Egyptian Journal of Aquatic Biology & Fisheries
Zoology Department, Faculty of Science,
Ain Shams University, Cairo, Egypt.
ISSN 1110 - 6131 Vol. 21(1): 1-9 (2017)
www.ejabf.js.iknito.com

Karyological Characterization of Three Fish Species (Family: Characidae)

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ARTICLE INFO
Article History:
Received: Dec. 2016
Accepted: Jan. 2017
Available online: May 2017

Keywords:
Zoology
Cytogenetics
Karyotype
Metaphase
Fishes
family Characidae

ABSTRACT

The number of cytogenetic studies of fresh water fishes was increased in the recent years. Fish groups, such as Family: Characidae, comprises many of fishes which have economic importance. In the present study, the metaphase chromosomes and their karyotypes have been studied in three species of that family by using cytogenetic analysis. Fish species were *Gymnocorymbus ternetzi, Moenkhausia sanctaefilomenae* and *Metynnis argenteus*. All samples were collected from ornamental fish farms in Egypt. The diploid chromosome number and fundamental numbers of the three species under study were 2n = 50 and FN = 80, 2n = 50 and FN = 100 and 2n = 62 and FN = 122, respectively.

INTRODUCTION

Characidae is the largest family of the order Characiformes with approximately 776 species and 152 genera [Froese & Pauly, 2005]. The study of chromosomes had become an important biodiversity-detection tool and could be also used to measure the biodiversity evolutionary aspects [Bertollo *et al.*, 2000]. In addition, it enables the development of evolutionary, taxonomic, and phylogenetic inferences resulting from the support provided by the conservation of Neotropical fish species [Jacobina *et al.*, 2011].

Chromosomes are cytological units comprised of highly condensed DNA and associated with a series of proteins. When the chromosomes are ordered according to their size and shape and identified by differential staining, they constitute the karyotype, which is believed to be unique for the great majority of species. Karyotypic data have contributed to the studies of biology, genetics, and systematic of fish fauna. This is particularly true in respect to diagnosis of sibling species [Nakayama, 1997].

Karyological study can be useful for addressing a variety of evolutionary and genetic questions about animals and may permit detection of changes that modified an ancestral karyotype as it evolved into new lines and chromosomal analysis is

important for genetic control, taxonomy and evolutionary studies [Suleyman *et al.*, 2004].

The order Characiformes have with range 12 families which revealed that Characidae are characterized by the highest rate of chromosomal changes. Karyotype of Characiformes have demonstrates great diversity in diploid values. It covers from *Nannostomus unifasciatus* 2n = 22 To *Potamorhina altamazonica* 2n = 102.

Most fishes studied have a diploid chromosome number 2n = 50 and show high different values in karyotypic formula [Pazza & Kavalco, 2010].

The 88 Genera of the family Characidae belonging to the incertae sides group, only (20%), have been cytogenetically studied. Therefore, little is known about the karyotype structure of this group. Some species which cytogenetic studies have been conducted are: 2n = 50 of *Bryconamericus*, 2n = 50 of *Deuterodon stigmaturus*, [Pazza, *et al.*, 2006], 2n = 50 of *Gymnocorymbus ternetzi* [Arefjav, 1990], 2n = 50 of *Moenkhausia sanctafilamenae* [Mendes *et al.*, 2011], 2n = 62 of *Metynnis argenteus* [Arai, 2011].

The aim of this study was to provide information about the chromosome numbers and karyotypes of the three species of family characidae: *Gymnocorymbus ternetzi*, *Moenkhausia sanctaefilomenae* and *Metynnis argenteus* by using cytogenetic analysis. These species are closely related and they will be studied in order to understand the types of chromosomes changes that might have occurred during their differentiation. Different cytogenetic techniques were applied to characterize taxonomic relationship and patterns of distribution.

MATRIALS AND METHODS

Samples of three species of ornamental fresh water fishes were collected from the ornamental fish farms in Port-said, *Gymnocorymbus ternetzi*, *Moenkhausia sanctaefilomenae* and *Metynnis argenteus* of family Characidae. They were caught and transported to the lab and kept alive until processed. Mitotic chromosomes were prepared from head kidney, liver and gills as described by Nirchio & Cequea [1998]. Each specimen was injected with 0.05% Colchicines (1ml / 100g fish weight) the fish were maintained in a well aerated aquarium and after 2hr they were sacrificed. The kidneys, liver and gills were removed and placed in a hypotonic solution of 0.56% KCl after nearly 30 min. The tissues were immersed three times in a mixture of ethanol-acetic acid glacial 3:1 every time was taken 20min, then the tissues squashed in 60% acetic acid.

