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Full Length Research Paper

Karyotypic analysis of chickens and other birds

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The karyotypic studies on chickens (2n= 78), duck (2n= 80), dove (2n= 76) and quail (2n= 78) demonstrated species-specific differences in total length (TL), relative length (RL), centrometric index (CI) and arm ratio (AR) values. The estimated genomic sizes (in µm) in these birds were 97.13, 89.1, 94.9 and 39.04, respectively. The information could be helpful for species identification and detecting genetic diseases. Moreover, impacts of the findings on production performance, management practices, haemato-biochemical and serological parameters, coupled with those on karyotypes in relation to the incidences of AI and other diseases in poultry farms of the Northern regions of Bangladesh have been discussed.

Key words: Karyotype, poultry, chromosome

INTRODUCTION

The science of cytogenetics is concerned with the mechanisms and transmission of heredity and variability at the cellular level which is important for speciation and identifies the genetic diseases of the organism. The chromosomes in different organisms as well as in the same cell besides their absolute and relative sizes may show a definite individuality in their genomic pattern as are evident from their size, shape, position of centromere and in such additional features as secondary construction and satellites (Stebbins, 1950). There are consequently effective research into >2000 chicken quantitative traits loci which were encoding for disease susceptibility, immunology, leanness, egg production etc (Liu *et al.,* 2001; Mariani *et al.,* 2001; Tatasuda and Fujanaka, 2001). In recent years there have been several comparative mapping studies; experiments and refining the information between chicken, human and, mouse and on chickens macro- and micro-chromosomes (Croojimans *et al.,* 2001; Suchyta, 2001; Buitenhuis, 2002; Jennen, 2002). Thus chicken is a primary model for of quantitative inheritance study in humans and other vertebrates (Jeurissen *et al.,* 2000; Ledur *et al.,* 2000, Le Bihan-Duval, 2001) and being successfully used in gene disruption experiments (Winding & Berchtold, 2001). A karyotypic study provides wealth information for the animals' infertility, diseases, tumorigenesis as well as low resolution of whole genome (Masabanda *et al.,* 2004). Chromosomes of the chickens can be identified at the metaphase stage by the use of peripheral blood techniques (Musa *et al.,* 2005). In the present study, an attempt has been made to compare the karyotypes of chicken and other birds to understand the cytogenetics of the birds under study. Chickens, like other avian species, differ from mammals in that their female is heterogametic (ZW) and male is homogametic (ZZ), the Z and W chromosomes showing heteromorphism. The chicken chromosomes are mostly euchromatic with the exceptions of a large terminal C-band on the Z 9 lineage. In the early 1990s, the chicken standard karyotype at the molecular level revived the international interest. The international cytogenetics meeting in 1992 in Netherlands, and then in 1993 at the University of

Guelph, indicated that the longitudinal banding patterns obtain from each of techniques is differing from each other individuals. On the other hands progress in quail karyotype was done, in Japanese quail the Centro mere region of chromosome No. 4 is the site of heteromorphism. Recently we studied Chinese Native chicken karyotype analysis; our comment is that the technique of peripheral lymphocyte culture was suitable for avian chromosome preparation. All species studied presented a diploid number of 78 chromosomes, with 10 pairs of macro chromosomes including the sex chromosome and 29 pairs of micro chromosomes. Comparison on karyotype and G-banded patterns between the domestic fowl and quail showed that they had a diploid number of 78, but the positions of centromere were different from each other. Similarly, the difference was found in chromosome No. 1 and No. 2 **(**Musa *et al*., 2005).

