromatin, neither As-51 satellite DNA. Mestriner *et al.* (2000) suggested that

the As-51 DNA distribution pattern found in *A. scabripinnis* and *A. fasciatus* may be an ancestral feature. The two other species possibly occupy a more derived position. Furthermore, *A. scabripinnis* showed different number of clusters and distribution patterns of such satellite DNA (Mestriner *et al.*, 2000; Mantovani *et al.*, 2004), as did *Astyanax fasciatus* (Pazza *et al.*, 2006). The distribution of 5S rDNA sites in *Astyanax* also pointed to the occurrence of two main groups, which is in agreement with the data herein reported. Almeida-Toledo *et al.* (2002) identified a marker metacentric pair in five *Astyanax* species. This pair was also observed in *A. scabripinnis* and *A. paraguayae*, and was absent in *A. giton* and *A. intermedius* (Kavalco *et al.*, 2004a). The large number of 5S rDNA sites in the two latter species may reflect their close relationship and their phylogenetic distance from the other species.

Acknowledgements

The authors wish to thank PhD Paulo A. Buckup for the taxonomic identifications. This work was supported by FAPESP (Proc. 01/00713-0 and 01/05185-5) and CNPq.

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Associate Editor: Fausto Foresti