Three droplets of the cellular suspension were dropped on a clean microscope slide, previously chilled in a freezer, from a height of 50 cm. The slides were briefly passed over a flame and then allowed to air-dry. For conventional karyotype the preparations were stained for 40 min with 5% Giemsa in phosphate buffer ph 6.8. The slides were examined under a research light microscope using ×10 or ×15 eyepieces, together with × 15 objectives for chromosomal analysis. Karyotypes were made from good spreads of chromosomes. Classification of chromosomes in karyotype studies relating to centromeric index was done according to [Levan *et al.*, 1964].

RESULTS

The chromosomal analysis of three species of family Characidae: **(***Gymnocorymbus ternetzi*, *Moenkhausia sanctaefilomenae* and *Metynnis argenteus)* including chromosome number, Fundamental number and karyotypes were

investigated. The chromosomal numbers of the first two species under study were the same 2n = 50, and differ from the third species and all of them differ in the karyotype formula.

Gymnocorymbus ternetzi

The metaphase and karyotypes of this species were found to have a diploid chromosome number of 2n = 50 and fundamental number (FN) = 80 as shown in (Fig.1, 2). The karyotype consists of four different groups formed: group A composed of two metacentric pairs of chromosomes with relative lengths varies from 5.2 % and 7.93%, arm ratios ranging from 1.36 and 1.64 and centromeric indices 37.83 and 42.26.

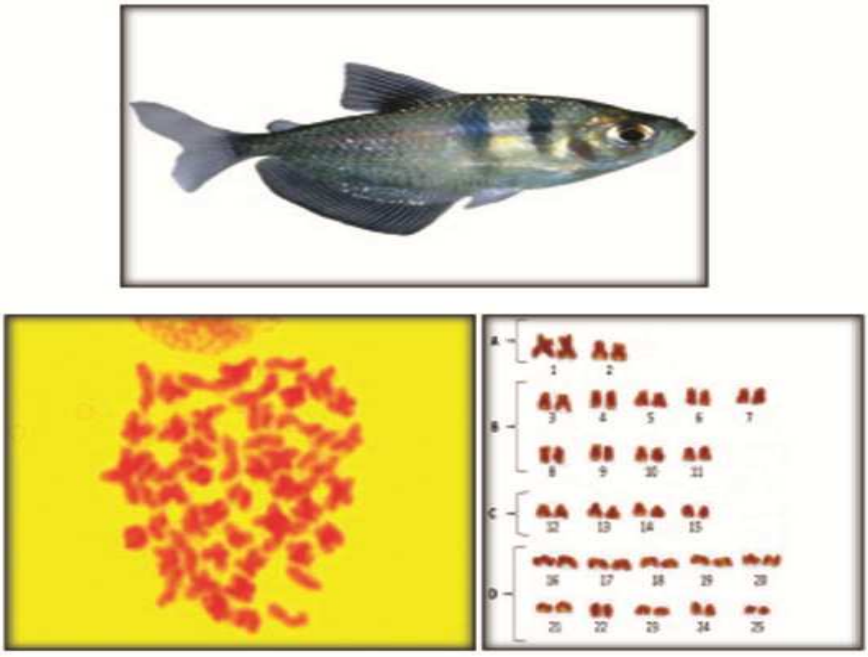

Fig. 1: A coloured photograph, Chromosomes spread and karyotype of *Gymnocorymbus ternetzi.*

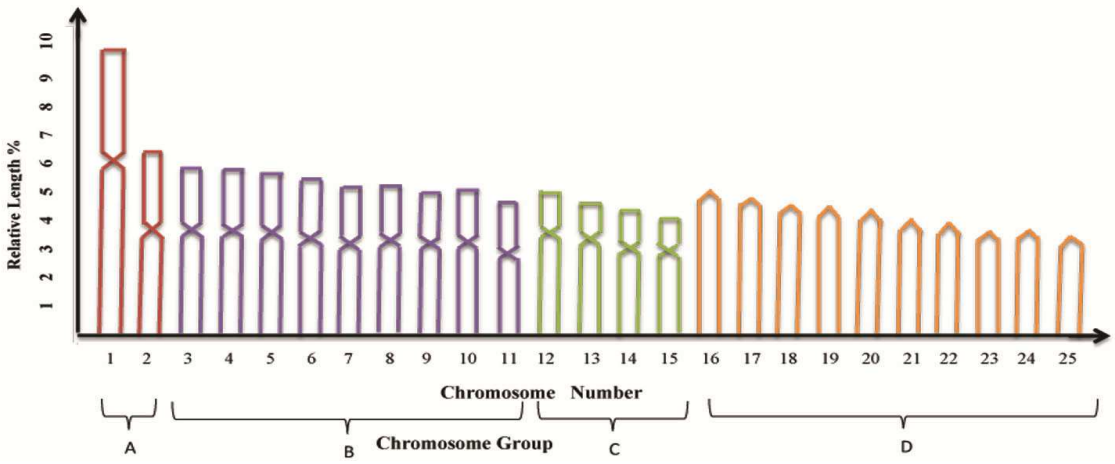

Fig. 2: Ideogram of chromosome of *Gymnocorymbus ternetzi* which constructed in respect to relative length.