MATERIALS AND METHODS

Preparation of slides

The present study included four different taxa of birds *viz*., the domestic chicken *Gallus gallus domesticus,* the domestic duck *Anas platyrhynchos* var*.,* the Chinese spotted dove *Streptopelia chinensis* and the Japanese quail *Coturnix coturnix japonica*. The birds were injected interperitoneally with 0.5 ml of colchicine (0.1 % w/v.). Testis and ovary were taken and washed in NaCl 1% twice, after that they were cut into small pieces in 0.56% KCl then incubated at 37^0C for 15-20 minutes and the germ tissues were gently shook for 5 minutes at room temperature. The meiotic cell suspension was centrifuged (4000 rpm.) for 5 minutes; the pellet was then fixed with cooled fresh fixative (3 methanols: 1 acetic acid). The fixed cells were incubated at room temperature for 30 minutes and washed twice with the same fixatives. Small drop of cell suspension were dropped on slides and air-dried. The meiotic cells from each bird were divided into two major groups-the first group was prepared for normal and conventional Geimsa staining and into macro- and microchromosomes according their size. All the operations were performed *in vivo* in the laboratory of the Department of Genetic Engineering and Biotechnology, University of Rajshahi. The molar (M) stock solution was made in dimethyl sulfoxide. For micronuclei method the animals' bone marrow smear were made in 1:1 phosphate buffer: calf serum where the slides were stained in May Grunwal's Giemsa stain (Schmid, 1973; 1975).

Squash technique

Follicle cells were dissected out in ringer solution (0.65gm NACL+0.25gm $CaCl_2$ +0.02gm $NaHCO_3$ +100cc distilled water). On a drop of 1% aceto-orcein (1gm of orcein stain powder +22cc glacial acetic acid + 4cc distilled water + 28cc lactic acid) or a drop of aceto-carmine (0.5gm carmine powder + 45cc glacial acetic acid + 55cc of distilled water) stain was taken on a slide, a follicle of birds gonad was kept for 10 minutes for staining. Sometimes a gentle heat was applied with the help of a sprit lamp. Then a cover slip was placed on the stained tissue and placing a piece of blotting paper on the cover slip, the follicle was squashed by pressing firmly with the help of a thumb. Then the follicular cells were dissociated. The squash technique described by Darlington & La Cour (1976) was followed.

Fixation

For increasing nuclear and chromosomal spreading, the selected cells were treated with 45% acetic acid in water, which was removed shortly and the material transferred to freshly prepared fixative; Carnoy's fluid (3 parts of absolute methanol + 1 part of glacial acetic acid) and leave for 30 minutes at room temperature. In case of eleven chemicals, the treated animals were sacrificed after 24 hours treatment. The chemicals were administered in the same dose sequence as in the micronuclei assay for the single treatment in the case of four chemicals; the treatment schedule was 4, 8, 12 and 16 days durations with 3, 7 11 and 15 injection at the interval of 24 hours respectively. Three hours prior to dissection, the animals were colchicinized with 0.1 ml/bird of 0.48 colchicine. The bone marrow cells were swollen in 0.075 M KCl treatment and then fixed in 1: 3 acetic acid: methanol. The slides were prepared according to the usual air drying technique and stained in carbol fuchsin (Carr & Waker, 1961).

Chromosome spreading and staining

For the rapid dissociation and good chromosome spreading, the tissue was transferred to a drop of 60% aqueous acetic acid on a warmed slide. Slight maceration was needed for proper dissociation. A number of chromosome stains were tried with varying degree of success like aceto-carmine, aceto-orcein, giamsa stain (1gm of Giemsa powder + 60cc methyl alcohol + 60cc distilled water). Staining with 1% of aceto-orcein made

Table1. Chromosome complement of chicken with its mean length and centrometric position

