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KARYOTYPE CHARACTERISTICS OF FORTY-ONE SPECIES OF ORTHOPTERA AND THEIR EVOLUTIONARY TRENDS AT THE FAMILY LEVEL

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INTRODUCTION

Orthopterans form a large and prominent group in the class Insecta which includes more than 20,000 described species (Yadav and Yadav, 1986). Their abundance and world wide distribution makes them conspicous in the animal world. Ever since the pioneer work of McClung (1905) at the dawn of the 20th century plethora of information on the karyology of this group has accrued. However, the chromosome biology of the Indian Orthoptera is comparatively less than those from the other parts of the world. It was Asana (1928) who initiated the chromosome study of insects in India. Yadav and Yadav (1986) have presented the chromosome number and sex determining mechanism in thirty species of Orthoptera confining mostly to northwest India. Since there is no separate list of the karyologically analysed species of Orthoptera from south India, present authors present the chromosome number, form and sex determining mechanism of 14 species of acridids, 14 species of tettigonids and 13 species of gryllids and an attempt has been made to discuss the evolutionary trends at the respective family levels. Table 1, 2 and 3 present the chromosome number and the morphology of previously published species in addition to unpublished data of some species.

MATERIALS AND METHODS

All the specimens of all the subgroups of Orthoptera were collected within a radius of 10 Kms of Manasagangotri Campus Mysore (south India). Testes and hepatic caecae were utilized for chromosomal preparations by applying the usual air dry Giemsa method.

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Table 1. : Number and morphology of chromosomes in Acrididae.

Sl. No.	Species	2n ♂	Chromosome morphology
	OXYINAE		
1.	*Oxya nitidula* Walker	23	all acro (l, m, s) XL
	CATANTOPINAE		
2.	*Brachyxenia* sp.	23	all acro (l, m, s) Xm
3.	*Catantops pinguis innotabilis* Walker		all acro (l, m, s) Xm
	ACRIDINAE		
4.	*Acrida turrita* Linnaeus	23	all acro (l, m, s) XL
	OEDIPODINAE		
5.	*Aiolopus* sp. 1	23	all acro (l, m, s) XL no. 5 pair with a/sm or sm/sm
6.	*Aiolopus* sp. 2	23	all acro (l, m, s) XL
7.	*Heteropternis respondens* Walker	23	all acro (l, m, s) XL
8.	*Acrotylus humbertianus* Saussure	23	all acro (l, m, s) XL
9.	*Gastrimargus africanus orientalis* Sjost	23	all acro (l, m, s) XL except no. 6, 7 and 9 pairs with variant morphs
10.	*Oedaleus abruptus* Thunberg	23	all acro (l, m, s) XL
11.	*Sphingonotus* sp.	23	all acro (l, m, s) XL
	HEMIACRIDINAE		
12.	*Spathosternum prasiniferum* Walker	23	all acro (l, m, s) XL
	CALLIPTAMINAE		
13.	*Acorypha glaucopsis* Walker	23	all acro (l, m, s) XL
	COPTACRIDINAE		
14.	*Coptarca punctoria* Walker	23	all acro (l, m, s) XL (except no. 6, 9 and 10 pairs with variant morphs

Note : l–long; m–medium; s–small; L–longer.
Publication : no. 9 and 14 published, others unpublished.
In *Gastrimargus africanus orientalis* and *Coptarca punctaria* no individual sample had all acrocentric chromosomes.
In *Aiolopus* sp. 1, 5th pair showed a/sm or sm/sm; a/a condition not observed.

Table 2. : Number and morphology of chromosomes in Tetigoniidae.

