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# The Chromosome Complement of *Arius felis* (Siluriformes, Ariidae)

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Hinegardner and Rosen (1972) presented an extensive study of nuclear DNA content in teleosts. They, like Ohno (1970a, b), were impressed with the diversity of genome size in bony fishes and found a mean DNA content close to 1.2 pg/haploid genome for most siluriform families. DNA values in the families Ictaluridae, Bagridae, Siluridae, Schilbeidae, Clariidae, Malapteuridae, Mochokidae and Pimelodidae were between 0.88 and 1.2 pg. Eight species of callichthyid catfishes exhibited elevated DNA contents with values between 1.7 and 4.4 pg/haploid genome. Two ariid catfishes (*Arius felis* and *Bagre marinus*) were studied. *Arius felis* had a haploid DNA content of 2.5 pg while *B. marinus* was found to have a DNA content of 2.4 pg. Gosline (1975a, b) noted that ariids, pimelodids, ictalurids, bagrids and doradids probably form an assemblage close to the basal siluriform stock. The approximate doubling of DNA in ariids compared to the presumeably related bagrids, pimelodids and ictalurids suggested a possible diploid-tetraploid relationship. To determine if chromosome number and form provided support for such a hypothesis, *A. felis* was karyotyped and compared to published karyotype accounts for other catfishes. This paper presents the first description of the chromosome complement from this family of marine and estuarine catfishes.

## Materials and methods

Specimens of *A. felis* were collected in Caminada Bay at Grand Isle, Louisiana, USA on 28 August 1976. Karyotype preparations were successfully made in the field from four juvenile (sex not determined) specimens. Tissues utilized were the kidney and the spleen. Techniques for the preparation of chromosome slides followed those outlined in LeGrande and Fitzsimons (1976). Each fish received an intraperitoneal injection of Velban (0.5 mg/ml) and was sacrificed $2\frac{1}{2}\sim 3\frac{1}{2}$ hr later. Tissues were excised, minced in 1.0% sodium citrate solution, fixed in methanol-acetic acid fixative, dropped on slides, flame dried and stained in diluted Giemsa solution. Voucher specimens have been deposited in the fish collections of the Museum of Natural History, University of Wisconsin, Stevens Point, Wisconsin, USA. Terminology for centromeric position is based on Levan et al. (1964).

## Results

Thirty-five well spread metaphase plates were counted from the *A. felis* specimens. The following counts were observed: 2N=54 (31 cells), 53 (2), 51 (1), 50 (1). The sharp modal count of 2N=54 indicates that this is the normal diploid number for this species. The same mode was observed in each of the four specimens examined. The karyotype (Fig. 1) was composed of 26 metacentric-submetacentric (msm) and 28 subtelocentric-acrocentric (stt) chromosomes. All chromosomes had identifiable second arms that ranged in size from large and well developed to small and knob-like. Because of the gradual change in size and morphology of the chromosomes, homologous pairs could not be identified with certainty in most cases. The larger msm chromosomes tended to be submetacentric, while the smaller msm's were mostly metacentric. One pair of marker chromosomes was noted in the stt series; it was distinguished by the presence of distinct satellites in a number of the spreads (Fig. 1).

## Discussion

LeGrande (1978 and in press) presented evidence suggesting a primitive siluriform karyotype of 2N=58 with a high (>80) arm number. This conclusion was based on chromosome data from 30 species of ictalurid catfishes (LeGrande, 1978; Hudson, 1976) as well as a survey of published karyotypes for all catfishes. Most (82.3%) of the siluriforms that have been karyotyped have diploid numbers between 40 and 60; the mean diploid number for the order is $\bar{X}=56.2$. If the DNA content in *A. felis* were indicative of tetra-