Group B: is composed of nine submetacentric pairs of chromosomes with relative lengths varies from 3.8 % to 4.71%, arm ratios ranging from 1.75 to 1.84 and centromeric indices from 35.21 to 37. Group C: composed of four subtelocentric

pairs of chromosomes with relative lengths varies from 3.2 % to 3.96% ,arm ratios ranging from 3 to 3.11and centromeric indices from 24.32 to 25 and group D: composed of ten acrocentric pairs of chromosomes with relative lengths varies from 2.84 % to 3.91% , arm ratios ∞ and centromeric index zero. All these measurements are shown in Table (1).

Table 1: Averages of chromosomes measurements and classification, obtained from observations on ten cell spreads of *Gymnocorymbus ternetzi.*

Chromosome Number	Chromosome Length			Relative Length %			Arm Ratio Mean ± S.D.	Centromeric Index Mean ± S.D.	Classification
	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.			
1	0.92±0.09	0.56±0.05	1.48±0.09	4.93±0.04	3.0±0.08	7.93±0.12	1.64±0.04	37.83±1.03	M
2	0.56±0.07	0.41±0.03	0.97±0.05	3.00±0.09	2.20±0.06	5.2±0.11	1.36±0.09	42.26±1.08	M
3	0.56±0.08	0.32±0.04	0.88±0.07	3.00±0.06	1.71±0.04	4.71±0.09	1.75±0.07	37±1.05	SM
4	0.55±0.06	0.31±0.02	0.86±0.06	2.95±0.08	1.66±0.03	4.61±0.08	1.77±0.05	36.04±1.04	SM
5	0.54±0.05	0.30±0.06	0.840.04±	2.89±0.05	1.61±0.06	4.5±0.10	1.8±0.04	35.71±1.06	SM
6	0.51±0.08	0.31±0.03	0.82±0.03	2.73±0.04	1.61±0.03	4.34±0.12	1.76±0.03	37.03±1.02	SM
7	0.50±0.04	0.29±0.04	0.79±0.08	2.68±0.07	1.55±0.08	4.23±0.13	1.76±0.08	36.70±1.08	SM
8	0.49±0.03	0.28±0.06	0.77±0.06	2.63±0.03	1.50±0.07	4.13±0.09	1.75±0.06	36.36±1.05	SM
9	0.48±0.06	0.27±0.05	0.75±0.05	2.57±0.07	1.44±0.05	4.01±0.08	1.77±0.05	36±1.04	SM
10	0.47±0.08	0.26±0.05	0.73±0.04	2.52±0.05	1.39±0.09	3.91±0.07	1.8±0.07	35.61±1.03	SM
11	0.46±0.05	0.25±0.04	0.71±0.03	2.46±0.06	1.34±0.04	3.8±0.11	1.84±0.04	35.21±1.07	SM
12	0.56±0.06	0.18±0.06	0.74±0.03	3.00±0.04	0.96±0.03	3.96±0.13	3.11±0.07	24.32±1.05	ST
13	0.51±0.04	0.17±0.03	0.68±0.08	2.73±0.05	0.91±0.05	3.64±0.12	3±0.06	25±1.04	ST
14	0.48±0.03	0.16±0.02	0.64±0.06	2.57±0.08	0.85±0.06	3.42±0.11	3±0.05	25±1.07	ST
15	0.45±0.09	0.15±0.06	0.6±0.05	2.41±0.04	0.80±0.04	3.2±0.09	3±0.08	25±1.02	ST
16	0.73±0.03	Zero	0.73±0.03	3.91±0.06	Zero	3.91±0.06	∞	Zero	Acro.
17	0.71±0.06	Zero	0.71±0.06	3.81±0.07	Zero	3.81±0.07	∞	Zero	Acro.
18	0.69±0.05	Zero	0.69±0.05	3.70±0.03	Zero	3.70±0.03	∞	Zero	Acro.
19	0.67±0.03	Zero	0.67±0.03	3.59±0.02	Zero	3.59±0.02	∞	Zero	Acro.
20	0.65±0.04	Zero	0.65±0.04	3.48±0.04	Zero	3.48±0.04	∞	Zero	Acro.
21	0.63±0.06	Zero	0.63±0.06	3.38±0.05	Zero	3.38±0.05	∞	Zero	Acro.
22	0.61±0.08	Zero	0.61±0.08	3.27±0.06	Zero	3.27±0.06	∞	Zero	Acro.
23	0.59±0.06	Zero	0.59±0.06	3.16±0.03	Zero	3.16±0.03	∞	Zero	Acro.
24	0.57±0.05	Zero	0.57±0.05	3.05±0.04	Zero	3.05±0.04	∞	Zero	Acro.
25	0.53±0.04	Zero	0.53±0.04	2.84±0.03	Zero	2.84±0.03	∞	Zero	Acro.
SUM			18.63±0.27						

M:metacentric, SM:submetacentric, ST:subtelocentric and Acro: acrocentric chromosome.