Sl. No.	Species	2n ♂	Chromosome morphology
	LISTROSCELINAE		
1.	*Euhexacentrus annulicornis* Stol	12	4p meta, 1p micro meta, X meta Y micro meta
2.	*Euhexacentrus* sp.	9	4p meta, X acro
	CONOCEPHALINAE		
3.	*Conocepalus maculatus* Le Guillum	21	7p meta, 2p sm, 1p sa, X meta
4.	*Euconcocephalus incertus* Walker	21	3p meta, 1p sm, 6p acro, X meta
	PHANEROPTERINAE		
5.	*Elimaea securigera* Brunner	27	All acro, X Acro Variant karyotype
6.	*Holochlora spectabilis* Walker	29	All acro X Acro
7.	*Letana nigrosparsa* Walker	29	All acro, X Acro, Variant sat. Chro. Pair No. 8 sa
8.	*Himerta kinneari* Uvarov	31	All acro, X Acro
9.	*Himerta* sp.	31	All acro, X Acro
	MECOPODINAE		
10.	*Mecaopoda elongata* Linnaeus	29	1p Meta, 7p meta, 5p sa, 1p acro X meta
11.	*Mecopoda* sp.	27	1p meta, 7p meta, 1p sm 44 sa, X meta
	PSEUDOPHYLLINAE		
12.	*Sathrophyllia femorata* Linnaeus	35	All acro, X Acro
13.	*Phyllozelus pectinatus* Retd	35	All acro, X Meta
	MECONEMATINAE		
14.	*Xiphidiopsis* sp.	33	1p meta, 2p sm, 3p sa, 10p acro X meta

Note : meta–med metacentric; sm–submetacentric; sa–subacrocentric; acro–acrocentric, Meta–large-metacentric; Acro–large acrocentric.

Publication : no. 1, 2 and 5 to 14 published (see Reference).

Euhexacentrus annulicomis is included under the subgroup INCERTAE SEDIS by Elzbeita Warchalowska-Sliwa (see *Folia biologica* (Krakow) 46 No. 3–4, 143–176, 1998).

Table 3. : Number and morphology of chromosomes in *Grylloidea*.

Sl. No.	Species	2n ♂	Chromosome morphology
	Fam GRYLLIDEA		
1.	*Gryllopsis maculithorax* Chopard	19	1p meta, 8p acro, X meta
2.	*Gryllodes sigillatus* Walker	21	All auto acro, X Meta
3.	*Plebeiogryllus guttiventris* Walker	21	All auto acro, X Meta
4.	*Velarifictorus maindroni* Chopard	21	3p meta, 3p sm, 2p sa, 2p acro, X Meta
5.	*Velarifictorus dehradunensis* Tandon and Shishodia	25	6p sm, 5p sa, 1p acro, X Meta
6.	*Teleogryllus* sp.	27	10p meta, 2p sm, 1p acro, X Meta
7.	*Gryllus bimaculatus* DeGeer	29	3p meta, 4p sm, 3p sa, 4p acro, X Meta
	Fam : NEMOBIINAE		
8.	*Pteronemobius taprobanesis* Walker	15	3p meta, 2p sm, 2p acro, X sm
9.	*Pteronembius csikii* Boliver	17	4p meta, 4p acro, X meta
	Fam OECANTHIDAE		
10.	*Oecanthus* sp.	18	All auto acro, 1p l, 2p m, 5p s, X meta, Y acro
	Fam TRIGONIDIIDAE TRIGONIDIINAE		
11.	*Trigonidium cicindelodes* Ramber	11	1p l sm, 4p meta, X meta
12.	*Trigonidium humbertianum* Saussare	11	3p meta, 2p sm, X Meta
13.	*Trigonidium* sp.	15	3p l. meta, 2p m. meta, 2p sm, X Meta

Note : meta–medium metacentric; sm–submetacentric; acro–acrocentric; l–large, m–medium; s–small.

Oecanthus sp. Neo-XY sex determining mechanism.

Publications : Published No. 1 and 6.

