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Institute of Environmental Medicine

CYTOGENETIC STUDY OF THE STRIPED BASS Morone saxatilis FROM THE HUDSON RIVER

REPORT
To

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From

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September, 1976

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CYTOGENETIC STUDY OF THE STRIPED BASS, Morone saxatilis (WALBAUM) FROM THE HUDSON RIVER ESTUARY, NEW YORK.

ABSTRACT

Striped bass larvae of 10 mm total length were utilized in obtaining chromosome spreads from epithelial tissue. Karyotypic analysis revealed a diploid chromosome number of 48, consisting of all acrocentric chromosomes with a size range of 1.25 μm-2.75 μm. Pairing of homologous chromosomes was not accomplished due to the small size of the chromosomes.

Introduction

Fishes are the most varied of the vertebrates, comprising more than 20,000 species, or about one third of all living vertebrate species. Despite the variety, abundance and importance of fishes, chromosomes have been reported for less than 600 fish species and of this total, karyotypes have been reported for fewer than 300 species (Denton, 1973). Included among the species studied for chromosomes and karyotypes are several forms common to the Hudson River Estuary (Table 1) including the two Ichthyopercids, Morone saxatilis and M. americana (Kerby, 1972).

The majority of fishes which have been studied have 48 chromosomes (Roberts, 1967; Denton, 1973). Fifty percent of the species likely to be found in the lower Hudson Estuary have been identified as having 48 chromosomes. Ohno, et al. (1969) suggested that ancestral fishes had 48 chromosomes and that many forms have retained the ancestral, diploid complement throughout more than 400 million years of evolution.

Chromosome number, morphology and complete karyotypic analysis have been used extensively in population studies of fishes (Denton, 1973; Fisher and Rachlin, 1972; Arcement and Rachlin, 1976; Kerby, 1972; Chen and Ruddle, 1969). Evidence exists that karyotypic analysis may be used to discern genetic divergence of isolated populations (Arcement and Rachlin, 1976) and perhaps to identify different genetic stocks in mixed populations.

Table 1. Chromosome numbers for estuarine and euryhaline fish species common in the lower Hudson River.

Species	Chromosome Number 2N	N	Reference
Sea lamprey	168		Potter & Rothwell, 1970
American eel	38		Sick, 1962
Alewife	48	24	Mayers & Roberts, 1969
Rainbow trout	60		Simon & Dollar, 1963
Brown trout	80		Svardson, 1945
Goldfish	94 - 104	(47)	Post, 1965 Ohno & Atkin, 1966 Chiarelli, et al., 1969
Carp	104	52	Makino, 1939
Golden shiner	50		Leippman & Hubbs, 1969
Banded killifish	48	24	Chen & Ruddle, 1970 Arcement & Rachlin, 1976
Mummichog	48	24	Chen & Ruddle, 1970 Fisher & Rachlin, 1972
Striped killifish	48	24	Chen & Ruddle, 1970 Fisher & Rachlin, 1972
Fourspine stickleback	46	23	Chen & Ebeling, 1970
Redbreasted sunfish	48	24	Roberts, 1964
Pumkinseed	48	24	Roberts, 1964
Largemouth bass	46	23	Roberts, 1964
White crappie	48	24	Roberts, 1964
White perch	48		Kerby, 1972
Striped bass	48		Kerby, 1972

The present study was undertaken to establish a karyotype for striped bass of Hudson River origin, and to compare that karyotype with that of a population of striped bass studied by Kerby (1972) captured from the James River, Virginia.

The assistance of Dr. J.W. Rachlin, Dept. of Biological Sciences, Herbert Lehman College, C.U.N.Y. in carrying out these studies is greatly appreciated.

Materials and Methods

Karyotypic analysis was performed on striped bass larvae of average total length of 10 mm. Larvae were obtained from the Hudson River Striped Bass Hatchery operated by Texas Instruments, Inc. Verplanck, New York.

