

Post-zygotic modifications and intra- and inter-individual nucleolar organizing region variations in fish: report of a case involving *Leporinus friderici*

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Silver nitrate staining, a rapid and efficient method, has proven to be excellent for nucleolar organizing region (NOR) studies in fish. Some fish appear to have only two NOR-bearing chromosomes in their karyotype, whereas others probably have several. In the present study we analyzed the NORs of *Leporinus friderici*, a species that, on the basis of previous studies, has been considered as representative of species with NORs carried by a single chromosome pair. The analyses were performed by a combination of three methods, i.e. silver nitrate staining, staining with the GC-specific fluorochrome chromomycin A₃, and *in situ* hybridization with digoxigenin-labeled probes. The results showed that, although more frequent and conspicuous in a single chromosome pair, the NORs of this species are present in multiple chromosomes. Intra- and inter-individual variations observed by the three methods strongly suggest the occurrence of post-zygotic modifications involving NORs. NOR identification in fish, almost exclusively performed by the silver nitrate method, is currently being re-evaluated by methods such as chromomycin A₃ staining and *in situ* hybridization, which may provide important information leading to a better understanding of chromosome evolution in these animals.

Key words: fish, fluorescent CMA bands, *in situ* hybridization, NOR polymorphisms

Introduction

Since the late 1970s, nucleolar organizer regions (NORs) have been identified in the karyotype by a rapid and easy technique involving impregnation with silver nitrate (Goodpasture & Bloom 1975, Howell & Black 1980). This method has revealed that most fish studied so far have only a single pair of homologous Ag-NOR-bearing chromosomes (e.g. Gold 1984, Moreira Filho *et*

al. 1984), while others show Ag-NOR sites distributed among multiple chromosomes (e.g. Almeida Toledo *et al.* 1985, Galetti *et al.* 1985). Polymorphisms in these regions, however, are frequent (Foresti *et al.* 1981). In the genus *Leporinus* Ag-NOR sites are characteristically found in only two chromosomes in the complement. Their location in different chromosome pairs in different species may confer a significant cytotaxonomic value on this trait (Galetti *et al.* 1984).

Previous studies on *Leporinus friderici* have identified Ag-NOR sites on the short arm of the second largest chromosome of the complement (Galetti *et al.* 1984). These results were later confirmed in specimens from a different population (Galetti *et al.* 1991). However, in this later study, one individual was identified as presenting as many as five chromosomes bearing Ag-positive sites, suggesting a larger number of NORs in the complement. According to the authors, since silver staining only detects rDNA sites that are active in the preceding interphase (Hsu *et al.* 1975, Miller *et al.* 1976) the number of inactive NORs might be underestimated in those fish with only two Ag-NORs.

It has been frequently observed that, regardless of any genetic activity, the NORs of certain lower vertebrates, especially amphibians and fish, can be identified in the karyotype by the use of fluorochromes such as chromomycin A₃ and mitramycin A, which preferentially bind to GC-rich sequences in DNA (e.g. Schmid 1980, Mayr *et al.* 1985, Amemiya & Gold, 1986, 1988, Schmid & Guttenbach, 1988). The association of fluorochromes and silver studies has been useful for the detection of polymorphisms at these sites (Phillips *et al.* 1989a,b, Sola *et al.* 1992a,b, Galetti & Rasch 1993a,b). Besides these methods, non-isotopic *in situ* rDNA hybridization, especially with biotin-labeled probes and fluorescence detection (FISH), has several times been

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considered decisive in a more precise identification of NOR sites in the complement, and has been increasingly used in fish studies (Pendás *et al* 1993a,b, 1994).

In the present paper we report a chromosome analysis carried out on *Leporinus friderici* specimens using silver nitrate and chromomycin A₃ staining. C-banding and *in situ* hybridization with digoxigenin-labeled rDNA probes. The combined use of these methods allowed us to detect a major pair of NOR-bearing chromosomes and at least two other pairs showing secondary NORs, which often varied from cell to cell in the same individual.