Chromosome no.	Mean length of short arm (s)	Mean length of long arm (l)	Total length (s+l)	Relative length (RL)	Centrometric index (CI)	Arm ratio (AR)	Centrometric type
1	2	4	6	0.06	33.33	1.5	Submetacentric
2	2	4	6	0.06	33.33	2	Submetacentric
3	3	1	4	0.04	75	1.5	Telocentric
4	3	1	4	0.04	75	5	Acrocentric
5	3	1	4	0.04	75	0.75	Telocentric
6	3	1	4	0.04	75	0.56	Telocentric
7	0.2	1.8	2	0.02	10	0.56	Telocentric
8	0.2	1.8	2	0.02	10	9	Metacentric
9	0.1	1.9	2	0.02	5	19	Telocentric
10	0.1	1.9	2	0.02	5	19	Telocentric
11	0.2	1.8	2	0.02	10	9	Telocentric
12	0.1	1.9	2	0.02	5	19	Telocentric
13	0.1	1.9	2	0.02	5	19	Telocentric
14	0.1	1.9	2	0.02	5	19	Telocentric
15	0.1	1.9	2	0.02	5	19	Telocentric
16	0.1	1.9	2	0.02	5	19	Telocentric
17	0.1	1.9	2	0.02	5	19	Telocentric
18	0.2	1.8	2	0.02	5	9	Telocentric
19	0.2	1.8	2	0.02	10	9	Telocentric
20	0.2	1.8	2	0.02	10	9	Telocentric
21	0.2	1.8	2	0.02	10	9	Telocentric
22	0.2	1.8	2	0.02	10	9	Telocentric
23	0.2	1.8	2	0.02	10	9	Telocentric
24	0.2	1.8	2	0.02	10	9	Telocentric
25	0.1	1.9	2	0.02	5	19	Telocentric
26	0.1	1.9	2	0.02	5	19	Telocentric
27	0.1	1.9	2	0.02	5	19	Telocentric
28	0.1	1.9	2	0.02	5	19	Telocentric
29	0.1	1.9	2	0.02	5	19	Telocentric
30	0.1	1.9	2	0.02	5	19	Telocentric
31	0.1	1.9	2	0.02	5	19	Telocentric
32	0.1	1.9	2	0.02	5	19	Telocentric
33	0.1	1.9	2	0.02	5	19	Telocentric
34	0.1	1.9	2	0.02	5	19	Telocentric
35	0.1	1.9	2	0.02	5	19	Telocentric
36	0.1	1.9	2	0.02	5	19	Telocentric
37	0.1	1.9	2	0.02	5	19	Telocentric
38	0.1	1.9	2	0.02	5	19	Telocentric
Z	0.53	0.50	1.03	7.67	48.82	5	Acrocentric
W	2	2.1	4.1	4.77	48.78	1.05	Metacentric

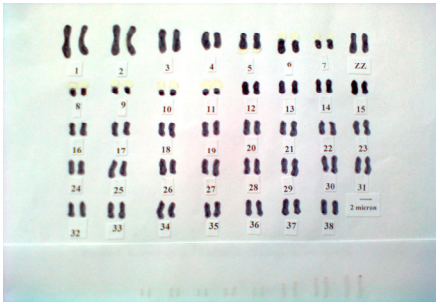

Plate 1. Karyotype of chicken

good result. A cover slip was placed over the tissue and to spread chromosomes, the tissue was squashed with applying pressure on the cover slip by the thumb. Thus the slide became ready for chromosomal study.

Slide preparation and mounting

Another drop of Carnoy's fluid was added to the preparation and till the slide in all directions to ensure a maximum spreading. The slide was then warmed gently over a flame of sprit lamp, which assists dispersion and evaporation. The dried slides were placed in acetic ethanol (1 part of glacial acetic acid in 3 parts of absolute ethanol) for about four hours to reduce cytoplasmic staining. The stained slides were mounted carefully only with the cover slip, no mounting medium was used because the refractive index of canada balsam does not coincide with the chromosomes. So, the tissue was mounted by attaching with the normal gum or nail polish only surrounding the cover slip.