RESULTS AND DISCUSSION

Acrididae

All the acridids of the present study have a diploid number of 23 in males and the length and form of the chromosomes of all the species is tabulated (Table 1). The chromosomes of all the species are acrocentric including the X chromosome except in *Gastrimargus africanus orientalis* and *Coptarca punctaria* in which a few chromosomes are biarmed, keeping the diploid number intact. In *G. a. orientalis* 3 pairs of chromosomes namely 6^{th}, 7^{th} and 9^{th} exhibit variant morphs in different individuals. Of the 3 pairs, the 9^{th} pair is highly dynamic in that one homologue is always metacentric and the other partner is either acrocentric, subacrocentric, submetacentric or metacentric whereas the 7^{th} pair is heteromorphic with acrocentric/subacrocentric. Further, the 6^{th} pair is heteromorphic with meta/acrocentric (Aswathnarayana *et al.*, 1981, Ashwath, 1981). Similarly such structural variation has been encountered in *Coptarca punctaria* involving 6^{th}, 9^{th} and 10^{th} pairs in different individuals. The 9^{th} pair shows homomorphic metacentric, submetacentric and heteromorphic with metacentric/submetacentric chromosomes. The 6^{th} pair is heteromorphic with meta/acrocentric and the 10th pair having meta/acrocentric condition (Umadevi and Aswathanarayana, 1987). In general, in the above mentioned species, no individual sample had all acrocentric chromosomes. These structural changes may be of the floating type or may be established in the karyotype as seen in one homologue of the 9th pair of *G. a. orientalis* as a metacentric. Such a change in the morphology of the chromosomes is attributed to pericentric inversion. With regard to the formation of a bi armed or metacentric chromosome, White (1973) stated that in acridids, although very short pericentric inversions might have been established in a few species, there appeared to be a 'special barrier' operating against longer inversions to establish metacentric morphology' The above examples confirm that only short inversions can give rise to biarmed chromosomes. Though Yadav and Yadav (1986) have analysed 29 species of acridids they did not discover structural variation in autosomes which may be due to geographical conditions.

Tettigonoidea

The tettigonids form a highly diversified group with chromosome number varying from 9 to 35 (Table 2). The diploid number of 9 is found in *Euhexacentrus* sp. (Aswathanarayana, 1998) and 2n = 35 in species of *Pseudophyllinae* (Aswathanarayana and Ashawath, 1996). In Phaneropterinae subgroup, 2n = 27 occurs in *Elimaea securigera*, 2n = 29 in *Holochlora spectabitis* and *Letana nigrosparsa* and 2n = 31 in *Himerta kinneari* and *Himerta* sp. In these species the chromosomes are all acrocentric including the large X-chromosome (Aswathanarayana and Ashwath, 1996). Rarely a few individuals exhibit variation in the morphology of a few chromosomes of the karyotype (they are called variant karyotypes). For example in *E. securigera* pairs 3, 4, 5 and 7 show structural changes. The pair no. 3 is heteromorphic with acrocentric/subacrocentric whereas pair nos. 4

and 5 are homomorphic with submetacentric and pair no. 7 has homomorphic subacrocentric chromosomes (Aswathanarayana and Srinivasa, 1993). In *L. nigrosparsa* pair no. 2 has satellited chromosomes and pair no. 8 is homomorphic with subacrocentric chromosomes. The structural changes in both the species are due to pericentric inversions. The sat-chromosome formation seem to be a secondary feature (Aswathanarayana, 1996). In Phaneropterinae, the typical karyotype has 2n = 31 having all acrocentrics (probably has been ancestral) and it is possible that some species with lower numbers (for example 2n = 29 and 27) must have evolved by tandem fusions (Aswathanarayana and Ashwath, 1996) Mecopodinae shows 2n = 29 in *M. elongata* which has 8 pairs of metacentrics (one pair is large), 5 pairs of subacrocentrics and one pair of acrocentrics and the X is a large metacentric whereas *Mecopoda* sp. has 2n = 27 which agrees with the *M. elongata* in all aspects except that it has only one pair of submetacentric and 4 pairs of subacrocentrics (Table 2). If the basic karyotype of the genus *Mecopoda* is assumed to be 2n = 31 with all acrocentrics, then the karyotypes of both the above 2 species are considered to be derived from such a basic karyotype by centric fusion and pericentric inversion (Aswathanarayana and Ashwath, 1994). Even in Listroscelinae, the basic karyotype must have had 2n = 33 as in the genus *Hexacentrus* (Aswathanarayana, 1998) with all acrocentrics from which *E. annulicornis* (2n = 12) and *Euhexacentrus* sp. (2n = 9) might have evolved by centric fusion, tandem fusion and pericentric inversion. Since many structural mechanisms are involved in the process, differentiation must have taken considerable span of time (Aswathanarayana, 1998).