Entire larvae were used in the preparation of chromosome spreads for analysis, and the method of Arcement and Rachlin (1976) was followed throughout. Groups of larvae were pre-treated in an hypotonic solution for 1.0 to 1.5 hours. Following pre-treatment the larvae were fixed in a methanol/acetic acid solution for 1/2 hour, divided into three 10 minute intervals, using fresh cold fixative for each 10 minute interval.

Larvae were removed from the fixative with forceps and "flocked" onto xylene-cleaned glass slides. The epithelial cells which adhered to the slides, after removal of scales and other gross debris, were allowed to air dry prior to staining. The slides were stained with buffered (pH 9.0)

Giemsa stain (Patil, et al., 1971), cleared in xylol and mounted for examination. After initial screening, chromosomes were examined for number and types, and the best preparations were used both for camera lucida drawings and photography for more careful study.

Results

An examination of Figures 1, 2 and 3 show that the chromosome complement of these striped bass larvae consists of a total of 48 acrocentric chromosomes. This is in contrast with the preliminary work of Kerby (1972) who reported that the striped bass from the James River, Virginia, had a chromosome complement of 48 chromosomes of which 46 were acrocentric and two were metacentric.

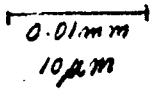
An examination of the idiogram in Figure 1, prepared from the camera lucida drawing in Figure 1 also indicates that there are only acrocentric and no metacentric chromosomes associated with the chromosome complement prepared from the larvae obtained from the Hudson River Striped Bass Hatchery. Further, Table 2 demonstrates that the size range of these chromosomes is from 1.25 to 2.75 µm. A further examination of Table 2 demonstrates that one chromosome is 2.75 µm, four are 2.5 µm, 10 are 2.25 µm, nine are 2.2 µm, 12 are 2.0 µm, four are 1.75 µm, one is 1.7 µm, five are 1.5 µm and two are 1.25 µm long.

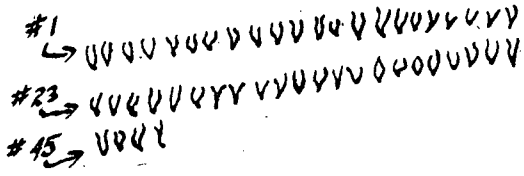
Figure 1

Camera Lucida drawing of Chromosome spread of Roccus saxatilis = Morone saxatilis (Walbaum)

Striped Bass
Roccus saxatilis = Morone saxatilis
Fish #14C
Larvae 10mm Total length
Epithelial spread

