Indian J.Sci.Res. 16 (1): 98-103, 2017

ISSN: 0976-2876 (Print)
ISSN: 2250-0138(Online)

CHARACTERIZATION OF CHROMOSOMAL MORPHOLOGY OF *Channa gachua* OF TONS (TAMSA) RIVER IN AZAMGARH

FATIMA ANUM[a1], REETU DEVI[b] AND S.Z.ALI[c]

[abc]Department of Zoology, Shibli National (P.G.) College, Azamgarh, U.P. India

ABSTRACT

In the study, the characterizations of a stream fish *Channa gachua* was carried out in Tons river of Azamgarh. The study particularly deals with diploid chromosomes count as well as chromosomes morphology which consist of fundamental arm number and total complement length also. The current observation have been recorded to discuss the phylogenetic relationship and karyotypic evolution in fishes.

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

Fishes are unique in that it is quite possible to separate chromosomes from their tissues in a short period that is 2 to 3 hours for further analysis. However, the analysis of fish chromosome is quiet difficult because most of the fishes have chromosomes relatively dense and small to extract. The present chromosomal study is not only limited to ichthyologists but also to genetics due to the advancement in techniques. In fishes, apart from taxonomy, chromosomal information serves as an important tool in classification as well as in understanding the process of speciation with many difficulties. In addition, the karyotopic data in them can help in understanding of vertebrate evolutionary pathways. The utilization of cytogenetics in fish breeding and fish-culture would be significant in genesis. Chromosomal analysis can illustrate whether hybridization in the real terms has taken place or not. Moreover, Chromosomal anomalies study can be of immense help in determining genesis of fish pathology.

Different reports on the chromosomes of species were published internationally by number of workers. In India S.Z.Ali et al (2013) illustrated his research work on chromosomal morphology of *Barilius vagra* of Kota stream in Jammu. Sharma et al (2002) presented a review of chromosomal banding in fishes and reported karyotypic diversity in genus Mystus (Bagridae: pisces). In addition, Khuda-Bukhsh et al (1978, 1975) reported data on somatic chromosomes of an esturine fish, *Trypauchen vaginaas* well as an exotic fish, *Puntius japonicus*. Subsequently, various works on fish karyotypes were reported (Choudhury et al, 1982 ; Barat et al, 1986). Different studies on somatic chromosomes of various individuals have been reported by Chakraborty et al (1989).

A good deal of research have been carried out of the chromosomes of different species of fishes for karyotypic evolution and also elucidating the phylogenetic relationships respectively.

MATERILAS AND METHODS

Fish specimens were collected from Mansarlake in Jammu, by cast- net collecting method were examined. Afterwards, they were pretreated with 0.5% colchicine solution via intramuscular route for 3-5 hours to procure metaphase stages. In the next stage, dissection was performed and tissues like liver, kidney, gill arches were separated and washed with distilled water and immediately transferred to hypotonic solution and fixed respectively. After that, cytological preparations were prepared by applying 2-3dops of cell suspension on a clean slide, air dried and then stained with 4% Giemsa buffer solution. Micrometry was performed to measure the chromosomal length using camera lucida sketches, photographs 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 chromosoms of the diploid set. TCL% and relative length of each pair chromosomes were work out from total compartment length of diploid set by the formuls given below:

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

---

[1]**Corresponding Author**

Relative length = $\frac{Absolute\ length\ of\ chromosomes}{absolute\ length\ of\ the\ largest\ chromosome\ of\ the\ component}$

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

Standard deviation= $\sqrt{\sum}\,(x - x)2/n$

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

RESULTS AND DISCUSSION

Table 1: Karyomorphometric Analysis of somatic metaphase chromosomes of complement of *Channa gachua*