Moenkhausia sanctaefilomenae

The chromosomal analysis of the studied samples demonstrated that the diploid chromosomal number was 2n=50 and fundamental number (FN) = 100 (Figs. 3, 4).

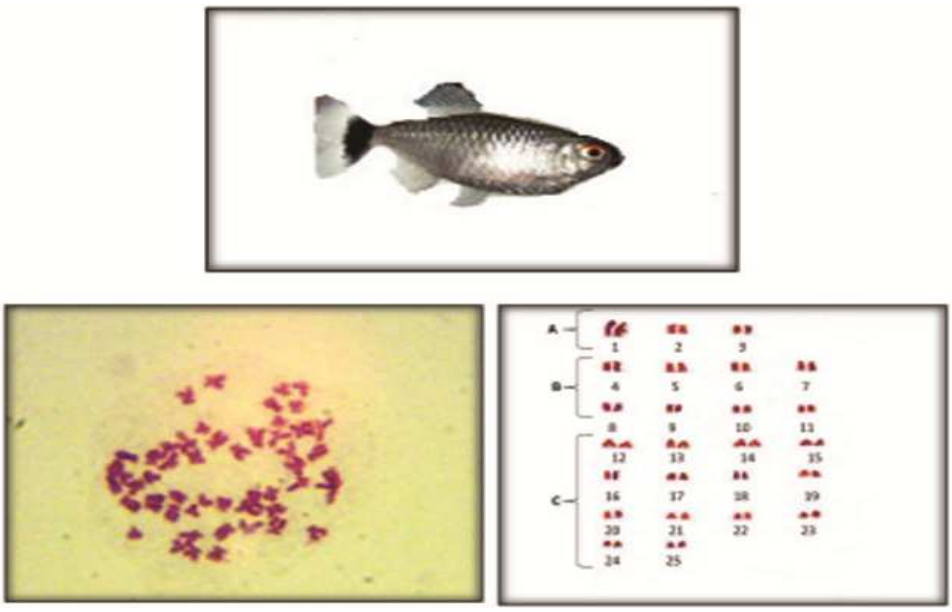

Fig. 3: A coloured photograph, Chromosomes spread and karyotype of *Moenkhausia sanctaefilomenae.*

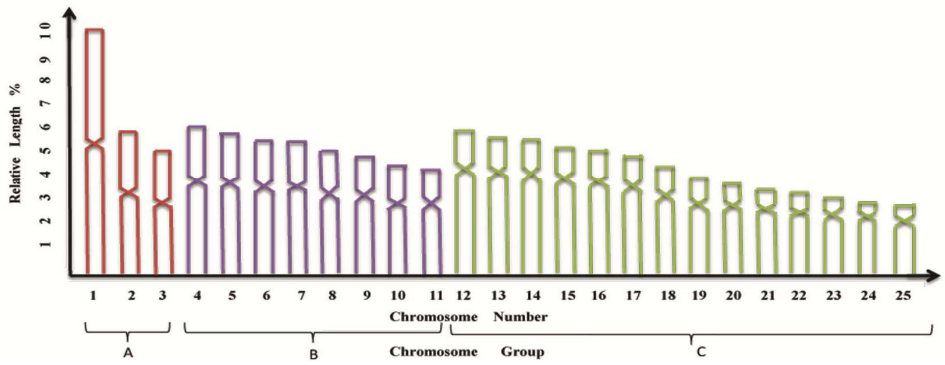

Fig. 4: Ideogram of chromosome of *Moenkhausia sanctaefilomenae* which constructed in respect to relative length.

Chromosomes were arranged in three different groups formed: group A composed of three metacentric pairs of chromosomes with relative lengths varies from 4.2 % to 8.3%, arm ratios ranging from 1.12 to1.33 and centromeric indices 42.85 to 46.98. Group B: eight submetacentric pairs of chromosomes with relative lengths varies from 3.5 % to 5 %, arm ratios ranging from 1.77 to 2.18 and centromeric indices from 31.42 to 36 and Group C: composed of 14 subtelocentric pairs of chromosomes with relative lengths varies from 2.2 % to 4.8%, arm ratios ranging from 3 to 4.6 and centromeric indices from 18 to 25 as shown in Table (2).

Table 2: Averages of chromosomes measurements and classification, obtained from observations on ten cell spreads of *Moenkhausia sanctaefilomenae*.

