



KARYOTYPIC CONSERVATISM AMONG DIFFERENT FAMILIES OF LIZARDS

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ABSTRACT

Chromosomal studies were carried out on members of 4 families of Lizards viz. *Scincella himalayanum* (Family Scincidae), *Agama tuberculata* (Family Agamidae), *Hemidactylus flaviviridis* (Family Gekkonidae) and *Varanus bengalensis* (Family Varanidae). The specimens were collected from different places of J&K (UT) viz. Bhaderwah, Kishtwar, Jammu and Kathua. Tissues such as bone marrow, spleen, liver, kidney and testes were used for chromosomal preparation using Air drying technique. *S. himalayanum* exhibits $2n=30$ (16 macro and 14 microchromosomes), *A. tuberculata* exhibits $2n=34$ (12 micro and 22 microchromosomes), *V. bengalensis* exhibits $2n=40$ (16 macro and 24 microchromosomes) and *H. flaviviridis* exhibits $2n=40$ with all chromosomes exhibiting regular gradation in chromosomes from larger to smallest. The species under study exhibits great variation in number of chromosome but all show karyotypes with well differentiated macro and microchromosomes except in family gekkonidae. Hence karyotype is highly conserved in case of lizards whatever variation is observed is just because of some para or pericentric inversions and translocation of chromosomes.

KEYWORDS:-Gekkonid, Karyotypic, *H. flaviviridis*, *A. tuberculata*, macrochromosomes and microchromosomes.

INTRODUCTION

A significant problem faced by animal taxonomist is the difficulty of finding reliable morphological characters when attempting to break down a wide spread and variable species into more acceptable taxonomic units but cytogenetic studies of individuals from different population can often provide the way to such problem. The chromosome number and karyomorphology are important species specific characters. Nature favors one karyotype over other depending on the degree of phenotypic fitness it provides, as karyotypic variations would affect the phenotype thus from genetic point of view it offers genotypic information for study. Moreover it's realized that karyological information could be of use towards the elucidation of taxonomical problems that can contribute to our knowledge and degree of affinity between species belong to some genera or familial or even higher systematic categories.

Lacertilia constitute largest group of reptiles. They originated in Jurassic period and are still in stage of differentiation. It comprises of 365 living genera and approx 3200 species worldwide. In India there are present only few species but in J&K only 23 species of lizards have been reported (Sahi, 1979). Lizards are cytologically divided into 16 families but taxonomically they have been arranged in 23 families. So far only 490 species have been cytologically worked out. A unique feature of reptilian karyotype is the presence of macro and micro chromosomes. Though there exist wide variation in the chromosomes number in reptiles but the number tends to be highly conserved at generic and familial level. Matthey (1949) categorized reptilian karyotype into 3 complexes viz. Scincolacertid, Gekkonid and Iguanid. During the

present investigation species i.e. *S. himalayanum* belongs to Complex Scincolacertid, *A. tuberculata* and *V. bengalensis* belongs to Complex Iguanid and *H. flaviviridis* belongs to the Complex Gekkonid.

MATERIAL AND METHODS

Live specimens of all the species under study were collected from Bhaderwah, bani, Env. Park (Jammu) and kathua district with the help of hand net during the month of March to October (Since reptiles come out in summer only). Specimens were brought to laboratory where they were injected intraperitoneally with 0/9% colchicines @ 1ml/100gm body weight for 24hrs prior to dissection. Tissues such as bone marrow, spleen, kidneys and gonads were collected and hypotonised tissues were fixed in carnoys fixative (3 methanol and 1 acetic acid) for 30 minutes. Slides were prepared by dabbing and stained in 2% Giemsa stain. Well spread metaphase stages were photographed and karyotyped and assigned nomenclature as given by Levan *et al.* (1964).

RESULTS

COMPLEX SCINCOLACERTID

Family Scincidae

S. himalayanum- A study of about 105 well spread metaphase complement from different somatic and meiotic tissues of male *S. himalayanum* exhibits $2n=30$ consisting of 16 macro and 14 microchromosomes. The macrochromosomes include 10 meta, 2 submeta and 2 acrocentric chromosomes in male. There exist a heteromorphic pair having larger acrocentric 'X' and smaller micro 'Y' in male with NF=42. The micro-

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chromosomes size ranges from 0.9 micron to 0.45 micron (Table 1).

