

STUDY OF CHROMOSOMAL MORPHOLOGY OF *Barilius vagra* OF KOTA , STREAM IN JAMMU PART-2**UMMEY TAMIM AHRARI^{a1} AND S.Z. ALI^b**

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^aE-mail: tamim_007@gmail.com^bE-mail: dr.saaduz@gmail.com**ABSTRACT**

The paper deals with diploid chromosomes count and chromosome morphology including fundamental arm number and total complement length of a Stream fish *Barilius vagra*. Fishes collected from Kota, Stream of Jammu. The present observation have been employed to discuss the Phylogenetic Kinship and karyotype evolution in fishes.

KEYWORDS : Kota, Stream, Chromosomal morphology, Phylogenetic, Karyotype

The study of chromosomes have been the subject of interest not only the Ichthyologists but also the geneticists for several reasons. In fishes, the use of chromosomal information as tool in taxonomy has even an added importance. The Karyotypic data in them can help in the understanding of vertebrate evolutionary pathway. Their chromosomal analysis can, therefore, be useful in understanding the process of speciation. 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 Retziat (1890) on the agnathan, *Myxine glutinosa* and, *Pristiurus melanostomus*. In India, Sharma and Tripathi (1981) work on fish cytology and reported chromosomes number in case of three Indian teleosts. Thereafter, Verma (1960), Srivastava and Kour (1964) and Subrahmanyam (1969) published data on the fish chromosomes. On Indian sense most of the work has also been by Prasad and Manna (1971); Khuda-Buksh, (1975, 1979); Khuda-Buksh and Nayak (1982); Sharma and Agarwal, (1978, 1980); Sharma and Tripathi (1981, 1982); Choudhry et al., (1982).

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

MATERIALS AND METHODS

The specimens were collected from Kota, Stream of Jammu with the help of Hand net collecting method were

examined. 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:

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

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

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

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

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 Chromosomes Of Complement of *Barilius vagra* (Undifferentiated Sex)

Chromo-Somes Pair no.	Length of short arm (S)'μ'	Length of long arm (L)'μ'	Absolute length (L+S)'μ'	Arm ratio (L/S)	Chromo-somes morphology
1.	0.9	1.0	1.9	1.11	m
2.	0.8	0.9	1.7	1.125	m
3.	0.8	0.8	1.6	1.0	m
4.	0.7	0.8	1.5	1.14	m
5	0.7	0.8	1.5	1.14	m
6	0.8	1.6	2.5	2.0	sm
7	0.8	1.5	2.3	1.87	sm
8	0.7	1.5	2.2	2.14	sm
9	0.7	1.4	2.1	2.0	sm
10	0.6	1.3	1.9	2.16	sm
11	0.6	2.0	2.6	3.33	st
12	0.5	1.8	2.3	3.6	st
13	0.4	1.4	1.8	3.5	st
14	0.4	1.5	1.8	3.5	st
15	0.4	1.3	1.7	3.25	st
16	0.4	1.3	1.7	3.25	st
17	0.3	1.1	1.4	3.66	st
18	-	2.4	2.4	-	t
19	-	2.1	2.1	-	t
20	-	1.9	1.9	-	t
21	-	1.8	1.8	-	t
22	-	1.6	1.6	-	t
23	-	1.5	1.5	-	t
24	-	1.4	1.4	-	t
25	-	1.1	1.1	-	t

Diploid chromosomes number = 50

Diploid chromosomes formula = 10m+10sm+14st+16t

$$\text{Standard error} = \frac{\text{Standard deviation}}{\sqrt{n}}$$

RESULTS AND DISCUSSION

Seven individuals of undifferentiated sex were utilized for chromosome study. Thirty well-spread metaphase plates were selected for the determination of diploid chromosome number and morphology of the chromosomes 26 cells (86.66%) showed the presence of 50 chromosomes in the diploid complement. A study of karyotype showed 50 chromosomes to comprise 5 pairs of meta-, 5 pairs of submeta-, 7 pairs of subtelo- and 8 pairs of telocentric chromosomes. No heteromorphic chromosome pair could be distinguished. The

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fundamental arm number (NF) was calculated to be 84, whereas the haploid chromosome formula was found to be 5m+5sm+7st+8t.

Morphometric Analysis

The absolute size of the chromosomes (Table, 1) ranged from 2.38 to 1.84 in metacentrics, 2.82 to 2.26 in submetacentrics, 2.95 to 1.73 in subtelocentrics and 2.81 to 1.46 in telocentrics. The total complement length (TCL) was calculated to be 112.08 with standard deviation of 7.7279 and standard error of 2.4437 (Table 2).