Chromosome Number	Chromosome Length			Relative Length %			Arm Ratio Mean ± S.D.	Centromeric Index Mean ± S.D.	Classification
	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.			
1	0.44±0.04	0.39±0.05	0.83±0.04	4.40±0.11	3.90±0.11	8.3±0.10	1.12±0.09	46.98±1.16	M
2	0.27±0.03	0.21±0.02	0.48±0.06	2.70±0.12	2.10±0.12	4.8±0.08	1.28±0.11	43.75±1.12	M
3	0.24±0.08	0.18±0.04	0.42±0.03	2.40±0.14	1.80±0.15	4.2±0.12	1.33±0.10	42.85±1.13	M
4	0.32±0.05	0.18±0.06	0.5±0.05	3.20±0.17	1.80±0.14	5±0.09	1.77±0.08	36±1.17	SM
5	0.31±0.06	0.17±0.06	0.48±0.03	3.10±0.15	1.70±0.11	4.8±0.08	1.82±0.07	35.41±1.09	SM
6	0.30±0.04	0.16±0.02	0.46±0.02	3.00±0.12	1.60±0.12	4.6±0.06	1.87±0.09	34.78±1.08	SM
7	0.29±0.03	0.15±0.05	0.44±0.07	2.90±0.11	1.50±0.14	4.4±0.10	1.93±0.06	34.09±1.11	SM
8	0.28±0.07	0.14±0.02	0.42±0.05	2.80±0.13	1.40±0.17	4.2±0.12	2±0.11	33.33±1.08	SM
9	0.27±0.05	0.13±0.04	0.4±0.04	2.70±0.12	1.30±0.12	4±0.11	2.07±0.13	32.5±1.06	SM
10	0.25±0.04	0.12±0.03	0.37±0.07	2.50±0.15	1.20±0.10	3.7±0.09	2.08±0.09	32.43±1.04	SM
11	0.24±0.06	0.11±0.05	0.35±0.04	2.40±0.16	1.10±0.09	3.5±0.08	2.18±0.07	31.42±1.12	SM
12	0.36±0.04	0.12±0.04	0.48±0.02	3.60±0.17	1.20±0.08	4.8±0.10	3±0.12	25±1.09	ST
13	0.35±0.03	0.11±0.02	0.46±0.03	3.50±0.13	1.10±0.07	4.6±0.11	3.18±0.13	23.91±1.07	ST
14	0.34±0.07	0.11±0.06	0.45±0.06	3.40±0.14	1.10±0.10	4.5±0.08	3.09±0.11	24.44±1.05	ST
15	0.32±0.06	0.10±0.03	0.42±0.07	3.20±0.15	1.00±0.9	4.2±0.06	3.2±0.10	23.80±1.04	ST
16	0.31±0.04	0.10±0.02	0.41±0.05	3.10±0.12	1.00±0.12	4.1±0.09	3.1±0.09	24.39±1.09	ST
17	0.30±0.04	0.09±0.03	0.39±0.03	3.00±0.13	0.90±0.09	3.9±0.08	3.33±0.05	23.07±1.07	ST
18	0.27±0.03	0.09±0.04	0.36±0.06	2.70±0.11	0.90±0.08	3.6±0.11	3±0.08	25±1.03	ST
19	0.24±0.09	0.08±0.02	0.32±0.04	2.40±0.13	0.80±0.07	3.2±0.09	3±0.09	25±1.07	ST
20	0.23±0.07	0.07±0.03	0.3±0.03	2.30±0.11	0.70±0.10	3±0.06	3.28±0.11	23.33±1.09	ST
21	0.22±0.05	0.06±0.02	0.28±0.02	2.20±0.12	0.60±0.09	2.8±0.08	3.66±0.10	21.42±1.02	ST
22	0.21±0.03	0.06±0.01	0.27±0.06	2.10±0.13	0.60±0.08	2.7±0.07	3.5±0.06	22.22±1.08	ST
23	0.20±0.02	0.05±0.03	0.25±0.07	2.00±0.14	0.50±0.06	2.5±0.10	4±0.09	20±1.03	ST
24	0.19±0.08	0.04±0.02	0.23±0.03	1.90±0.11	0.40±0.09	2.2±0.05	4.61±0.08	18±1.08	ST
25	0.18±0.05	0.04±0.01	0.22±0.04	1.80±0.15	0.40±0.07	2.2±0.07	4.6±0.09	18.1±1.05	ST
SUM			9.99±0.31						

Metynnis argenteus

The photographs of cell spread and karyotype of this species intubated a diploid chromosome number of 2n = 62 and fundamental number (FN) = 122 in (Figs. 5, 6).

The karyotype consists of four different groups formed: group A composed of 15 metacentric pairs of chromosomes with relative lengths varies from 2.97 % to 4.92%, arm ratios ranging from 1.62 to 1.7 and centromeric indices 37 to 38.02.