COMPLEX IGUANIDAE

Family Agamidae

A. tuberculata has diploid count of 34 chromosomes (2n=34) comprising 12 macro and 22 micro chromosomes. All macro chromosomes are metacentric excepting the second largest pair which is sub -metacentric, in both male and female. All the microchromosomes are small dot like ranging from 0.6-1.05 micron in male and 0.42-0.54 micron in female and NF=46.

Family Varanidae

V. bengalensis has diploid count of 2n=40 as observed in almost 90 well spread metaphase stages. Their exist distinct bimodality in karyotype comprising 24 micro and 16 macrochromosomes with NF =54. All the macro

chromosomes are microcentric except 5th pair which is acrocentric. Among microchromosomes 9th pair is heteromorphic with larger acrocentric `W` and smaller metacentric `Z` and rest all microchromosomes are acrocentric. First pair of macrochromosomes shows secondary constriction on short arm. The length of microchromosomes ranges from 0.54 to 0.34 micron (excluding sex pair).

COMPLEX GEKKONID

Family Gekkonidae

H. flaviviridis mitotic metaphase reveals a diploid count of 2n=40 in both male and female. First pair is metacentric, 2nd is submetacentric and all others are subtelocentrics (with very small short arm) and telocentrics excepts the lastpairs which are metacentric. There is no heteromorphic pair in the karyotype of either male or female and NF=50.

TABLE 1: Morphometric data of somatic karyotype of male *Scincella himalayanum*

Chromosome Pair No:	Mean Length of Short arm (P) in μ	Mean length of long arm (q) in μ	RL % P+q ----*100 Mean haploid length	Arm ratio p/q	Centromeric Index CI=p/q+q	Nomenclature
1.	2.40	2.40	16.70	1.00	0.50	m
2.	2.25	2.25	15.60	1.00	0.50	m
3.	2.25	2.25	15.60	1.00	0.50	m
4.	1.95	1.95	13.50	1.00	0.50	m
5.	1.05	1.08	7.42	1.00	0.50	m
6.	0.27	1.08	4.70	1.00	0.50	st
7.	0.27	1.08	4.70	1.00	0.50	st
X	0.27	1.08	4.70	1.00	0.50	st
Total length of haploid macrocomplement			= 24.48 μ			
Total Length of microcomplement			= 4.20 μ			
Total length of haploid set			=28.68 μ			

TABLE: 4 Morphometric data of somatic karyotype of *Hemidactylus flaviviridis*.

Total length of haploid set of male =27.57 μ
Total length of diploid set of male =55.14 μ

Chromosome Pair No:	Mean Length of Short arm (P) in μ	Mean length of long arm (q) in μ	RL % P+q ----*100 Mean haploid length	Arm ratio p/q	Centromeric Index CI=p/q+q	Nomenclature
1.	1.27	1.80	11.13	1.50	0.43	m
2.	0.75	1.30	7.43	1.73	0.37	sm
3.	0.43	1.57	7.25	3.48	0.25	t
4.	0.24	1.80	7.25	9.00	0.16	t
5.	0.30	1.50	6.54	5.00	0.16	t
6.	-----	1.80	6.54	-----	-----	t
7.	-----	1.74	6.31	-----	-----	t
8.	0.26	1.01	4.61	3.88	0.20	t
9.	-----	1.20	4.35	-----	-----	t
10.	-----	1.20	4.35	-----	-----	t
11.	-----	1.20	4.35	-----	-----	t
12.	-----	0.90	3.26	-----	-----	t
13.	-----	0.90	3.26	-----	-----	t
14.	-----	0.80	3.26	-----	-----	t
15.	-----	0.90	3.26	-----	-----	t
16.	-----	0.90	3.26	-----	-----	t
17.	-----	0.60	2.17	-----	-----	t
18.	0.60	0.60	4.35	1.00	0.50	m
19.	0.60	0.60	2.35	1.00	0.50	m
20.	0.39	0.30	2.82	1.00	0.50	m

TABLE 3 : Morphometric data of somatic karyotype of female *Varanus bengalensis*.

