

CHROMOSOME CHARACTERIZATION OF THE FISH *Trichogenes longipinnis*. A POSSIBLE BASIC KARYOTYPE OF TRICHOMYCTERIDAE

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ABSTRACT

A karyotypic study of 11 *Trichogenes longipinnis* specimens revealed a diploid number of $2n = 54$ and a chromosomal formula of $36M + 12SM + 6ST$. C-banding showed heterogeneous constitutive heterochromatin segments, some of which stained deeply while others were much less conspicuous. The nucleolar organizer region was located on the terminal portion of the long arm of a medium-sized metacentric pair.

INTRODUCTION

The Trichomycteridae are a typical South American family comprising two subfamilies (Trichomycterinae and Vandellinae) and characterized by advanced traits within the Siluriformes group (Baskin, 1973). Although this family has many species and is widely distributed throughout Brazil, very little is known about the karyotype of these fish. The only study carried out thus far on the chromosomes of this group has reported the haploid number ($n = 32$) for *Vandellia cirrhosa*, Vandellinae (Scheel, 1973). No information on Trichomycterinae chromosomes is available in the literature.

A genus in this group, *Trichogenes*, recently described by Britski and Ortega (1983), presents *sui generis* traits within the family which are related to the fact that it is apparently endemic in the coastal rivers of southeastern Brazil. According to these investigators, *Trichogenes* is very close to the species *Nematogenys inermis* from

central Chile and is considered to be the most generalized group related to Trichomycteridae. Thus, *T. longipinnis* is believed to possibly represent one of the most basic species in this family (Pinna, personal communication). It should be pointed out that, even though the Trichomycteridae are considered to be monophyletic (Baskin, 1973), the morphological traits that have been generally used in studies on this family are not appropriate to determine the variability existing within the group, nor do they permit establishing consistent phylogenetic relationships (Pinna, in press).

In view of these considerations, we undertook the present study to characterize the chromosomes of the species *T. longipinnis* in order to identify the chromosomes that may represent the basic karyotype of the family and thus contribute to a survey of traits that may be of help in clarifying the phylogenetic relationships of the group.

MATERIAL AND METHODS

Trichogenes longipinnis specimens were collected at a typical site for the species, Cachoeira dos Amores, km 3 on the Parati-Ubatuba highway (SP) and have been deposited at the Zoology Museum of the University of São Paulo under number MZUSP 40238.

The karyotype was studied by the standard cell suspension method described by Bertollo *et al.* (1978), using kidney cells. The nucleolar organizer regions (NORs) were identified by the colloidal silver method (Howell and Black, 1980) and constitutive heterochromatin distribution was visualized by the C-banding method of Sumner (1972).

RESULTS

Analyses carried out on 6 @ and 5 @ specimens of *T. longipinnis* showed a diploid number equal to 54 chromosomes in 76% of 331 metaphases observed. The chromosome formula detected was 36 metacentrics (M) + 12 submetacentrics (SM) + 6 subtelocentrics (ST). No numerical or structural differences were observed between the sexes (Figure 1). In most of the chromosomes of this species (approximately 20 pairs), the C-banding technique revealed either weakly staining bands or no staining at all. The seven remaining pairs (2, 3, 8, 21, 23 and 26) exhibited conspicuous C-banded blocks, usually close to the centromere.

The NOR was identified at the end of the longer arm of a single chromosome pair which corresponded to the eighth in size in the metacentric group (Figures 2 and 3). A weakly staining C-banded segment coincided with the NOR.