Materials and methods

We studied the mitotic chromosomes of 10 *Leporinus friderici* specimens (Anostomidae, Characiformes) from two different hydrographic systems, *i.e.* the Candeias

River, a tributary of the Madeira River in the Amazon basin, and the Mogi-Guaçu River of the upper Paraná basin. Except for animals 5891 and 5892, the only two obtained from the second collection site, all fish had been previously studied for NORs by the silver nitrate method (Galetti *et al.* 1991).

Chromosome banding.

The NORs were reanalyzed using colloidal silver nitrate emulsion (Howell & Black, 1980). In addition, C-banding analyses were performed using the method described by Sumner (1972), and chromomycin A₃ staining was carried out in combination with the counterstain distamycin A as described by Schweizer (1976) and Schmid (1980), with some adaptations to fish chromosome studies (Galetti & Rasch 1993a).

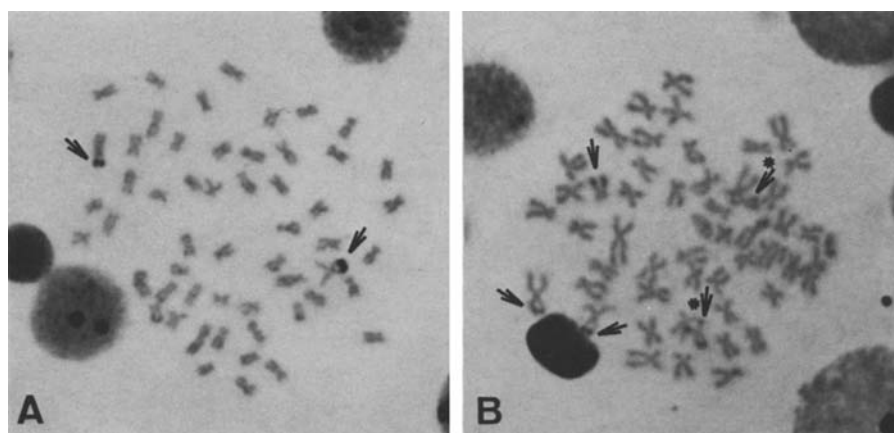


Figure 1. Silver nitrate stained metaphases. **A** The two major NOR-bearing chromosomes corresponding to pair 2 in the complement are indicated. **B** Five Ag-NOR-bearing chromosomes detected in the specimen 4976. The asterisk-marked arrows show Ag-NOR sites in both telomeres of a median sized metacentric (pair 13).

Table 1. NOR-bearing chromosome frequencies of *L. friderici* shown by silver nitrate (Ag-NOR), chromomycin A₃ (CMA) and *in situ* hybridization with digoxigenin-labeled probes (DIG)

	Ag-NOR						CMA						DIG					
	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6
4976	14	16	4	2	6				2	4	6		1	4				
5241	1	16							1	8	1	2						
5243								15	7	2	1		2	1	1		1	
5643		11					2	5	4	1				2				
5644	1	8					3	9		2								
5648	7	9					18	14	5					5	2			1
5649	1	21						1	5					4		5	1	
5682							2									1		1
5891							1	2	2	1			3					
5892							10	10										
Total	24	81	4	2	6	0	36	56	26	18	8	2	6	16	3	6	2	2

In situ hybridization

Hybridization assays were carried out with human rDNA 18S probes labeled with digoxigenin and identified by the immunocytochemical method with anti-digoxigenin-alkaline phosphatase stained with nitroblue tetrazolium (NBT) as described by the supplier (Boehringer Mannheim, Germany).

Results and Discussion

Analysis of the NORs by silver nitrate staining confirmed previous studies (Galetti *et al.* 1984) indicating that Ag-NORs are present only in the telomere of the short arm of the second metacentric pair (Figure 1A). In specimen 4976, however, at least five chromosomes with conspicuous silver labeling were observed (Table 1, Figure 1B), corroborating results previously reported by Galetti *et al.* (1991). In this specimen, in addition to the Ag-NOR sites on chromosome pair 2 in the complement, other sites were observed in both telomeres of a metacentric pair of intermediate size (pair 13) and in the subterminal portion of the long arm of one of the chromosomes of pair 26, a small submetacentric. Conspicuous associated C-banding-positive blocks were also detected in all of these segments (Figure 2C).