Chromosomes pair no.	Length of short arm (S) µ	Length of long arm (L) µ	Absolute length (L+S) µ	Arm ratio (L+S)	Chromosomes morphology
1	1.6	1.7	3.3	1.06	m
2	1.5	1.6	3.1	1.06	m
3	1.4	1.4	2.8	1	m
4	1.2	1.4	2.6	1.16	m
5	0.9	0.9	1.8	1	m
6	0.9	2.2	3.1	2.44	sm
7	0.9	1.8	2.7	2	sm
8	0.8	1.7	2.5	2.125	sm
9	0.7	1.5	2.2	2.142	sm
10	0.6	1.3	1.9	2.166	Sm
11	0.6	2.1	2.7	3.5	St
12	0.6	2	2.6	3.3	St
13	0.5	1.8	2.3	3.6	St
14	0.5	1.7	2.2	3.4	St
15	0.5	1.6	2.1	3.2	St
16	0.5	1.6	2.1	3.2	St
17	0.4	1.5	1.9	3.75	St
18	-	2.5	2.5	-	T
19	-	2.4	2.4	-	T
20	-	2.3	2.3	-	t
21	-	2.3	2.3	-	T
22	-	2	2	-	T
23	-	2	2	-	T
24	-	1.8	1.8	-	T
25	-	1.7	1.7	-	T
26	-	1.7	1.7	-	T
27	-	1.6	1.6	-	T
28	-	1.6	1.6	-	T
29	-	1.6	1.6	-	T
30	-	1.5	1.5	-	T

31	-	1.5	1.5	-	T
32	-	1.5	1.5	-	T
33	-	1.4	1.4	-	T
34	-	1.4	1.4	-	T
35	-	1.3	1.3	-	T
36	-	1.3	1.3	-	T
37	-	1.3	1.3	-	T
38	-	1.2	1.2	-	T
39	-	0.8	0.8	-	T

Diploid chromosomes number = 78
Diploid chromosomes formula = 10m+10sm+14st+44t
Fundamental arm number (NF) = 112
Total complement length = 157.2µ

Channa gachua's eight individuals of undifferentiated sex were selected for the present study. Diploid number of chromosomes in this species were determined by utilizing 34 metaphase plates. 28 metaphase plates (82.35%) depicted the presence of 78 elementsin the diploid complement. Given Karyotype study illustrates 78 elementsto comprise 5 pairs of meta-, 5 pairs of submeta-, 7 pairs of subtelo- and 22 pairs of telocentric chromosomes. The fundamental arm number (NF) was found to be 112, subsequently the haploid chromosomes formula was calculated as 5m+5sm+7st+22t.

MORPHOMETRIC ANALYSIS

Chromosome's absolute length ranged between 3.32µ and 1.71 µ in metacentrics, 3.1 µ to 1.93 µ in submetacentrics, 2.71 µ to 1.88 µ in subtelocentrics and 2.53 µ to 0.8 µ in telocentrics (Table 2). The total complement length was calculated to be 123.74 with the standard deviation of 14.862 and standard error of 4.699

The first pair is the largest amongst all, having an absolute length 3.32 µ with TCL% of 2.119 and relative length of 100%. However, an absolute length of 0.8 µ is the smallest telocentric pair having TCL% 0.5107 and relative length of 24.096% (Table 2).

Table 2: Mean Absolute Length, Total Complement Length And Standard Deviation, Standard Error, Tcl%, Relative Length Of Chromosomes *Channa gachua*

X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X	S.D.	S.E.	TCL %	R.L. %
3.3	3.6	3.2	3	3	3	3.8	4	3.2	3.1	3.32	0.34	0.1075	2.1197	100
3.1	3.4	3	2.8	2.9	2.8	3.6	3.7	3	3	3.13	0.3067	0.097	1.9984	94.277
2.8	3	2.7	2.5	2.6	2.6	3.1	3.2	2.7	2.8	2.8	0.219	0.0692	1.7877	84.337
2.6	2.8	2.5	2.4	2.4	2.4	2.8	2.8	2.6	2.5	2.58	0.16	0.0505	1.6472	77.71
1.8	2	1.7	1.6	1.5	1.2	1.9	2	1.8	1.6	1.71	0.2343	0.074	1.0918	51.506
3.1	3.4	3	2.8	2.8	2.7	3.5	3.6	3.1	3	3.1	0.2932	0.0927	1.9793	93.373
2.7	2.9	2.6	2.4	2.5	2.5	3	3.4	2.5	2.4	2.69	0.3047	0.0963	1.7175	81.024
2.5	2.7	2.4	2.3	2.3	2.4	2.9	3.2	2.4	2.3	2.54	0.287	0.0907	1.6217	76.506