According to White (1973) it may be assumed that 2n = 31 is the basic (ancestral) chromosome number for most of the subfamilies of Tettigonoidea. But in Pseudophyllinae (2n = 35) and Meconematinae (2n = 33), the karyotype data are insufficient to draw any conclusion on evolutionary trends.

Grylloidea

Gryllids show a wide range of diploid numbers from 11 to 29. The lowest chromosome number of 2n = 11 is in the species of *Trigonidium* and the highest of 2n = 29 in *Gryllus bimaculatus*. In *Gryllodes sigillatus* (2n = 21) and *Plebeigryllus guttiventris* (2n = 21) and *Oecantrus* sp. (2n = 18) all the autosomes are acrocentric but the X-chromosomes are metacentric. In all the other species viz., *Gryllopsis maculithorax* (2n = 19), *Velarifictorius maindroni* (2n = 21) and *V. dehradunensis* (2n = 25). *Telegryllus* sp. (2n = 27) and *Gryllus bimaculatus* (2n = 29) the karyotypes have a combination of acrocentric and biarmed chromosomes. The X chromosome in all the species is a large metacentric except in *Pteronemobius taprobanensis* in which it is a large submetacentric. In this group 21, 19 and 15 are the commonest numbers. So it is difficult to designate the basic number for the whole group. However, it is possible to indicate the generic modal numbers for almost all the genera; for example, in the genus *Gryllus* it is 29. *Gryllodes sigillatus*, *Plebeiogryllus guttiventris* and *Oecanthus* sp. are considered to be more primitive than the other species of Gryllinae and all species of Nemobiinae and Trigonidiinae. In general, Robertsonian changes must have taken place during the evolution of this group.

Sex chromosomes and Sex determining mechanism

In general, the sex determining mechanism in all the 3 subgroups Acrididae, Tettigonoidae and Grylloidea is XX : XO type except in *Euhexacentrus annulicornis* (Tettigonidae) (Aswathanarayana and Ashwath, 1985) and *Oecanthus* sp. (Glylloidea) (Ashwath, 1981) which have neo-X Y condition. It is known that neo-X Y condition is produced by centric fusion between X (of XX : XO) and an autosome and the homologue of the fused autosome forms a neo-Y

In 14 species of the acridids (Table 1), the X-chromosome is the largest and measures ca. 10 to 15% of the haploid set in different species. No species exhibited neo-X Y condition. But Yadav and Yadav (1986) have recorded neo-X Y condition in 3 species from Kurukshetra (North-West India) and are considered to be of recent origin.

The evolution of the X chromosome in tettigonids is of special interest and importance because it is generally large and in some strikingly large irrespective of its morphology. The length varies from ca. 16 to 30% of the haploid genome in different species. White (1973) stated that the X-chromosome had an independent evolution and its acrocentric condition was considered to be primitive from which other forms seem to have arisen in tettigonids. The largeness of the X-chromosome may not be due to the addition of heterochromatin as evidenced by our preliminary C-banding studies, since the amount of heterochromatin was almost the same or even less than in some of the large autosomes (Aswathanarayana and Ashwath, 1985 and 1994). It is not clear how the X-chromosome attains large size. In gryllids all the 13 species have generally large metacentric X-chromosome except in one species which has large submetacentric morphology. The X-chromosome measures ca. 14 to 23% of the haploid genome in different species.

SUMMARY

The chromosome number, morphology and sex determining mechanism of 41 species of Orthoptera are described and the trends of karyotype evolution at the family level are discussed.

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