In fact, NOR polymorphism has been observed quite often in fish, and has been demonstrated by cytogenetic (*e.g.* Foresti *et al.* 1981, Gold 1984, Moreira Filho *et al.* 1984, Phillips *et al.* 1989b, Sola *et al.* 1992a,b) and also by molecular methods (Monaco *et al.* 1988, Phillips *et al.* 1989a). Owing to their repetitiveness in the genome of different organisms, these cistrons are highly susceptible to pre- and post-zygotic structural modifications as a result of unequal crossing over, regional duplications, transpositions and other rearrangements. However, when NORs are identified with silver nitrate staining (Ag-NORs), variations due to structural modifications and those of functional origin are indistinguishable, since only truly functional sites are identified by silver nitrate (Hsu *et al.* 1975, Miller *et al.* 1976). In this case, those rDNA cistrons present in the genome but inactive as a result of regulation processes will remain masked (Schmid 1980).

In order to verify if the Ag-NOR polymorphism observed in *Leporinus friderici* is a product of genetic regulation or the result of true structural changes involving this chromosome region, analyses using chromomycin A₃ (CMA) were performed. Approximately 150 cells from different individuals were counted and considerable inter- and intra-individual variation in the pattern of CMA-positive bands was demonstrated

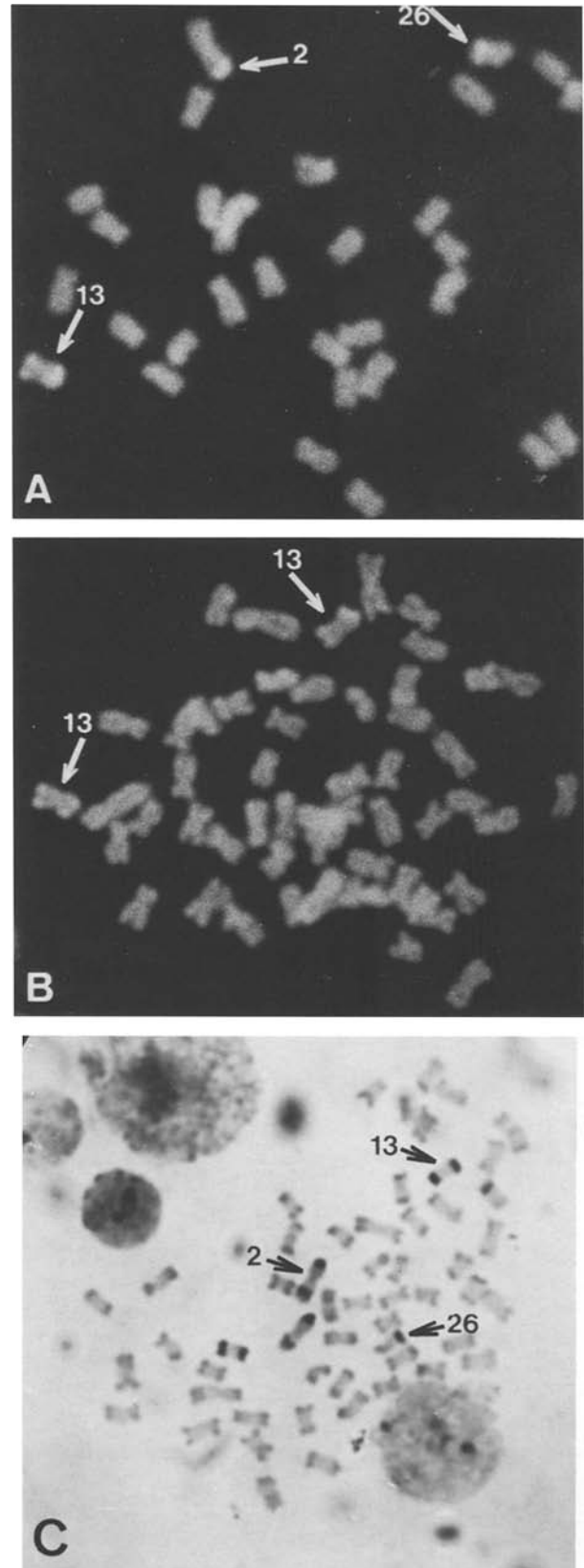


Figure 2. A & B Partial chromomycin A₃-stained metaphases. CMA fluorescent bands in the telomeres of a chromosome 2, 13 and 26 (A). Two chromosomes 13 with CMA bands in both telomeres (B) C C-banding metaphase. A chromosome of each pair 2, 13 and 26, bearing conspicuous heterochromatin blocks, is indicated.

(Table 1). Although CMA-positive fluorescent segments were always present in pair 2 in the complement, other CMA-positive bands were also observed (Figure 2A & B & 3). Approximately 50% of the cells analyzed showed 3–6 chromosomes bearing CMA-positive regions, consistent with the three homologous pairs bearing Ag-NOR sites in specimen 4976. In addition to these, some other small CMA-positive bands were sporadically detected, such as that appearing in the pericentromeric region of pair 18 in the complement and in the telomeric region of pairs 4 and 7. (Figure 3).

The same tendency to variation was also observed by analyzing chromosomes subjected to *in situ* hybridization with digoxigenin-labeled rDNA 18S probes that were visualized by NBT staining. Owing to methodological difficulties related to visualizing the usually small NBT deposits, this analysis was limited to a small number of metaphases in each individual, and only those cases in which there was no doubt were considered. Positive signals were identified at least at the sites present in pairs 2, 13 and 26 of the complement (Figure 4, centre). Heteromorphisms, such as a probable duplication in chromosome 2 or deletion of one of the telomeres of one chromosome 13, may occur. Thus, the results of hybridization appear to be consistent with the multiple Ag-NORs observed only in specimen 4976, reinforcing the observation of secondary constrictions in these regions (Figure 4, left) and the presence of CMA-positive bands (Figure 4, right) in the animals analyzed.