Measurement of chromosomes

In order to display the karyotype pictorially, the individual metaphase chromosome from the photograph were arranged by length and in pairs, later aligned in such a way that the centromeres were at the same level and the short arms were oriented upward. Centromeric formula was derived on the basis of l/s ratio proposed by Levan *et al.* (1962). Morphometric analysis was done from direct measurement by ocular micrometer, the scale of which was earlier standardized with the stage micrometer. One day old slides were exposed to Hoechst 33258 (0.5 µg/ml) for 30 minutes, washed in phosphate buffer (PH 7.4) and exposed to GE 20 watts light at 60^0C for 1 hour. They were then rinsed in phosphate buffer and stained in Gurr's Giemsa (4%). The differentially stained slides were observed under the microscope (Sobti *et al*., 1982; 1983). Well spreading metaphase stages were studied under oil immerson lens of the Carl Zeiss Jenaval microscope. The Japanese quail (*Coturnix japonica*) is the first bird species whose lamp brush chromosomes were investigated by using the method of light electron microscope (Kropotova & Gaginskaya, 1984).

Measurement of chromosomes was made using the following formulae:

$$\text{Relative length, RL} = \frac{\text{Length of a particular chromosome (s+l)}}{\text{Mean total length of the genome}}$$

$$\text{CI (Centrometric Index)} = \frac{s}{s+l} \times 100; \text{ and AR (Arm Ratio)} = \frac{l}{s}$$

$$\sum(s+l)$$

RESULTS AND DISCUSSION

Karyotype of chicken

The chromosome complement of the chicken *G. g. domesticus* is composed of 76 autosomes (AA) and a pair of sex-chromosomes (Z and W), thus making the total number of chromosomes, 2n=78 (Table 1; Plate 1). The karyotypic formula is 1AAm + 2AAsm + 1AAa + 34AAt + Za + Wm, where one pair of autosomes is metacentric (chromosome 8), two pairs are sub-metacentric (chromosomes 1 and 2), majority of the autosomes are telocentric (34 pairs), the Z chromosome is acrocentric and the W chromosome is metacentric. The estimated total length of the genome consisting of 78 chromosomes is 97.13 µm. The diploid chromosome number of the chicken is 78 with 1 pair sex chromosome as revealed by the total number of the chromosome plates. The karyotype was made by arranging the chromosome from larger to shorter. The chromosome had the following break up of the autosome 38 pairs were 1 metacentric, 2 pairs submetacentric, 1 pair acrocentric and 34 pairs telocentric. The quantitative characteristics of the chromosomes showed a structural range of the mean total length of the arms between 2-6 µm of which Z was smallest, W was 4.1 µm in length. The relative length of the autosomes ranged between 0.02-0.06 and relative length of Z and W chromosome is 7.67 and 4.77. Arm ratio of the metacentric ones chromosome were 9, submetacentric ones were 1.5-2, acrocentric 5 and telocentric from 0.56-19. The centrometric indices range from 5-75. The present results lend support to those of Masabanda *et al.* (2004) and Musa *et al.* (2005).

Karyotype of duck

The chromosome complement of the duck *A. platyrhynchos* is composed of 78 autosomes (AA) and a pair of sex-chromosomes (Z and W), thus making the total number of chromosomes, 2n=80 (Table 2; Plate 2). The karyotypic formula is 15AAsm + 15AAa + 9AAt + Za + Wa, where nine pair of autosomes is telocentric (chromosome 11-19), fifteen pairs are sub -metacentric

Table2. Chromosome complement of duck with its mean length and centrometric position