Chromsome Count
48 acrocentics

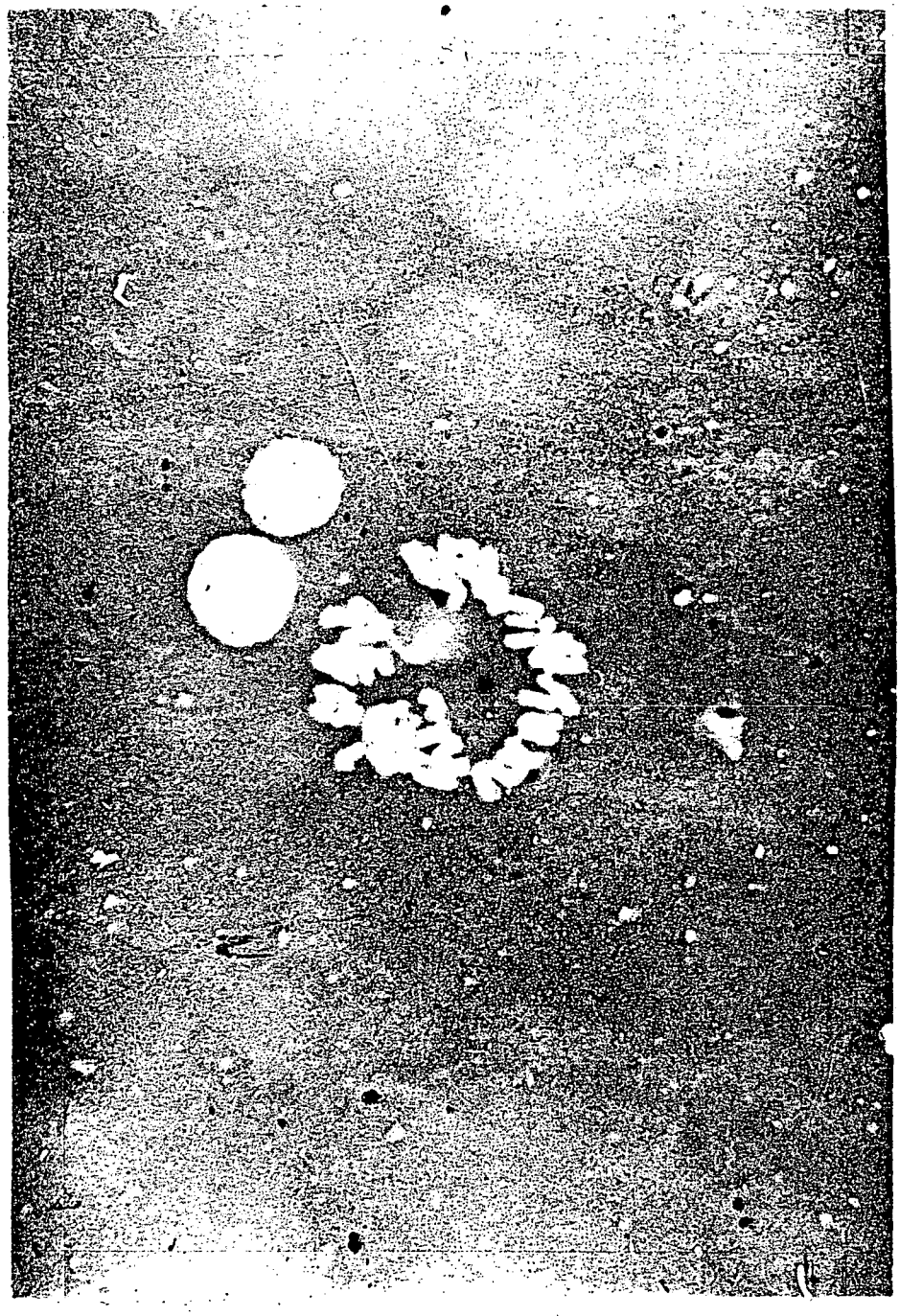




Idiogram of Above Chromosome Spread

Figure 2

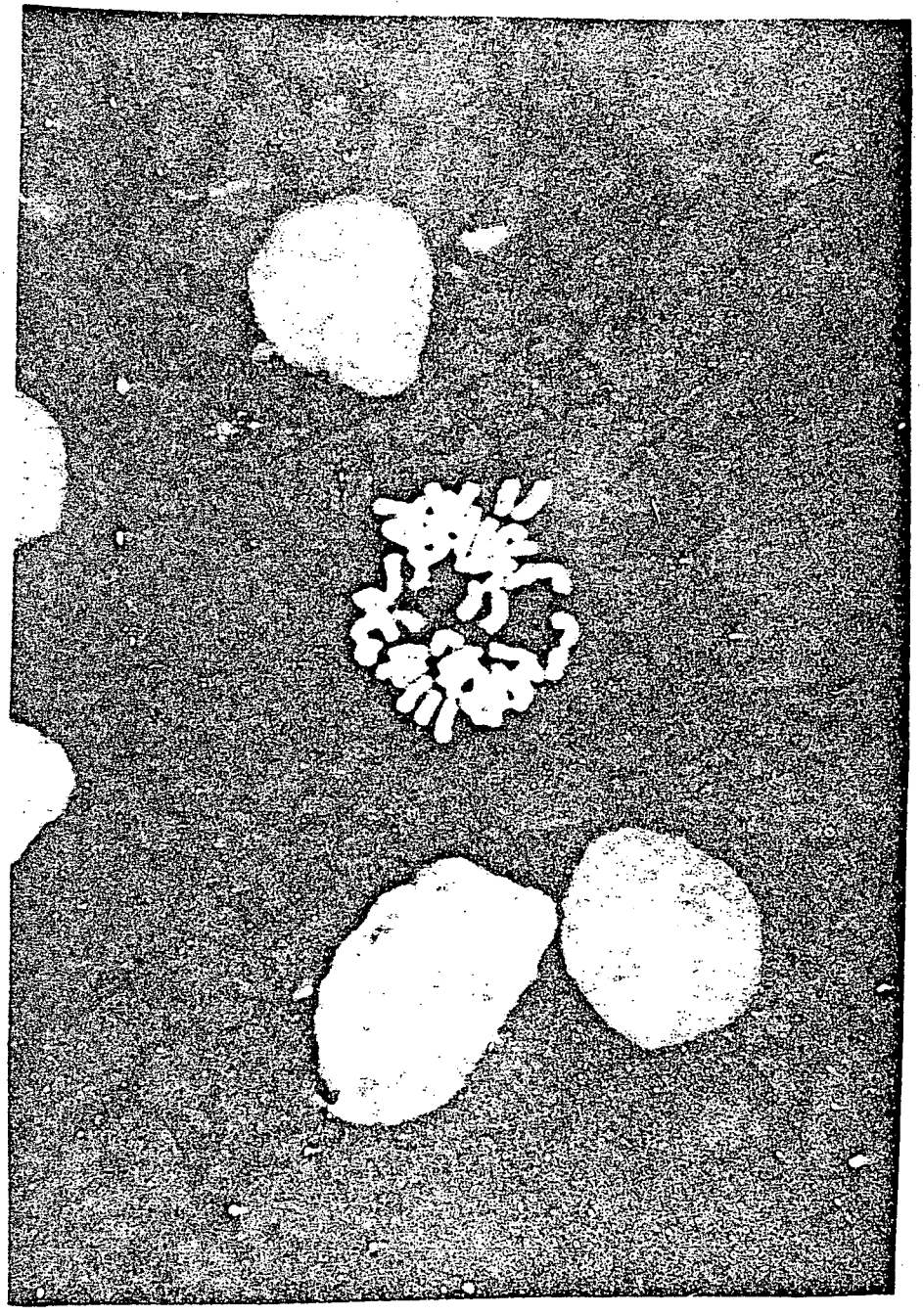
Metaphase chromosome spread from *Morone saxatilis*



10 μm

Figure 3

Metaphase chromosome spread from Morone saxatilis



10 μm

Examination of the slides indicated presumptive banding, however, due to the tightness of coiling of the chromosomes and their small size, one could not resolve the banding with enough precision to use the technique as a means of pairing the homologous chromosomes.

Discussion

A karyotype of striped bass larvae, derived by artificial spawning of adult striped bass captured in the Hudson River Estuary, has been prepared. This karyotype consists of 48 acrocentric chromosomes and resembles closely the published karyotype for the white perch, Morone americana (Kerby, 1972). It differs from the published karyotpye of striped bass, Morone saxatilis, from the James River, Virginia (Kerby, 1972), in that the James River striped bass were reported to have a karyotype consisting of 48 chromosomes of which 46 are acrocentric and two are metacentric. However, Kerby (pers. comm., June, 1976) has indicated that the initial classification of James Rivers striped bass chromosomes as consisting of 46 acrocentrics and 2 metacentrics may have been premature, and that further study of this karyotype is anticipated during the 1977 spawning season.

A difference of this magnitude between the chromosome complements of these two striped bass strains (Hudson River vs. James River) is possible, but unlikely between populations only partially isolated geographically for a relatively

brief period of time. It could be explained on the basis of Robertsonian inheritance, (Mayr, 1963) involving first a centromere division of the two metacentric chromosomes creating a karyotype consisting of 50 acrocentric chromosomes followed by a second event involving chromosome loss; perhaps by a non-disjunction, establishing, once again, a chromosome complement of 48 chromosomes, but now with only acrocentric chromosomes in the complement. Further discussion of this question depends upon additional information regarding karyotypes of striped bass from other populations.

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