Chromosome Pair No:	Mean Length of Short arm (P) in μ	Mean length of long arm (q) in μ	RL % P ⁺ q ————*100 Mean haploid length	Arm ratio p/q	Centromeric Index CI=p/q ⁺ q	Nomenclature
1.	2.25	2.25	16.40	1.00	0.50	m
2.	2.22	2.22	16.40	1.00	0.50	m
3.	1.20	1.20	8.75	1.00	0.50	m
4.	0.90	0.90	6.56	1.00	0.50	m
5.	----	1.75	6.38	----	----	t
6.	0.87	0.87	6.38	1.00	0.50	m
7.	0.81	0.81	5.90	1.00	0.50	m
8.	0.81	0.81	5.90	1.00	0.50	m
W	----	0.75	2.73	----	----	t
Z	-----	0.30	1.09	----	----	t
Total length of haploid macrocomplement				= 20.82 μ		
Total Length of microcomplement				= 6.60 μ		
Total length of haploid set				=27.42 μ		

TABLE 2: Morphometric data of somatic karyotype of female *Agama tuberculata*.

Chromosome Pair No:	Mean Length of Short arm (P) in μ	Mean length of long arm (q) in μ	RL % P ⁺ q ————*100 Mean haploid length	Arm ratio p/q	Centromeric Index CI=p/q ⁺ q	Nomenclature
1	3.40	3.60	21.03	1.05	0.48	m
2	1.98	3.00	14.90	1.50	0.39	sm
3	2.40	2.40	14.42	1.00	0.50	m
4	1.90	2.10	12.00	1.10	0.47	m
5	1.75	1.75	10.50	1.00	0.50	m
6	1.20	1.20	7.20	1.00	0.50	m
Total length of haploid macrocomplement				= 26.68 μ		
Total Length of microcomplement				= 6.60 μ		
Total length of haploid set				=33.28 μ		

DISCUSSION

Family Agamidae consist of 41 genera and 300 species (Smith 1943), but in India having only 50-60 species of which only 7 species were recorded from J&K (Sahi 1979). Majority of the genera of family Agamidae are difficult to recognize because of their being mixed characters and hence for those genera chromosomal studies were of great help in assigning proper taxa to a species. Till now only 33 species have been cytologically investigated with the diploid number ranging from $2n=34$ to $2n=48$ but $NF=48$ in this family. Sharma and Nakashi (1980) divided this family into 2 groups *i.e.* Group I includes species with low diploid number ranging from $2n=34-36$ with more banded chromosomes while Group II includes species with $2n=44-48$ and more number of unibanded chromosomes. In present study *A. tuberculata* belonging to family Agamidae has karyotype which is characteristic of Group I. On the basis of RL% of macrochromosomes *A. tuberculata* seems to be more closely related to *A. agronensis* and *Calotes versicolor* (Sharma and Kour 2004) than to other Agamids hence it is believed that speciation might have occurred due to translocation of genome from macro to micro and vice versa but still karyotype is highly conserved within this family.

Family Varanidae is monogeneric and includes world largest lizards of the 35 taxonomically known species only 20 have cytologically investigated. This group is highly conserved cytologically having $2n=40$ with 16 macro and 24 micro chromosome. Martens 1963 divided genus *varanus* into 6 sub genera but King (1973) divided family

into 6 karyotypic groups. Chromosomal re-arrangements are restricted to centromeric shifts caused by para and paracentric inversion in 5th to 8th macro chromosomes. During the present investigation *Varanus bengalensis* karyotype resembles that of Odatarian (D) of Kings (1981) of 6th karyotypic group. This species was also worked out by Singh *et al* in 1970 but the results do not co-accord with that of Singh, but the karyotype of *V. bengalensis* resemble typical varanid karyotype with well differentiated ZZ male ZW female type of sex mechanism. Family gekkonids is also highly conserved, the diploid number ranges from $2n=28$ to $2n=46$ but $2n=40$ are most common, more over chromosomal studies on number of gekkonids suggests that the ancestors gekkonids karyotype has $2n=38$ with gradual size diminution. King recognized 8 putative ancestral karyomorphs ($2n=32, 34, 36, 38, 40, 42, 44$ and 46) all acrocentric and telocentric chromosomes within the sub-family and postulated that each of the known karyotype has been derived from one of these prototypes through chromosomal re-arrangement. The results obtained during present investigation do not co accord completely with work already done (King 1976, Nakamura 1932, Sharma and Nakashi 1992, Bhatnagar 1962, Adegoke 1985,) the results shows variations in N.F. which is attributed again to translocation and inversion which leads to speciation. Family Scincidae is the most species rich family including almost 1000 species all over the world. Till now only 57 species have been cytological investigated. The amount of data on the cytotaxonomy is not satisfactory. According to King (1973) the divergence in the chromosome number and morphology is attributed