2.2	2.4	2.1	2	2	2.1	2.6	3	2	2	2.24	0.3168	0.1001	1.4302	67.469
1.9	2.1	1.8	1.7	1.7	1.7	2.3	2.5	1.8	1.8	1.93	0.2647	0.0837	1.2322	58.132
2.7	2.9	2.6	2.5	2.5	2.5	3.1	3	2.7	2.6	2.71	0.2071	0.0654	1.7303	81.626
2.6	2.8	2.5	2.4	2.4	2.4	2.8	2.8	2.5	2.5	2.57	0.1615	0.051	1.6409	77.409
2.3	2.5	2.3	2.1	2.1	2.2	2.5	2.6	2.4	2.5	2.35	0.1688	0.0533	1.5004	70.783
2.2	2.4	2.1	2	2.1	2.1	2.5	2.5	2	2.3	2.24	0.1685	0.0532	1.4302	67.469
2.1	2.3	2.1	1.9	1.9	2	2.4	2.4	1.8	2.2	2.14	0.1743	0.0551	1.3663	64.457
2.1	2.2	2	1.8	1.8	1.9	2.3	2.3	2.7	2.1	2.05	0.1746	0.0552	1.3089	61.746
1.9	2.1	1.8	1.7	1.7	1.7	2.1	2.2	2.5	1.8	1.88	0.1777	0.0562	1.2003	56.626
2.5	2.7	2.4	2.3	2.3	2.4	2.8	2.9	2.4	2.5	2.53	0.1951	0.0617	1.6153	76.204
2.4	2.6	2.3	2.2	2.2	2.3	2.7	2.8	2.2	2.4	2.42	0.1989	0.0629	1.5451	72.891
2.3	2.5	2.2	2.1	2.1	2.2	2.6	2.6	2.1	2.3	2.32	0.172	0.0544	1.4812	69.879
2.3	2.4	2.1	2.1	2.1	2.1	2.6	2.6	2.2	2.2	2.27	0.19	0.06	1.4493	68.373
2	2.2	1.9	1.8	1.9	2	2.3	2.4	1.9	1.9	2.03	0.19	0.06	1.2961	61.1443
2	2.1	1.9	1.8	1.8	1.9	2.2	2.3	1.8	1.8	1.96	0.1743	0.0551	1.2514	59.036
1.8	2	1.7	1.6	1.6	1.8	2.1	2.2	1.7	1.8	1.83	0.1951	0.0617	1.1684	55.12
1.7	1.9	1.7	1.5	1.5	1.7	2	2.1	1.7	1.7	1.75	0.1857	0.0587	1.1173	52..710
1.7	1.8	1.6	1.5	1.5	1.6	2	2.1	1.7	1.6	1.71	0.192	0.06074	1.0918	51.506
1.6	1.8	1.6	1.5	1.4	1.6	1.9	2	1.6	1.6	1.66	0.1743	0.0551	1.0598	50
1.6	1.7	1.5	1.4	1.4	1.5	1.8	2	1.6	1.5	1.6	0.1788	0.0565	1.0215	48.192
1.6	1.7	1.5	1.4	1.3	1.4	1.8	2	1.5	1.5	1.57	0.2002	0.0633	1.0024	47.289
1.5	1.6	1.4	1.4	1.3	1.4	1.7	1.9	1.5	1.4	1.51	0.17	0.0537	0.9641	45.481
1.5	1.6	1.4	1.3	1.3	1.3	1.7	1.9	1.4	1.4	1.48	0.1886	0.0596	0.9449	44.578
1.5	1.6	1.3	1.3	1.2	1.3	1.6	1.8	1.4	1.3	1.43	0.1791	0.0566	0.913	43.072

