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STUDY OF CHROMOSOMAL MORPHOLOGY OF *Xenenthodon cancila* OF GHO-MANASHA STREAM IN JAMMU PART-1

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ABSTRACT

The paper deals with diploid chromosomes count and chromosome morphology including fundamental arm number and total complement length of a Stream fish *Xenenthodon cancila*. Fishes collected from Gho-manasah stream of Jammu. The present observation have been employed to discuss the phylogenetic relationship and karyotype evolution in fishes.

KEYWORDS : Biological yield, Harvest index, Test-weight, Trichloroacetic acid (TCA),Nessler's reagent

The study of chromosomes have been the subject of interest not only the Ichthyologi-sts but also the geneticists for several reasons. In fishes,the use of chromosomal information as tool in taxonomy has even an added importance. The Karyotopic data in them can help in the understanding of vertebrate evolutionary pathway. Their chro-mosomal analysis can, therefore, be useful in understanding the process of speciatrion. The use cytogenetics in fish breeding and fish culture can be of immense help. A chromosomes study of suspected polyploidy fishes would be significant in understanding the role of polyploidy in a speciation in fishes.

First report on fish chromosomes were published by different works. In India , sharma and Agarwal, (1978) work on fish cytology and reported chromosomesnumber in case of three Indian teleosts. Thereafter , Srivastava and Kour, (1964) and Subrahmanyam, (1969) published data on the fish chromosomes. On Indian sense most of the work has also been by Khuda-Buksh (1975,1979);Khuda-Buksh and Nayak,(1982) ; Rishi and Kaul, (1983) ; Sharma and Agarwal (1980);Sharma and Tripathi (1981,1982) and Choudhrari et al., (1982).

The present investigation would be significant in identifying the fish species for hybridiz-Ation experiments and also elucidating the phylogenetic relationships in fishes.

MATERIALS AND METHODS

The specimens were collected from Gho-manasah stream of Jammu with the help of Hand net collecting method were examined from May 2008 . Before the dissection. The fishes were pretreated with colchicine solution to produce metaphase stages. After pretreatment the fishes were dissected and tissue like kidney, gill arches, liver taken out and wash with distilled water. For determination of cytological preparation the slide were prepared by dropping 2-3 drop of cell suspension on a clean slide. The slide were air dried and then slide were stained with 4% Giemsa buffer solution. The chromosomal length was measured using camera lucida sketches , photograph and stage micrometer. The various parameter such as the length of short arm(s) , length of long arm(L), arm ratio (L/S) were used to established karyotype of species. The TCL(Total Complement Length) was calculated adding of absolute length of each chromosomes of the diploid set. TCL% and relative length of each pair chromosomes were work out from total complement length of diploid set by the formula given below:

$$TCL\% = \frac{\text{Absolute length of Chromosomes}}{\text{Total complement length(TCL)}}$$

$$\text{Relative length} = \frac{\text{Absolute length of Chromosomes}}{\text{Absolute length of the largest Chromosome of the complement}} \text{ X } 100$$

The standard deviation standard error for length of each chromosome pair and total complement length (TCl) were calculated in the following way:

$$\text{Standard deviation} = \sqrt{\frac{\sum(x\text{-}x)^2}{n}}$$

Where 'X' is the value for chromosomal length and is different for different complements and 'n' is the number of observations made .

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Table 1: Karyomorphometric analysis of somatic metaphase complement of *Xenentodon cancila*