Group B: is comprises of 12 submetacentric pairs with relative lengths varies from 1.73 % to 2.97%, arm ratios ranging from 1.86 to 2.2 and centromeric indices from 29.16 to 34.88 and group C: composed of three subtelocentric pairs of chromosomes with relative lengths varies from 3.74 % to 4.36%, arm ratios ranging from 3.2 to 3.9 and centromeric indices from 20.37 to 23.80 and group D: composed of one acrocentric pair of chromosomes with relative lengths 2.28 %, arm ratios ∞ and centromeric index zero, as shown in Table (3).

The results of cytogenetic analysis (karyotyping) was compared with those obtained from the classical methods in taxonomy using morphological and anatomical characters. This work could be considered a pilot that reporting the chromosomes numbers, karyotypic characters analysis of the three species, *Gymnocorymbus ternetzi*, *Moenkhausia sanctaefilomenae* and *Metynnis argenteus* found in Egypt.

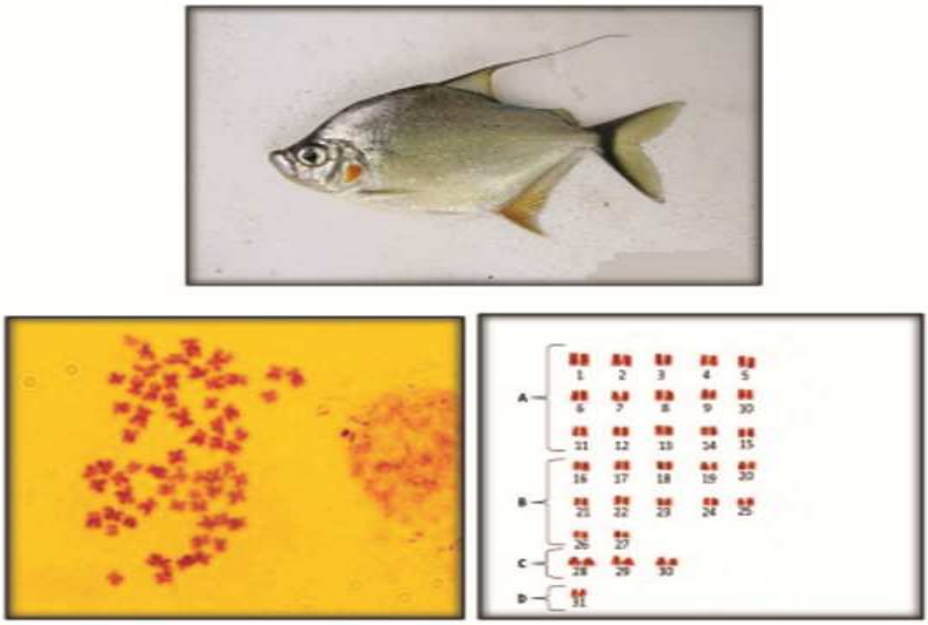

Fig. 5: A coloured photograph, Chromosomes spread and karyotype of *Metynnis argenteus*.

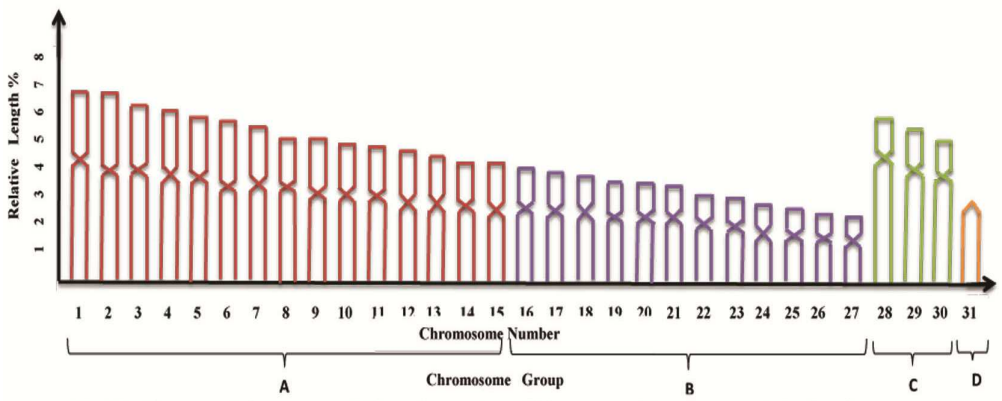

Fig. 6: Ideogram of chromosome of *Metynnis argenteus* which constructed in respect to relative length.