1.4	1.5	1.3	1.3	1.2	1.2	1.6	1.8	1.3	1.3	1.39	0.1813	0.0573	0.8874	41.867
1.4	1.5	1.2	1.2	1.2	1.2	1.5	1.7	1.2	1.2	1.33	0.1734	0.0548	0.8491	40.06
1.3	1.4	1.2	1.2	1.1	1.1	1.5	1.5	1.2	1.2	1.27	0.1417	0.0448	0.8108	38.253
1.3	1.4	1.2	1.1	1.1	1.1	1.4	1.4	1.1	1.1	0.22	0.1326	0.0419	0.7789	36.746
1.3	1.3	1.1	1.1	1	1	1.4	1.3	1.1	1	1.16	0.1428	0.0451	0.7406	34.939
1.2	1.2	1	1	0.9	1	1.3	1.2	1	1	1.08	0.1248	0.0394	0.6895	32.53
0.8	0.9	0.8	0.7	0.7	0.7	0.9	1	0.8	0.7	0.8	0.1	0.0316	0.5107	24.096
157.2	169.8	149.4	141.4	140.8	144	177.2	185.6	151	149.8	156.62	14.8621	4.6997		

The standard deviation and standard error analysis (Table 2) for the length of each chromosomes demonstrated the maximum standard deviation (0.34) and standard error (0.1075) for the first pair, while the minimum standard deviation (0.10) and standard error (0.0316) was found for 39th pair (telocentric pair). A diploid count of 78 chromosomes in *Channa gachua*reported by Manna and Parasad (1973) comprising 12 meta-, 12 submeta-, and 54 telocentrics (NF=102). Sharma and Agarwal (1981) mentioned varied chromosome morphology *i.e.* 2n=78, 10 meta-, 8 submeta-, 8 subtelo- and 52 telocentric chromosomes having NF=104. The present study of 78 chromosomes in the diploid complement with 10 meta-, 10 submeta-, 14 subtelo-, 44 telocentric chromosomes and NF=112 in *Channa gachua* has been reinvestigated from Azamgarh based on application of conventional geimsa staining and C-banding technique therefore the present observation gives an accurate information about karyotype of *Channa gachua*.

REFERENCES

Ahrari UT, Ali S. STUDY OF CHROMOSOMAL MORPHOLOGY OF Barilius vagra OF KOTA, STREAM IN JAMMU PART-2. Indian Journal of Life Sciences. 2013;2(2):91.

Barat A, Khuda-Bukhsh A. Karyomorphological studies in two species of fishes, Lepidocephalichthys guntea (fam: Cobitidae) and Mystus corsula (fam: Bagridae). Perspectives in Cytology and Genetics. 1986;5:115-8.

Bhattacharya P. overview of genetical research in the animal kingdom. Genetical research in India/[chief editor, PL Jaiswal]. 1983.

Chakraborty S, Kagwade P. CHROMOSOME COUNTS OF NIBEA SEMILUCTUOSA AND JOHNIUS BELANGERH (PISCES: SCIAENIDAE). Indian Journal of Fisheries. 1986;33(1):115-8.

Chakraborty S, Kagwade P. Somatic chromosomes of two marine teleosts. Fish Genetics in India. 1989:63-8.

Chatterjee K, Majhi A. Chromosomes of Mugil parsia Hamilton (Teleostei, Mugiliformes: Mugilidae). Genen Phaenen. 1973;16(2):51-4.

Choudhury RC, Prasad R, Das CC. Karyological studies in five tetraodontiform fishes from the Indian Ocean. Copeia. 1982;1982(3):728-32.

Das P, Jhingran AG. Fish genetics in India. Proceedings. 1989.

Dhar N, Chatterjee K. Chromosomal evolution in Indian murrels (Channiformes: Channidae). Caryologia. 1984;37(4):359-71.

Kaur D, Srivastava M. The structure and behaviour of chromosomes in five fresh-water teleosts. Caryologia. 1965;18(2):181-91.

Sharma O, Tripathi N, Sharma K. A review of chromosome banding in fishes. Some aspects of chromosome structure and functions: Springer; 2002. p. 109-22.

Sharma O, Tripathi N. Karyotypic diversity in genus Mystus (Bagridae: pisces). Cytologia. 1986;51(1):1-9.

Khuda-Bukhsh A. Somatic chromosomes of an esturine fish, Trypauchen Vagina (Fam: Gobidae) from Sagar Island [India]. Current Science (India). 1978.

Khuda-Bukhsh A. Somatic chromosomes of an exotic fish Puntius japonicus. J Cytol Genet Cong Suppl. 1975:118-20.