S.NO.	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X	S.D.	S.E.	TCl%	R.L.%
1.	3.6	4.0	4.0	3.8	3.6	3.6	3.8	3.5	4.0	3.8	3.77	0.1791	0.0566	3.046	100.00
2.	3.4	3.8	3.8	3.6	3.4	3.4	3.6	3.3	3.8	3.6	3.57	0.1791	0.0566	2.885	94.694
3.	3.2	2.8	2.9	2.8	3.0	3.0	2.8	2.6	2.9	2.8	2.88	0.1536	0.0485	2.327	76.392
4.	3.0	2.6	2.8	2.7	2.8	2.8	2.7	2.5	2.7	2.7	2.73	0.1268	0.0401	2.206	72.413
5.	2.8	2.5	2.7	2.6	2.7	2.6	2.5	2.3	2.6	2.6	2.59	0.13	0.0411	2.093	68.700
6.	2.4	2.4	2.5	2.4	2.5	2.4	2.4	2.2	2.5	2.4	2.41	0.0830	0.0262	1.947	63.925
7.	2.3	2.1	2.3	2.2	2.3	2.3	2.3	2.1	2.2	2.3	2.24	0.08	0.0252	1.810	59.416
8.	3.2	3.5	3.2	3.1	3.2	3.1	3.1	2.9	3.3	3.2	3.18	0.1469	0.0464	2.569	84.350
9.	2.8	2.9	2.9	2.8	2.8	2.9	2.9	2.7	2.9	3.0	2.86	0.08	0.0252	2.311	75.862
10	2.7	2.8	2.8	2.7	2.7	2.7	2.8	2.6	2.8	2.8	2.74	0.0663	0.0209	2.214	72.679
11.	2.5	2.5	2.6	2.5	2.5	2.5	2.6	2.4	2.7	2.7	2.55	0.0921	0.0291	2.060	67.639
12.	2.3	2.4	2.5	2.4	2.3	2.4	2.5	2.3	2.6	2.4	2.41	0.0943	0.0298	1.947	63.925
13.	2.2	2.3	2.3	2.2	2.2	2.2	2.3	2.1	2.4	2.2	2.24	0.08	0.0252	1.810	59.416
14.	2.1	2.2	2.2	2.1	2.1	2.1	2.2	2.0	2.3	2.1	2.14	0.08	0.0252	1.729	56.763
15.	2.0	2.1	2.1	2.0	2.0	2.0	2.1	1.9	2.2	2.0	2.04	0.08	0.0252	1.648	54.111
16.	2.6	2.9	2.9	2.8	2.6	2.7	2.8	2.7	2.9	2.8	2.77	0.11	0.0347	2.238	73.474
17.	2.5	2.7	2.8	2.7	2.5	2.5	2.7	2.5	2.8	2.5	2.62	0.1248	0.0394	2.117	69.496
18.	2.4	2.5	2.6	2.5	2.4	2.4	2.6	2.4	2.7	2.4	2.49	0.1044	0.0330	2.012	66.047
19.	2.3	2.3	2.4	2.3	2.3	2.3	2.5	2.3	2.5	2.3	2.35	0.0806	0.0254	1.899	62.334
20.	2.1	2.3	2.3	2.2	2.2	2.1	2.3	2.1	2.3	2.2	2.21	0.0830	0.0262	1.786	58.620
21.	2.3	3.0	2.9	2.9	2.7	2.5	2.9	2.7	2.9	2.6	2.74	0.2107	0.0666	2.214	72.679
22.	1.9	2.4	2.5	2.4	1.9	1.9	2.5	2.3	2.5	2.3	2.26	0.2457	0.0777	1.826	59.946
23.	1.9	2.2	2.3	2.2	1.9	1.8	2.3	2.1	2.3	2.2	2.12	0.1777	0.0562	1.713	56.233
24.	1.8	2.1	2.1	2.0	1.8	1.7	2.1	1.8	2.2	2.0	1.96	0.1624	0.0513	1.583	51.989
TCl	120.6	126.6	128.8	123.8	120.8	119.8	126.6	116.6	130.0	123.8	123.74	4.0763	1.2890		

RESULTS AND DISCUSSION

Six individuals of undifferentiated sex of Xenentodon cancila were procured for the resent study . A study of karyotype revealed 7 pairs of meta- ,8 pairs of submeta- ,5 pairs of subtelo and 4 pairs of telocentric chromosomes.No heteromorphic chromosome pair could be identified . the fundamental arm number has been calculated to be 88 . The haploid chromosome formula has been found to be 7m+8sm+5st+4t.