Chromosome no.	Mean length of short arm (s)	Mean length of long arm (l)	Total length (s+l)	Relative length (RL)	Centrometric index (CI)	Arm ratio (AR)	Centrometric type
1	3	6	9	0.15	33.33	2	Submetacentric
2	2.83	5.67	8.5	0.14	33.29	2	Submetacentric
3	2	6	8	0.14	25	3	Acrocentric
4	2	4	6	0.10	33.33	2	Acrocentric
5	2	4	6	0.10	33.33	2	Acrocentric
6	1	3	4	0.07	25	3	Acrocentric
7	1	3	4	0.07	25	3	Acrocentric
8	0.5	1	1.5	0.03	33.33	2	Acrocentric
9	0.47	0.93	1.4	0.02	33.57	1.98	Submetacentric
10	0.5	1	1.5	0.02	33.33	2	Submetacentric
11	0.3	1	1.3	0.02	23.08	3.33	Telocentric
12	0.3	1	1.3	0.02	23.08	3.33	Telocentric
13	0.3	1	1.3	0.02	23.08	3.33	Telocentric
14	0.3	1	1.3	0.02	23.08	3.33	Telocentric
15	0.4	1	1.4	0.02	28.57	2.5	Telocentric
16	0.1	0.8	0.9	0.02	11.11	8	Telocentric
17	0.1	0.8	0.9	0.02	11.11	8	Telocentric
18	0.1	0.8	0.9	0.02	11.11	8	Telocentric
19	0.1	0.8	0.9	0.02	11.11	8	Telocentric
20	0.3	0.5	0.8	0.01	37.5	7	Submetacentric
21	0.3	0.5	0.8	0.01	37.5	7	Submetacentric
22	0.3	0.5	0.8	0.01	37.5	7	Submetacentric
23	0.3	0.5	0.8	0.01	37.5	7	Submetacentric
24	0.3	0.4	0.7	0.01	42.86	6	Submetacentric
25	0.3	0.4	0.7	0.01	42.86	6	Submetacentric
26	0.3	0.4	0.7	0.01	42.86	6	Submetacentric
27	0.3	0.4	0.7	0.01	42.86	6	Submetacentric
28	0.3	0.4	0.7	0.01	42.86	6	Submetacentric
29	0.3	0.4	0.7	0.01	42.86	5	Submetacentric
30	0.2	0.4	0.6	0.01	33.33	5	Submetacentric
31	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
32	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
33	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
34	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
35	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
36	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
37	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
38	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
39	0.1	0.5	0.6	0.01	16.67	5	Acrocentric
Z	0.2	0.7	0.9	0.02	22.22	3.5	Acrocentric
W	0.5	1	1.5	0.03	33.33	2	Acrocentric

Plate 2. Karyotype of duck

Table3. Chromosome complement of dove with its mean length and centrometric position

Chromosome no.	Mean length of short arm (s)	Mean length of long arm (l)	Total length (s+l)	Relative length (RL)	Centrometric index (CI)	Arm ratio (AR)	Centrometric type
1	1.9	2	3.9	0.04	48.72	1.05	Submetacentric
2	1.8	2	3.8	0.04	47.37	1.11	Submetacentric
3	0.7	3	3.7	1.04	18.92	4.29	Acrocentric
4	2	2.1	4.1	0.04	48.78	1.05	Submetacentric
5	1.9	2	3.9	0.04	48.72	1.05	Submetacentric
6	0.8	2	2.8	0.03	28.57	2.5	Acrocentric
7	0.6	2.3	2.9	0.03	20.69	3.83	Acrocentric
8	0.3	2	2.3	0.02	13.04	6.67	Acrocentric
9	0.4	2	2.4	0.03	16.67	5	Acrocentric
10	0.2	2	2.2	0.02	9.09	10	Acrocentric
11	0.1	2	2.1	0.02	4.76	20	Acrocentric
12	0.1	2	2.1	0.02	4.76	20	Acrocentric
13	0.1	2	2.1	0.02	4.76	20	Acrocentric
14	0.1	2	2.1	0.02	4.76	20	Acrocentric
15	0.1	2	2.1	0.02	4.76	20	Acrocentric
16	0.2	2	2.2	0.02	9.09	20	Acrocentric
17	0.2	2	2.2	0.02	9.09	10	Acrocentric
18	0.2	2	2.2	0.02	9.09	10	Acrocentric
19	0.2	2	2.2	0.02	9.09	10	Acrocentric
20	0.2	2	2.2	0.02	9.09	10	Acrocentric
21	0.3	2	2.3	0.02	13.04	10	Acrocentric
22	0.3	2	2.3	0.02	13.04	6.67	Acrocentric
23	0.1	2	2.1	0.02	4.76	6.67	Acrocentric
24	0.1	2	2.1	0.02	4.76	20	Acrocentric
25	0.1	2	2.1	0.02	4.76	20	Acrocentric
26	0.2	2	2.2	0.02	9.09	10	Acrocentric
27	0.2	2	2.2	0.02	9.09	10	Acrocentric
28	0.1	2	2.1	0.02	4.76	20	Acrocentric
29	0.2	2	2.2	0.02	9.09	10	Acrocentric
30	0.3	2	2.3	0.02	13.04	6.67	Acrocentric
31	0.1	2	2.1	0.02	4.76	20	Acrocentric
32	0.2	2	2.2	0.02	9.09	10	Acrocentric
33	0.2	2	2.2	0.02	9.09	10	Acrocentric
34	0.3	2	2.3	0.02	13.04	6.67	Acrocentric
35	0.1	2	2.1	0.02	4.76	20	Acrocentric
36	0.1	2	2.1	0.02	4.76	20	Acrocentric
37	0.1	2	2.1	0.02	4.76	20	Acrocentric
Z	0.9	1	1.9	0.02	47.37	1.11	Submetacentric
W	0.83	1.67	2.5	0.03	33.2	2.01	Acrocentric