Table 2 : Mean Absolute Length, Total Complement Length And Standard Deviation, Standard In Error, Tci%, Relative Length of Chromosomes *Barilius vagra*

CH. 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.	1.9	2.6	2.2	2.2	2.4	2.6	2.4	2.4	2.5	2.6	2.38	0.2135	0.0675	2.123	80.677
2.	1.7	2.5	1.0	2.1	2.5	2.5	2.3	2.4	2.4	2.5	2.26	0.2497	0.0789	2.016	76.610
3.	1.6	2.2	1.8	1.8	2.2	2.2	2.6	2.2	2.2	2.3	2.04	0.22	0.0695	1.820	69.152
4.	1.5	2.1	1.7	1.8	2.1	2.1	2.0	2.0	2.0	2.1	1.93	0.19	0.0600	1.721	65.423
5.	1.5	1.9	1.7	1.7	2.0	2.0	1.9	1.9	1.9	2.0	1.84	0.1496	0.0473	1.641	62.372
6.	2.4	2.8	2.7	2.8	3.0	3.0	2.9	2.8	2.8	3.0	2.82	0.1720	0.0544	2.516	95.593
7.	2.3	2.6	2.6	2.6	2.8	2.8	2.7	2.6	2.6	2.8	2.64	0.1428	0.0451	2.355	89.391
8.	2.2	2.5	2.5	2.5	2.6	2.6	2.6	2.6	2.6	2.6	2.54	0.1280	0.0404	2.266	86.101
9.	2.1	2.4	2.4	2.4	2.6	2.6	2.5	2.5	2.4	2.5	2.44	0.1356	0.0428	2.177	82.711
10.	1.9	2.2	2.2	2.2	2.4	2.4	2.4	2.3	2.3	2.3	2.26	0.1428	0.0451	2.016	76.610
11.	2.6	2.9	2.8	2.8	3.1	3.1	3.0	2.9	3.0	3.2	2.95	0.1802	0.0570	2.632	100.00
12.	2.3	2.6	2.6	2.6	2.8	2.8	2.8	2.7	2.7	2.8	2.67	0.1486	0.0470	2.382	90.508
13.	1.8	2.3	2.2	2.2	2.3	2.3	2.3	2.4	2.4	2.5	2.27	0.1791	0.0566	2.025	76.949
14.	1.8	2.2	2.1	2.1	2.2	2.2	2.3	2.3	2.3	2.3	2.19	0.1513	0.0478	1.953	74.237
15.	1.7	2.1	2.0	2.0	2.1	2.1	2.2	2.2	2.1	2.2	2.07	0.1417	0.0448	1.846	70.169
16.	1.7	2.1	1.9	1.9	2.1	2.1	2.1	2.1	2.0	2.1	2.01	0.13	0.0411	1.793	68.135
17.	1.4	1.8	1.6	1.7	1.8	1.8	1.8	1.8	1.8	1.8	1.73	0.1268	0.0401	1.543	58.644
18.	2.4	2.6	2.7	2.7	2.9	2.9	3.0	2.9	2.9	3.0	2.81	0.1920	0.0607	2.507	95.254
19.	2.1	2.4	2.4	2.5	2.7	2.7	2.7	2.7	2.7	2.8	2.57	0.2051	0.0648	2.293	87.118
20.	1.9	2.2	2.2	2.3	2.3	2.3	2.4	2.4	2.5	2.5	2.31	0.17	0.0537	2.061	78.305
21.	1.8	2.1	2.1	2.1	2.3	2.3	2.3	2.2	2.3	2.4	2.19	0.1640	0.0518	1.953	74.237
22.	1.6	2.0	1.8	1.8	2.1	2.1	2.2	2.2	2.2	2.2	2.02	0.2039	0.0644	1.802	68.474
23.	1.5	1.9	1.7	1.8	2.0	2.0	2.6	2.0	2.1	2.0	1.89	0.17	0.0537	1.686	64.067
24.	1.5	1.8	1.7	1.7	1.8	1.8	1.8	1.8	1.8	1.8	1.75	0.0921	0.0291	1.561	59.322
25.	1.1	1.6	1.4	1.4	1.5	1.5	1.4	1.5	1.6	1.7	1.46	0.1562	0.0493	1.302	49.491
TCL	92.6	112.8	106	107.4	116.6	117.6	116.0	115.6	116.2	112.0	112.08	7.7279	2.4437		

The 11th pair (1st subtelocentri pair) is largest in the complement having absolute length of 2.95 with TCL % of 2.632 and relative length of 100% (Table, 2). The 25th pair (last telocentric pair) is smallest in the complement having absolute length of 1.46 with TCL % of 1.302 and relative length of 49.49 %.

The standard deviation and standard error analysis (Table, 2) for the length of each chromosome pair revealed the maximum standard deviation (0.2497) and standard error (0.0789) for 2nd pair. the minimum standard deviation (0.0921) and standard error (0.0291) was found for 24th pair.

Cyprinidae is the largest family of order Cypriniformes and includes about 175 genera 1600 species .of these only about 317 species including present work have so far been cytologically studied. During the course of present study seven species belonging to 6 genera have been karyologically worked , of which 3 have been studied for the first time viz., *Schizothoracichthys labiatus*, *Ptychobarbus conirostris* and *Barilius vagra*.

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