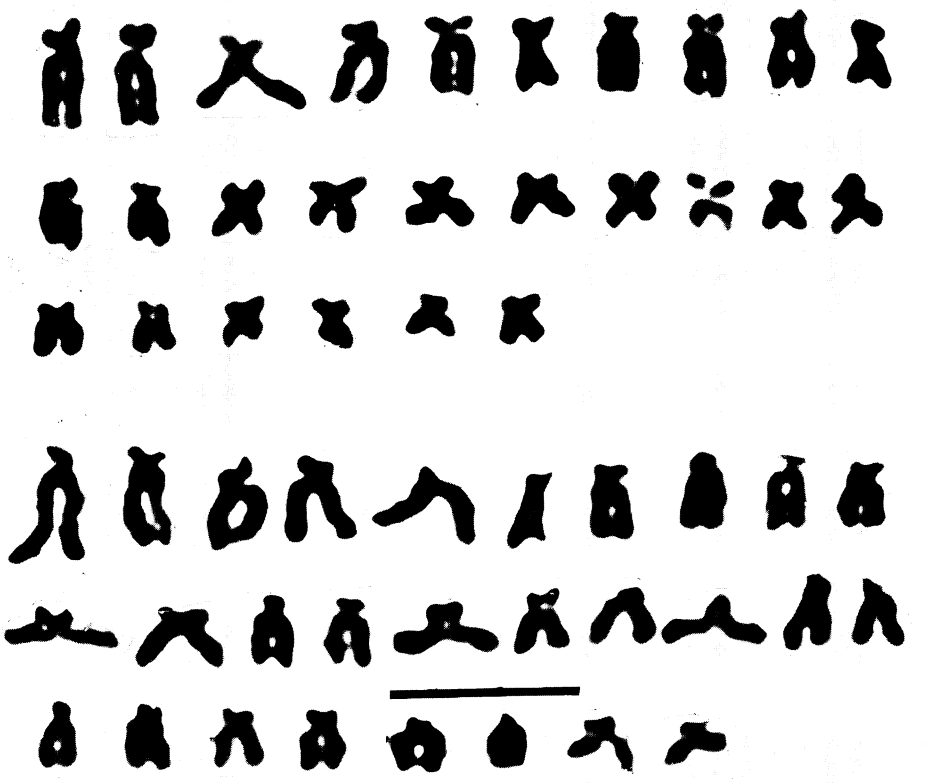

Fig. 1. Karyotype of *Arius felis* from Caminada Bay, Grand Isle, Louisiana, USA. Top group of chromosomes is metacentric-submetacentric. Lower group is subtelocentric-acrocentric chromosomes. Line is under a pair in the stt series that exhibited satellites.

ploidy with respect to most other siluriforms studied I would expect a higher 2N than observed in this species. Its 2N of 54 closely approaches the average 2N for siluriforms and the presumed ancestral 2N for the group. It seems unlikely that polyploidization in *A. felis* would have been followed by massive reduction in 2N to bring the karyotype back to a condition closely approximating the ancestral karyotype. More likely, the evolution of *A. felis*' karyotype was via a combination of Robertsonian and non-Robertsonian chromosomal rearrangements, reducing the 2N and resulting in the formation of some of the larger msm pairs. LeGrande (1978 and in press) has concluded that chromosomal rearrangement has played an important role in the evolutionary history of siluriforms. Catfishes show great diversity in both diploid and arm numbers indicating a complex pattern of chromosome restructuring.

Changes in DNA content with karyotype conservation has been documented in teleosts. Park and Kang (1976) observed DNA differences between two anguilliform species that exhibited the same karyotype. *Anguilla japonica* (family Anguillidae) and *Astroconger myriaster* (family Congridae) had karyotypes that were indistinguishable, including the presence of a distinct heteromorphic (sex chromosome?) pair in both. The DNA content of *Astroconger myriaster* was approximately 1.5 times that in *Anguilla japonica*. Data on the DNA content from ictalurid catfishes also supports the notion of non-polyploid DNA changes in catfish evolution. Hudson (1976) presented DNA values for 10 species in the family Ictaluridae, including 7 species of *Ictalurus*, *Pylodictis olivaris* and 2 *Noturus* species. There was no correlation between DNA content and 2N, even though both varied considerably between species.

*Noturus gyrinus* had the highest DNA content at 1.98 pg/haploid genome but possessed one of the lowest 2N's seen in 30 ictalurids that have been karyotyped. DNA values and chromosome numbers (Hinegardner and Rosen, 1972; Scheel et al., 1972) exhibit dramatic variation in callichthyid catfishes. While some members of the genus *Corydoras* have diploid numbers and elevated DNA contents that might be consistent with diploid-polyploid relationships, others exhibit DNA variation with relatively conservative karyotypic change (Hinegardner and Rosen, 1972). These data suggest that mechanisms of DNA change other than polyploidization may have frequently been operative in the evolution of catfishes.

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## ハマギギ科の一種 *Arius felis* の染色体

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アメリカ合衆国，ルイジアナ州，Caminada 湾で採集された 4 尾の *Arius felis* の染色体を観察した．実験方法としては，Velban 注入後 2.5～3.5 時間にじん臓およびひ臓を摘出し，air drying 法でプレパラートを作製した．

*Arius felis* の核型は，$2n=54$ で 26 本の中部・次中部着糸染色体と 28 本の端部・次端部着糸染色体とからなる．

一方，*Arius* ハマギギ属は DNA 量が多く，ギギ科や Ictaluridae のそれに比べて 2 倍以上ある．しかしながら，$2n$ は上記 2 科の魚と比べてほとんど変わらない．このことは，ナマズ類の進化を考える場合，染色体の倍数化では説明できない DNA 量増大のメカニズムの可能性を示唆すると考える．