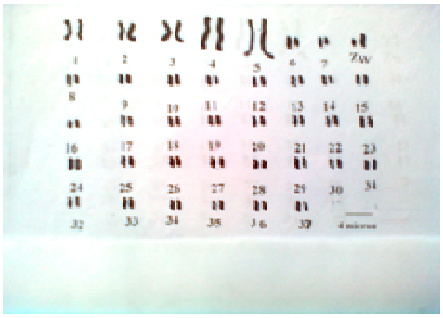

Plate3. Karyotype of dove

and acrocentric (chromosomes 1,2 and 20-30 and acrocentric chromosomes are from 3-8 and 31-39 with Z and W), majority of the autosomes are submetacentric (30 pairs) and the W and Z chromosomes are acrocentric. The estimated total length of the genome consisting of 80 chromosomes is 59.1 µm. The diploid chromosome number of the duck is 80 with 1 pair sex chromosome as revealed by the total number of the chromosome plates. The karyotype was made by arranging the chromosome from larger to shorter. The chromosome had the following break up of the autosome 39 pairs were 15 pairs submetacentric, 15 pair acrocentric and 9 pairs telocentric. The quantitative characteristics of the chromosomes showed a structural range of the mean total length of the arms between 0.6-9 µm of which Z was smallest, W was 1.5 µm in length. The relative length of the autosomes ranged between 0.01-0.15 and relative length of Z and W chromosome is 0.02 and 0.03. Arm ratio of the submetacentric chromosome were varied from 1.98-7, acrocentric 5-2 and telocentric from 2.5-8. The centrometric indices range from 11.11-42.86. Observed results are in agreement with that of Wojcik & Smalec (2007).

Karyotype of dove

The chromosome complement of the dove *Streptopelia chinensis* is composed of 74 autosomes (AA) and a pair of sex-chromosomes (Z and W), thus making the total number of chromosomes, 2n=76 (Table 3; Plate 3). The karyotypic formula is 4AAsm+33AAa+Zsm+Wa, where four pair of autosomes are submetacentric (chromosome 1,2,4,5 and Z), thirty three pairs are acrocentric (chromosomes 3 then 6-37 and W) which are the majority of the autosomes. The estimated total length of the genome consisting of 76 chromosomes is 94.9 µm. The diploid chromosome number of the dove is 76 with 1 pair sex chromosome as revealed by the total number of the chromosome plates. The karyotype was made by arranging the chromosome from larger to shorter. The chromosome had the following break up of the autosome 37 pairs were 4 pairs submetacentric, 33 pair acrocentric. The quantitative characteristics of the chromosomes showed a structural range of the mean total length of the arms between 2.1-3.9 µm of which Z was smallest, W was 2.5 µm in length (table 8.3 and plate 3.38). The relative length of the autosomes ranged between 0.02-1.04 and relative length of Z and W chromosome is 0.02 and 0.03. Arm ratios of the submetacentric chromosome were varied from 1.05-1.11 and acrocentric 2.5-20. The centrometric indices range from 4.76-48.78. This observation is similar to the study of Small *et al.* (1993).