Table 3: Averages of chromosomes measurements and classification, obtained from observations on ten cell spreads of *Metynnis argenteus.*

Chromosome Number	Chromosome Length			Relative Length %			Arm Ratio Mean ± S.D.	Centromeric Index Mean ± S.D.	Classification
	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.	Long Arm Mean ± S.D.	Short Arm Mean ± S.D.	Total Mean ± S.D.			
1	0.44±0.05	0.27±0.07	0.71±0.08	3.04±0.05	1.87±0.07	4.92±0.09	1.62±0.09	38.02±1.09	M
2	0.43±0.09	0.26±0.06	0.69±0.05	2.97±0.09	1.8±0.06	4.78±0.08	1.65±0.08	37.68±1.07	M
3	0.41±0.08	0.24±0.09	0.65±0.07	2.84±0.03	1.66±0.05	4.5±0.06	1.7±0.06	37±1.06	M
4	0.39±0.05	0.23±0.04	0.62±0.04	2.70±0.06	1.59±0.07	4.29±0.05	1.69±0.07	37.09±1.03	M
5	0.38±0.04	0.23±0.05	0.61±0.03	2.63±0.07	1.59±0.04	4.22±0.08	1.65±0.05	37.7±1.04	M
6	0.37±0.06	0.22±0.03	0.59±0.06	2.56±0.03	1.52±0.03	4.08±0.05	1.68±0.09	37.28±1.09	M
7	0.36±0.04	0.22±0.07	0.58±0.08	2.49±0.04	1.52±0.03	4.01±0.06	1.63±0.07	37.93±1.11	M
8	0.34±0.03	0.20±0.05	0.54±0.04	2.35±0.05	1.38±0.08	3.74±0.05	1.7±0.09	37.03±1.06	M
9	0.33±0.07	0.20±0.08	0.53±0.03	2.28±0.09	1.38±0.06	3.67±0.08	1.65±0.06	37.73±1.04	M
10	0.32±0.05	0.19±0.03	0.51±0.06	2.21±0.07	1.31±0.05	3.53±0.06	1.68±0.08	37.25±1.02	M
11	0.31±0.04	0.19±0.04	0.5±0.07	2.14±0.06	1.31±0.04	3.46±0.04	1.63±0.05	38±1.06	M
12	0.30±0.02	0.18±0.03	0.48±0.04	2.07±0.05	1.24±0.03	3.32±0.03	1.66±0.09	37.5±1.06	M
13	0.29±0.07	0.17±0.08	0.46±0.04	2.0±0.04	1.17±0.05	3.18±0.07	1.7±0.06	37±1.09	M
14	0.28±0.04	0.17±0.05	0.45±0.03	1.94±0.08	1.17±0.07	3.11±0.06	1.64±0.03	37.77±1.02	M
15	0.27±0.08	0.16±0.06	0.43±0.08	1.87±0.07	1.10±0.04	2.97±0.05	1.7±0.05	37±1.04	M
16	0.28±0.06	0.15±0.03	0.43±0.06	1.94±0.03	1.03±0.07	2.97±0.05	1.86±0.07	34.88±1.09	SM
17	0.27±0.04	0.14±0.04	0.41±0.05	1.87±0.04	0.97±0.06	2.84±0.07	2±0.08	34.14±1.07	SM
18	0.26±0.03	0.13±0.08	0.39±0.07	1.8±0.05	0.90±0.05	2.70±0.08	2±0.04	33.33±1.04	SM
19	0.25±0.04	0.12±0.06	0.37±0.03	1.73±0.07	0.83±0.04	2.56±0.06	2.08±0.02	32.43±1.08	SM
20	0.24±0.06	0.11±0.08	0.35±0.05	1.66±0.06	0.76±0.09	2.42±0.04	2.18±0.08	31.42±1.05	SM
21	0.23±0.03	0.11±0.05	0.34±0.09	1.59±0.04	0.76±0.05	2.35±0.07	2.09±0.06	32.35±1.04	SM
22	0.22±0.02	0.10±0.04	0.32±0.06	1.52±0.08	0.69±0.07	2.21±0.03	2.2±0.05	31.25±1.03	SM
23	0.21±0.05	0.10±0.03	0.31±0.07	1.45±0.06	0.69±0.03	2.14±0.07	2.1±0.04	32.25±1.09	SM
24	0.20±0.07	0.09±0.02	0.29±0.04	1.38±0.05	0.62±0.06	2.00±0.05	2.22±0.03	31.03±1.04	SM
25	0.19±0.04	0.09±0.06	0.28±0.03	1.31±0.04	0.62±0.05	1.94±0.04	2.11±0.08	32.14±1.07	SM
26	0.18±0.03	0.08±0.07	0.26±0.05	1.24±0.03	0.55±0.04	1.74±0.03	2.21±0.06	30.76±1.04	SM
27	0.17±0.06	0.07±0.05	0.24±0.06	1.17±0.03	0.55±0.08	1.73±0.06	2.2±0.05	29.16±1.03	SM
28	0.48±0.08	0.15±0.08	0.63±0.08	3.32±0.07	1.03±0.07	4.36±0.08	3.2±0.07	23.80±1.03	ST
29	0.46±0.05	0.13±0.02	0.59±0.06	3.18±0.06	0.9±0.05	4.08±0.06	3.5±0.05	22.03±1.02	ST
30	0.43±0.03	0.11±0.05	0.54±0.03	2.97±0.05	0.76±0.07	3.74±0.04	3.9±0.04	20.37±1.05	ST
31	0.33±0.02	Zero	0.33±0.04	2.28±0.04	Zero	2.28±0.03	∞	Zero	Acro.
SUM			14.43±0.26						