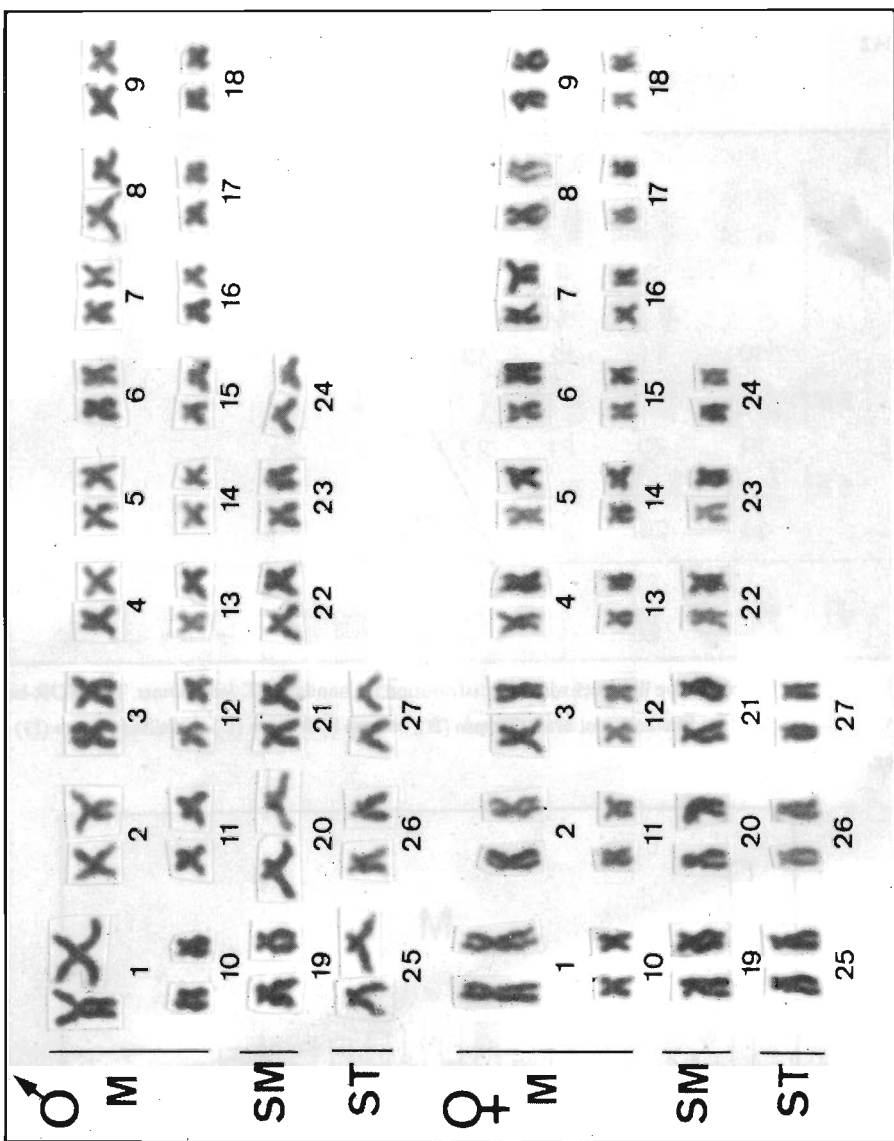


Figure 1 - Karyotype of *Trichogenes longipinnis* arranged into chromosome groups: (M) metacentrics, (SM) submetacentrics and (ST) subtelocentrics.



Figure 2 - (A) Constitutive heterochromatin distribution (C bands) in *T. longipinnis*. The NOR-bearing chromosome pair (no. 8) stands out after Giemsa (B), barium hydroxide (C) and silver nitrate (D) staining.