Karyotype of quail

The chromosome complement of the Japanese quail C. *coturnix japonica* is composed of 76 autosomes (AA) and a pair of sex-chromosomes (Z and W), thus making the total number of chromosomes, 2n=78 (Table 4; Plate 4). The karyotypic formula is 5AAm+1AAsm+2AAa+30AAt+Zm+Wt, where five pair of autosomes are metacentric (chromosome 8 and 10-13), one pair is submetacentric (chromosomes 9), two pairs are acrocentric (chromosome 1 and 20), majority of the autosomes are telocentric (30 pairs), the Z chromosome is metacentric and the W chromosome is telocentric. The estimated total length of the genome consisting of 78 chromosomes is 39.04 µm. The diploid chromosome number of the quail is 78 with 1 pair sex chromosome as revealed by the total number of the chromosome plates. The karyotype was made by arranging the chromosome from larger to shorter. The chromosome had the following break up of the autosome 38 pairs were 5 metacentric, 1 pair submetacentric, 2 pairs acrocentric and 30 pairs telocentric and of the sex chromosome was also Z metacentric and W Telocentric. The quantitative characteristics of the chromosomes showed a structural range of the mean total length of the arms between 0.9-6.07 µm of which W was smallest; Z was 5.79 µm in length (table 8.4 and plate 3.39). The relative length of the autosomes ranged between 0.003-1.24 and relative length of Z and W chromosome is 2.79 and 0.02. Arm ratio of the metacentric chromosome were varied from 1-1.03, submetacentric ones were 1.67, acrocentric 1.37-2.55 and telocentric from 3-52. The centrometric indices range from 1.89-50. This result is similar to the observation of Takashima *et al*. (1985).

Table4. Chromosome complement of quail with its mean length and centrometric position

Chromosome no.	Mean length of short arm (s)	Mean length of long arm (l)	Total length (s+l)	Relative length (RL)	Centrometric index (CI)	Arm ratio (AR)	Centrometric type
1	1.71	4.36	6.07	0.16	28.17	2.55	Acrocentric
2	1.82	2.5	4.32	0.11	42.13	1.37	Acrocentric
3	0.18	3.06	3.24	1.24	5.56	17	Telocentric
4	0.2	2.43	2.63	0.07	7.60	12.15	Telocentric
5	0.03	1.56	1.59	0.04	1.89	52	Telocentric
6	0.2	0.8	1	0.03	20	4	Telocentric
7	0.1	0.8	0.9	0.02	11.11	8	Telocentric
8	0.42	0.43	0.85	0.02	49.41	1.02	Metacentric
9	0.30	0.50	0.80	0.02	37.5	1.67	Submetacentric
10	0.40	0.41	0.81	0.02	49.38	1.03	Metacentric
11	0.34	0.34	0.68	0.02	50	1	Metacentric
12	0.32	0.33	0.65	0.02	49.23	1.03	Metacentric
13	0.30	0.31	0.61	0.02	49.18	1.03	Metacentric
14	0.1	0.4	0.5	0.01	20	4	Telocentric
15	0.1	0.3	0.4	0.01	25	3	Telocentric
16	0.1	0.3	0.4	0.01	25	3	Telocentric
17	0.1	0.4	0.5	0.01	20	4	Telocentric
18	0.01	0.09	0.1	0.003	10	9	Telocentric
19	0.01	0.09	0.1	0.003	10	9	Telocentric
20	0.05	0.15	0.2	0.01	25	3	Telocentric
21	0.05	0.15	0.2	0.01	25	3	Telocentric
22	0.05	0.15	0.2	0.01	25	3	Telocentric
23	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
24	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
25	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
26	0.1	0.3	0.4	0.01	25	3	Telocentric
27	0.1	0.3	0.4	0.01	25	3	Telocentric
28	0.1	0.3	0.4	0.01	25	3	Telocentric
29	0.1	0.3	0.4	0.01	25	3	Telocentric
30	0.1	0.3	0.4	0.01	25	3	Telocentric
31	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
32	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
33	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
34	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
35	0.07	0.23	0.3	0.01	23.33	3.29	Telocentric
36	0.07	0.3	0.4	0.01	25	3	Telocentric
37	0.1	0.3	0.4	0.01	25	3	Telocentric
38	0.1	0.3	0.4	0.01	25	3	Telocentric
Z	1.30	4.49	5.79	2.79	22.45	1.15	Metacentric
W	0.2	0.7	0.9	0.02	22.22	3.5	Telocentric