DISCUSSION

Studies on the chromosomes of fishes have not been widespread as in other vertebrate groups. Fish karyotypes are generally characterized by a large number of small chromosomes. Fishes represent more than half of all extant vertebrates with more than 32,000 recognized species [Eschmeyer & Fong, 2014], and are characterized by different morphology, behavior, and habitat. Family Characidae shows the greatest diversity of the order Characiformes, with about 950 species of fish described [Reis *et al.*, 2003]. It comprises 13 subfamilies, where the majority of the genera are included in the subfamily Tetragonopterinae. While there is a lack of evidence that this subfamily is a monophyletic group, these genera have been placed in an insert side group by [Lima *et al.*, 2003], based on phylogenetic systematics.

In family Characidae, Cytogenetic studies have been conducted are: 2n=48 of *Astyanax eignmanniorum*, 2n = 50 of *Bryconamericus*, 2n=50 of *Deuterodon stigmaturus*, 2n=52 of *Hemigrammus hyanuary* accepted with [Pazza *et al.*, 2006]. The present result, are in apparent with these reported by [Hashimoto *et al.*, 2011; Arefjav, 1990 and Foresti, *et al.*, 1989]. The detected chromosome number in fish species: *Gymnocorymbus ternetzi* and *Moenkhausia sanctafilamenae* was the same; 2n=50. In addition the number of chromosomes detected in fish *Metynnis argenteus* 2n=62 [Scheel, 1973].

In conclusion, the results of this study indicated that the first two species *Gymnocorymbus ternetzi* and *Moenkhausia sanctaefilomenae* have the same diploid chromosome number 2n=50, but different in karyotypic formula while the third

species *Metynnis argenteus* has different diploid chromosome number and karyotype. It can be concluded also that, studying of karyotypes structure could prove to be a useful tool for estimating the variability and various taxonomical degree among fish species.

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ARABIC SUMMARY

تمييز الأنماط الصبغية لثلاثة أنواع من أسماك عائلة الكاراسيدي

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تناولت هذه الدراسه التحليل الصبغي وعمل الخرائط الصبغيه لثلاثة انواع من أسماك الزينه التي تنتمي الى عائلة الكاراسيدي، حيث اظهرت الدراسة ان العدد الكروموسومى الزوجى والكريوتيب لكل الانواع محل الدراسه كانت كالتالي:

جايمينوكوريمبس تيرنتزي : *Gymnocorymbus ternetzi* الهيئة الصبغية له تحتوى علي عدد صبغى زوجى ٢ن = ٥٠، وعدد الاذرع الفعالة FN = ٨٠ ، وقد تم ترتيب الصبغيات فى أربع مجموعات وهى ٢ زوج وسطى السنترومير ، و ٩ زوج تحت وسطي السنترومير و٤ زوج تحت طرفي السنترومير و١٠ زوج طرفي السنترومير.

مونكوشيا سانكتافيلومنيا: *Moenkhausia sanctaefilomenae* أوضح التحليل الصبغي لهذا النوع أن العدد الزوجى للصبغيات هو خسة وعشرون زوجا ٢ن = ٥٠، و عدد الفتائل الفعالة FN = ١٠٠، وقد تم ترتيب الصبغيات فى ثلاث مجموعات: ٣ زوج وسطى السنترومير ، و ٨ زوج تحت وسطي السنترومير و١٤ زوج تحت طرفي السنترومير.

ميتننس ارجنتيس: *Metynnis argenteus* أوضح التحليل الصبغي لهذا النوع أن العدد الزوجى للصبغيات هو واحد وثلاثون زوجا ٢ن = ٦٢، و عدد الفتائل الفعالة FN = ١٢٢ ، وقد تم ترتيب الصبغيات فى أربع مجموعات هى: ١٥ زوج وسطى السنترومير ، و ١٢ زوج تحت وسطي السنترومير و٣ زوج تحت طرفي السنترومير و زوج واحد طرفي السنترومير.

وتمثل هذه الدراسة أهميه كبيره في علم التصنيف الحديث الذي أصبح يستخدم الانماط الصبغية في تصنيف الانواع هذا الي جانب الصفات المورفولوجيه والتشريحه ودراسة الإختلاف والترابط بين الانواع المختلفه وتعد هذه دراسه وراثيه خلويه رائدة على هذه الأنواع في مصر.