However, in contrast to silver staining, the results of both CMA staining and *in situ* hybridization would not be expected to vary within the same individual unless independent structural differences occur from cell to cell. Similar intra-individual variations in the fluorescent CMA bands have been identified recently in some other fish species (Galetti & Rasch 1993a,b, Mestriner 1993) and may be more common than initially suspected. Although methodological artifacts cannot be completely excluded as a source of some of the variability we have observed here, it seems unlikely that both CMA staining and *in situ* hybridization would be subject to the same technical flaws. Thus, there are two

main hypothesis to explain these findings. These variations might be exclusively due (1) to heteromorphisms of a GC-rich heterochromatin linked or not linked with NOR sites (Pendás *et al.* 1993a,b) or (2) to *de facto* changes in the set of rDNA cistrons. Our C-band analyses showed quite conspicuous NOR-associated heterochromatin segments in chromosome pairs 2, 13 and 26 in *L. friderici*. However, in many cells these segments were considerably reduced with chromomycin A₃, or could not be identified at all. These findings suggest that the reduction or lack of CMA-positive bands does not seem to be a direct response related to heterochromatin, but may rather be a strong indication of modifications at the level of rDNA cistrons. Furthermore, if variations occur within rDNA cistrons, they should result in heteromorphisms detectable by *in situ* hybridization, as was indeed the case for *L. friderici*. Post-zygotic modifications may be an important mechanism for variations among organisms and, since their discovery (McClintock 1956), transposons have been the best evidence that these changes occur continuously along the genome. The occurrence of these mechanisms modifying fish NORs may reflect the plastic condition of the genome of these animals. Plants, in general, are considered to be organisms of high plasticity from a genetic viewpoint, able to stand large variations in the genome such as polyploidization and aneuploidy. Several plants show NOR variation from cell to cell, suggesting that these cistrons or segments of them may jump along the chromosomes (Schubert & Wobus 1985). As a parallel example, fish as a group may perhaps represent one of the vertebrates of high genetic plasticity, with marked genomic variations. The results of *in situ* hybridization with rDNA probes as used here proved to be highly variable. Although artifacts cannot be ruled out completely and the method used may have been of considerably reduced efficiency, at least part of the variation observed in the hybridization assays is consistent with the idea that the NORs of these fish may be moving along the genome.