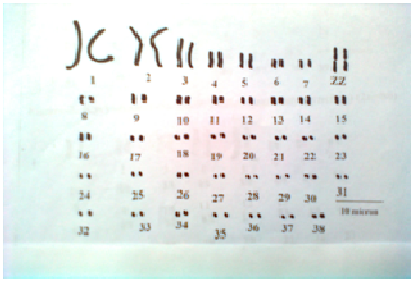

Plate4. Karyotype of quail

A comparative account of the karyotypes of chicken and other birds

The genome of the domestic chicken has a haploid number of 39 chromosomes, the ten largest are as macrochromosomes, and the other 29 are named microchromosomes (Yamashina, 1944). In chickens chromosomes have been numbered depending on its size. In comparison to man being the first six chromosomes are of similar size. However, much smaller than the smallest human chromosome **(**Bloom & Bacon, 1987). There is a size difference of 23 times between the largest and the smallest one in the chicken. In case of chicken the total chromosome number were 2n=78, while in duck 2n=80, in spotted dove 2n= 76 and lastly in quail 2n=78, suggesting that chicken and quail possess the same number of chromosomes. On the other hand the centrometric position for metacentric ranges between pairs from 1-5, submetacentric from 1-15, acrocentric from 1-15 and finally telocentric were from 9-34, so the telocentric chromosomes were highest in chicken and quail. Sex chromosomes were Z acrocentric and W metacentric whereas in quail Z metacentric and W telocentric, in case of duck both Z and W sex chromosome were acrocentric and in dove Z were sub metacentric and W were acrocentric. Most of the last numbers of chromosomes were dot like and the initial numbers were large.

CONCLUSION

A chromosome with its great potential of future achievements has become completely a new synthetic science due to advancement of technical aspects of the proper research on biochemistry, biophysics, cell physiology and genetics (Sharma, 1984). The shape and size of the chromosomes seem to be of great value in the cytotaxonomy and karyotypic evaluation. The universal occurrence of chromosome indicates that there is a clear evolutionary sequence in the complexity of the chromosomes from bacteria to the organism (Sharma & Sharma, 1965). The chromosome number is an important datum for a species than any other characteristics seemed significantly stable to merit taxonomic significance (Garber, 1978).The chromosomal numbers in different species, length, shape index and centrometric types were studied because of the importance for taxonomy and evolution. In animals karyotype analysis using to identify heredity disease and analyzing the mechanism of pathological change (Huang *et al*., 1995). Therefore, Standard cytogenetic analysis is used to detect abnormalities in chromosome number or microscopically visible of chromosomal material. With the advent of molecular cytogenetic techniques, such as fluorescence in situ hybridization (FISH), it is now possible to detect chromosomal rearrangements by light microscopy due to standard analysis. The use of FISH analysis for genetic diagnosis is made possible when a unique sequence of a gene or group of genes is known (Musa *et al*., 2005).

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