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to trans location from 12th to 6th pair or fusion in an ancestral Scincid karyotype (2n=32) leading to lose of centromere and hence reduction in the chromosome number to 30. Dallai Talluri (1969) have suggested that karyotypic evolution of the scincidae involves pericentric inversion. According to King (1973) Sciencidae karyotype is divided into 4 types i.e Scincus type with 2n=32, Chalcide type with 2n=28, Mabuya type with 2n=26 and Scincella type with 2n=30, of which first three types have NF=36 but Scincella type has NF=46 and hence is considered to be the primitive type. *S. himalayanum* has already been worked out by Duda and Gupta (1981) and reported 2n=30 (16 macro and 14 microchromosomes), all

macrochromosomes being metacentrics with no heteromorphic sex pair, while present study reveals 2n=30 comprising 14 somatic macro-(5 pairs of metacentrics, 1 pair of submetacentrics and 1 pair of acrocentrics) and XY sex pair (X-being large acrocentric macrochromosome and Y being largest microchromosome) and 14 somatic microchromosomes.

Hence present work further substantiate the fact that karyotype is highly conserved within family and genera level in reptiles, slight variation in the karyotype of the members of same family is because of the translocations and inversion that leads to speciation in this group.

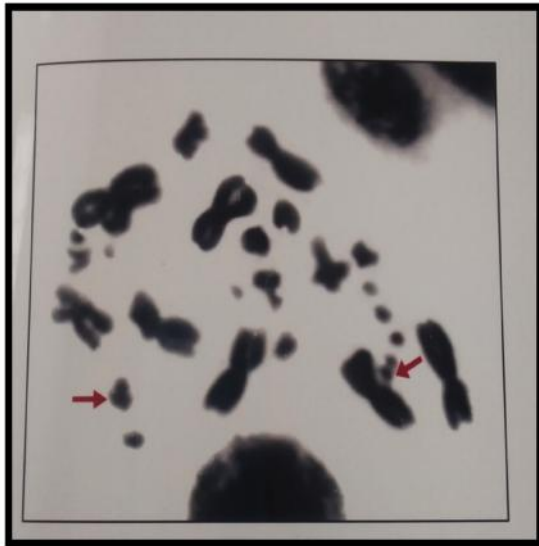


FIGURE 1 Showing complement of *S. himalayanum*

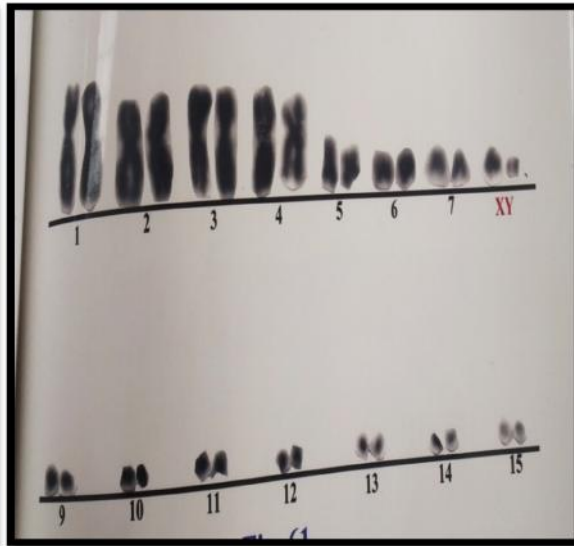


FIGURE 2 Showing karyotype of *S. himalayanum*



FIGURE 3 Showing complement of *A. tuberculata*

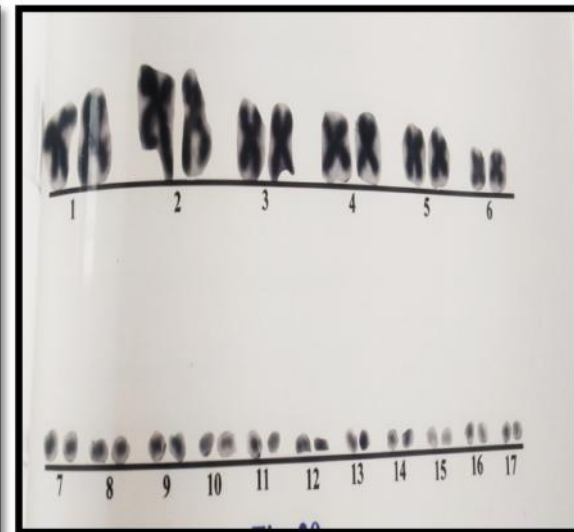


FIGURE 4 Showing karyotype of *A. tuberculata*

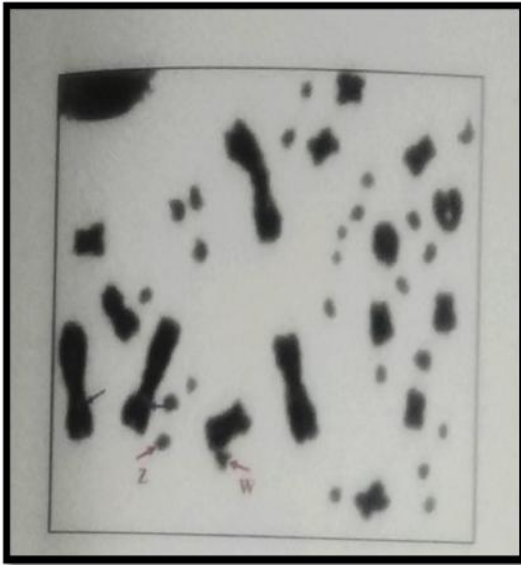


FIGURE 5 Showing complement of *V. bengalensis*

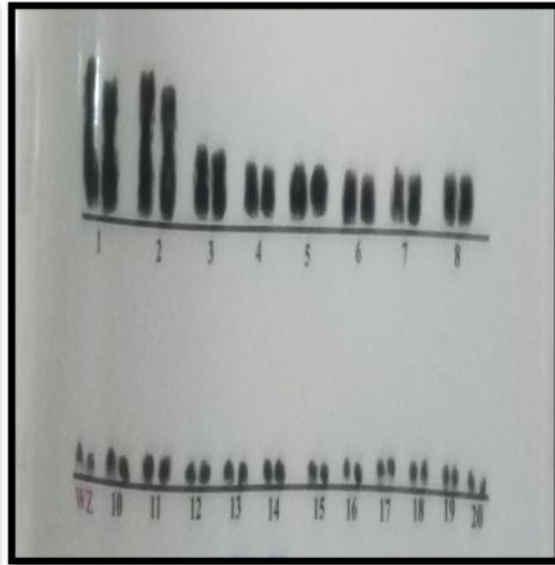


FIGURE 6: Showing karyotype of *V. bengalensis*



FIGURE 7 Showing complement of *H. Flaviviridis*

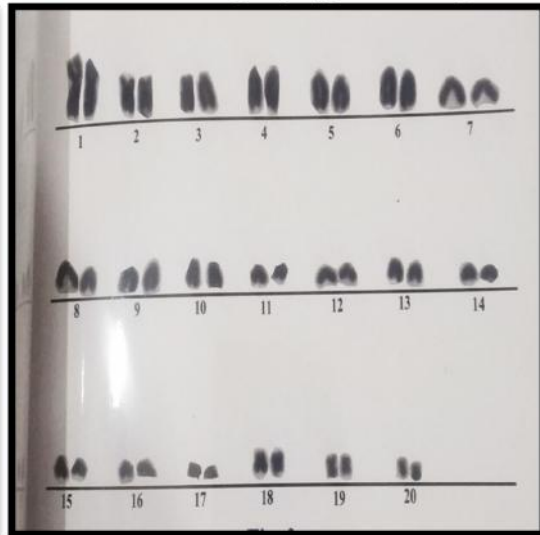


FIGURE 8 Showing karyotype of *H. Flaviviridis*

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