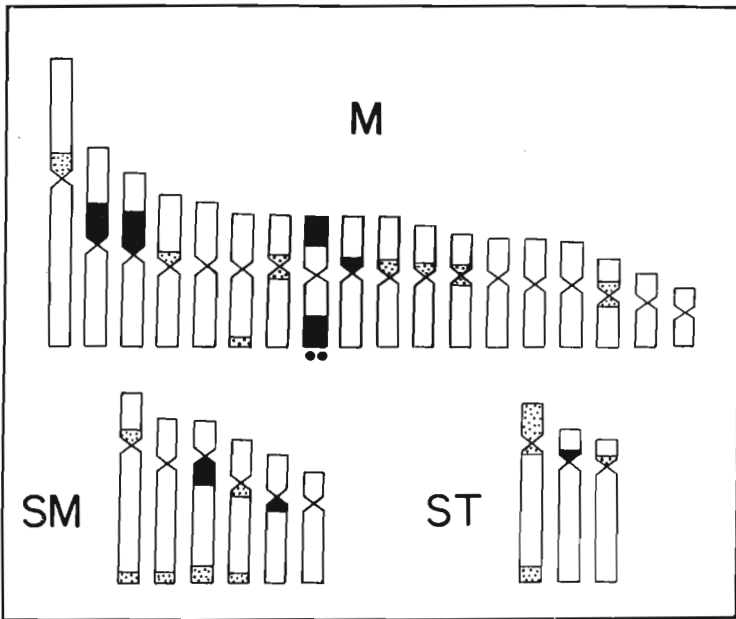


Figure 3 - Diagram representing the haploid set of *T. longipinnis*. The conspicuous C-positive bands are presented in black and the C-positive bands of low contrast are represented by dots. The location of the NOR is represented by two small filled circles.

DISCUSSION

Giemsa-stained karyotype of T. longipinnis

The karyotypic macrostructure of *T. longipinnis* is characterized by 54 bi-armed chromosomes with a predominance of metacentrics, followed by sub-metacentrics and subtelocentrics. Thus, there are no chromosomes of the acrocentric type, which is characteristic of many Siluriformes species. Variations in size between homologous elements are observed in both sexes. However, these variations are erratic and do not appear to be related to structural polymorphisms or even to sexual heteromorphism. Rather, they seem to result from small differences in condensation cycles between homologues.

C band and NOR distribution

As also observed in other fish (Galetti and Foresti, 1986), treatment with barium hydroxide (C-banding) revealed a heterogeneous pattern among the chromosomes of *T. longipinnis*. Differences in heterochromatin quality and/or quantity are probably the reason for this type of result (Galetti and Foresti, 1986). Studies with base-specific fluorochromes carried out on fish have confirmed the heterogeneous nature of heterochromatin from the point of view of composition (Galetti *et al.*, unpublished results).

The complement of *T. longipinnis* shows only 2 NOR-bearing chromosomes. Approximately 85% of the neotropical Siluriformes species studied thus far present, like *T. longipinnis*, show NORs of the simple type, *i.e.*, ribosomal cistrons concentrated in a single chromosome pair. This probably represents the primitive condition within the group. However, intraindividual variations in homologous AgNOR region size are observed. Variations of this type have been commonly reported in the literature and have been attributed to differences in ribosomal cistron number and/or to their differential activity (Ruiz, 1980), or to variation in the methylation and condensation of homologous rDNA segments (Angelier *et al.*, 1986).

Chromosomal studies performed on several Siluriformes groups (Le Grande, 1981; Dias, 1987; Fenocchio, 1987; Oliveira, 1988) have reported wide diversity in diploid number from $2n = 22$ to 132. Within these limits, however, Le Grande (1981) pointed out that most species studied have $2n = 48 - 58$, with most chromosomes being meta- and submetacentric. On the basis of a simple abundance criterion, this author hypothesized that the ancestral karyotype of Ictaluridae, and possibly of Siluriformes as a whole, may be $2n = 56 \pm 2$ and may consist mainly of bi-armed chromosomes. Starting from this complement, the different Siluriformes families may have undergone parallel chromosomal evolutions which gave rise to the diversity observed today. Very little can be said about the chromosomal evolution of

Trichomycteridae. In a preliminary analysis of the karyotype of a species of the genus *Trichomycterus* from the Corumbataí river, SP, we also noted $2n = 54$ chromosomes (unpublished data), with a rough karyotypic structure quite close to that observed in *T. longipinnis*. This observation may corroborate the hypothesis that the karyotype identified for *T. longipinnis* is basic among the Trichomycteridae and suggests a certain karyotypic stability within the group. However, any firmer conclusions with respect to this matter are still premature.

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RESUMO

O estudo do cariótipo de 11 exemplares de *Trichogenes longipinnis* revelou um número diplóide modal $2n = 54$ e fórmula cromossômica com $36M + 12SM + 6ST$. Os segmentos de heterocromatina constitutiva revelaram-se heterogêneos pela técnica de bandas-C, sendo alguns fortemente marcados e outros poucos conspícuos. A região organizadora dos nucléolos (NOR) localiza-se na porção terminal do braço longo de um par metacêntrico de tamanho mediano.

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