MORPHOMETRIC ANALYSIS

The absolute length of the chromosomes ranged from 3.77 to 2.24 in metacentrics , 3.18 to 2.04 in. Subtelocentrics , 2.77 to 2.21 in subtelocentrics and 2.74 to 1.96 in telocentrics (Table,2). The total complement length was calculated to be 123.74 with the standard deviation of 4.0763 and standard error of 1.2890.

The first metacentric pair is largest in the complement with an absolute length of 3.77 having TCl % of 3.046 and relative length of 100% . The 24th pair (last telocentric pair) is smallest in the complement (absolute length 1.96) with TCl % of 1.583 and relative length of 51.989% (Table ,1) .

The analysis of standard deviation and deviation and standard error (Table,2) revealed the maximum standard deviation of 0.2107 and standard error of 0.666 for 21st pair. The minimum standard deviation (0.0663) and standard error (0.0209) have been found for pair number 10 . *X . cancila* has already been studied by Srivastava and Kour (1964), Sharma and Tripathi , (1981); Srivastava and Kour, (1964) reported 50 acrocentric chromosomes in the diploid complement of *X. cancila* .Sharma and Tripathi, (1981) recorded 2n = 48 comprising 16 meta - , 18 submeta - , 6 subtelo - and 8 acrocentric chromosomes (NF=82) in the same species from gho-Manasah stream jammu. Khuda Bukhsh and Nayak, (1987) confirmed the diploid number 2n=48 for *X. cancila* ,but recorded different chromosomes morphology of 30 metacentrics 2 submetacentrics 2 subtelocentrics and 14 telocentrics with NF = 82 in Haldia (West Bengal) population . Sharma and Tripathi, (1981) and Khuda Bukhsh and Nayak ,(1987) considered subtelo-and telocentric as uniarmed .The present observations of 48 chromosomes in the diploid complement of Jammu population of *Xenentodon cancila* with 14 meta-, 16 submeta- , 10 subtelo- and 8 telocentrics

Table 2: Karyomorphometric analysis of somatic metaphase complement of *Xenentodon cancila*

Chromo-some Pair No.	length of short arm (S) "	Length of long arm (L) "	Absolute length (L+S) "	Arm ratio (L/S)	Chromosome morphology
1	1.7	1.9	3.6	1.11	m
2	1.7	1.7	3.4	1.0	m
3	1.5	1.7	3.2	1.13	m
4	1.5	1.5	3.0	1.0	m
5	1.3	1.5	2.8	1.15	m
6	1.1	1.3	2.4	1.18	m
7	1.1	1.2	2.3	1.09	m
8	1.0	2.2	3.2	2.2	sm
9	1.0	1.8	2.8	1.8	sm
10	0.9	1.8	2.7	2.0	sm
11	0.8	1.7	2.5	2.125	sm
12	0.6	1.7	2.3	2.83	sm
13	0.6	1.6	2.2	2.66	sm
14	0.6	1.5	2.1	2.5	sm
15	0.5	1.5	2.0	3.0	sm
16	0.5	2.1	2.6	4.2	st
17	0.5	2.0	2.5	4.0	st
18	0.5	1.9	2.4	3.8	st
19	0.4	1.9	2.3	4.75	st
20	0.4	1.7	2.1	4.25	st
21	-	2.1	2.1	-	t
22	-	1.9	1.9	-	t
23	-	1.9	1.9	-	t
24	-	1.8	1.8	-	t

Diploid chromosome number = 48
Diploid chromosome formula = 14m+16sm+10st+8t
Fundamental arm number = 88
Total complement length = 120.2

(NF = 88, considering subtelocentrics as biarmed) are based on studies made by application of both conventional Giemsa staining technique and G - banding technique, therefore the present recording provide an accurate karyotype of *X. cancila*.

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