The results obtained for *Leporinus friderici* show that studies of NOR identification in fish carried out exclusively using the silver nitrate method deserve re-

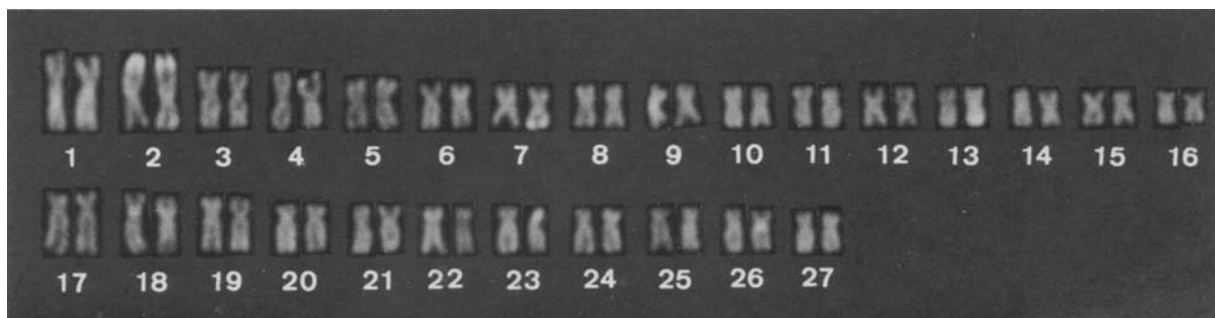


Figure 3. Karyotype of *L. friderici* showing the two major chromosomes (pair 2) bearing CMA fluorescent bands. Other minor CMA bands may be observed in the telomere of chromosomes 4 and 7 as well as in the centromeric region of chromosome 18.

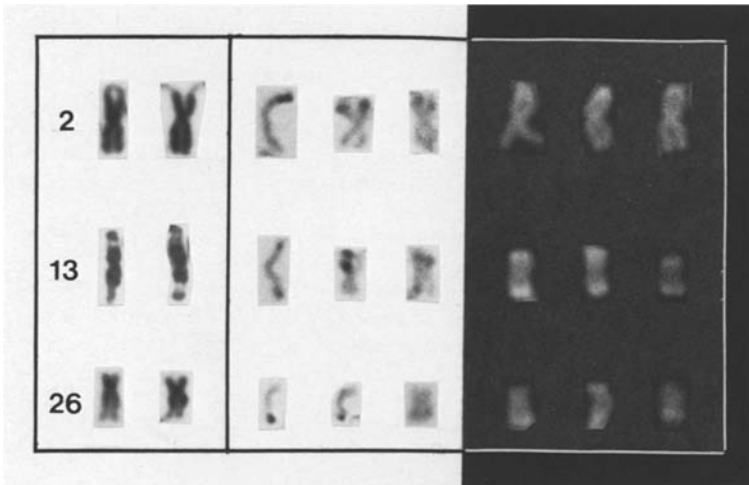


Figure 4. Giemsa-stained chromosome pairs 2, 13 and 26 showing secondary constrictions (left). The same chromosomes from different metaphases observed after *in situ* hybridization with digoxigenin-labeled rDNA 18S probes (center), and after CMA staining (right).

evaluation. The combined use of methods based on different mechanisms of action, as is the case for silver staining, chromomycin A₃ staining and *in situ* hybridization, should make new contributions to the understanding of the distribution of these cistrons in the chromosome complement of fish and to studies on the chromosome evolution of these animals.

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