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Cytogenetics Studies in Brazilian Species of Pseudophyllinae (Orthoptera: Tettigoniidae): $2n(\♂)=35$ and $FN=35$ the Probable Basic and Ancestral Karyotype of the Family TettigoniidaeAMILTON FERREIRA, ALEJO MESA[†]*Depto de Biologia, Instituto de Biociências, Unesp, Campus de Rio Claro, Av 24 A 1515, 13.5000-900, Rio Claro, SP, Brasil; amilton@rc.unesp.br; †in memoriam**Edited by Roberto A Zucchi – ESALQ/USP**Neotropical Entomology 39(4):590-594 (2010)*

ABSTRACT - The karyotypes of five species of Brazilian Pseudophyllinae belonging to four tribes were here studied. The data available in the literature altogether with those obtained with species in here studied allowed us to infer that $2n(\♂)=35$ is the highest chromosome number found in the family Tettigoniidae and that it is present in species belonging to Pseudophyllinae, Zaprochilinae and in one species of Tettigoniinae. In spite of that all five species exhibit secondary karyotypes arisen surely by a mechanism of chromosomal rearrangement of centric fusion, tandem fusion and centric inversion types from those with $2n(\♂)=35$ and $FN=35$, they share some common traits. The X chromosome is submetacentric ($FN=36$), heteropicnotic during the first prophase, the largest of the set but its size is rather variable among the species and the sex chromosomal mechanism is of the XO ($\♂$), XX ($\♀$) type. The chromosomal rearrangements involved in the karyotype evolution of the Pseudophyllinae and its relationship with those of the family Tettigoniidae are discussed and we propose that the basic and the ancestral karyotype of the Tettigoniidae is formed by $2n(\♂)=35$, $FN=35$ and not by $2n(\♂)=31$, $FN=31$, as usually accepted.

KEY WORDS: Chromosomal rearrangement, fusion and centric inversion, evolution

The family Tettigoniidae comprises approximately 1,155 genera and 6,521 species of which only 7.5% have been studied cytologically. Very little progress has been made so far in the chromosome survey of these insects. The main information concerning the karyotype evolution, chromosomal rearrangements, phylogenetic relationship and the structure of the chromosomes revealed by the use of C bands, Ag-NoR bands and by quantitative approaches has been made recently available. The Warchalowska's (1998) paper is meritorious once she makes a general review of all information available at that time. The document adds new data and discusses the karyotype evolution of the subfamilies and their relationship.

The family Tettigoniidae is characterized by a variation in its chromosome number that extends over a wide range, especially in the sub-families Phaneropterinae and Tettigoniinae. The numerical variability ranges from $2n(\♂)=33$ to $2n(\♂)=16$ in the Phaneropterinae (Pearson 1929, Dave 1965, Ferreira 1969, Cisneros-Barrios *et al* 1990), whereas in the Tettigoniinae it goes from $2n(\♂)=33$ to $2n(\♂)=15$ (Ueshima *et al* 1990, Warchalowska-Śliwa 1998). Despite this great variation, the family shows some traits that are commonplace and found in the majority of the species. The X chromosome is always heteropicnotic during the first prophase. It is rather variable in size among species, but always constitutes the largest unit of the

karyotype. Its morphology can be acrocentric, metacentric or submetacentric. Most of species have males with an XO sex chromosome mechanism. Only six species are at present known to have changed their XO sex mechanism to a more complex one (Dave 1965, White, Mesa & Mesa 1967, Ferreira 1969, 1976, Messina 1975).

The family Tettigoniidae is arranged according to different authors between 14 to 24 subfamilies (Kevan 1976, 1977, 1982, Rentz 1985, 1993, Eades & Otte 2009). Presently, we will take into consideration Eades & Otte (2009) who include the Pleminiini and Pseudophyllini in the subfamily Pseudophyllinae.

The pioneer cytological work in the Pseudophyllinae is from the beginning of last century. Woolsey (1915) described the karyotype of three species of *Jamaicana*. *Jamaicana flava* (Caudell) has $2n(\♂)=35$ and $FN=35$, while *J. unicolor* (Brunner von Wattenwil) and *J. subguttata* (Walker) have $2n(\♂)=33$ and $FN=35$. Asana (1938) published the karyotype of *Satrophylia* sp. as formed also by $2n(\♂)=35$ and $FN=35$, whereas Piza (1950) reported for the first time the karyotype of *Meroncidius intermedius* (Piza) a Brazilian species formed by $2n(\♂)=31$ and $FN=35$.

According to Yadav & Yadav (1986) and Aswathanarayama & Aswath (1996), *Sathrophyllia rugosa* (Thunberg) has $2n(\♂)=31$, $FN=31$ and *S. femorata* (Fabricius) $2n(\♂)=35$, $FN=35$.

In this paper, we studied the chromosomes of five species of Pseudophyllinae belonging to four tribes, discuss the chromosomal mechanism involved in the karyotype evolution of the sub-family and propose a tentative karyotype model for the family Tettigoniidae.

Material and Methods

All species studied in here, *Bliastes viridifrons* Piza (Cocconotini), *Diophanes amazonensis* Piza (Pterophyllini), *Diophanes scaberrimus* Piza (Pterophyllini), *Leptotettix crassiceri* Piza (Leptotettigini) and *Leptotettix humaita* Piza (Leptotettigini), were collected in the vicinities of Humaita, state of Amazonas, Brazil. All specimens were dissected in the field and the testes fixed in a mixture of ethyl alcohol-acetic acid (3:1) and stored at low temperature. Squash preparations of the chromosomes were stained with 2% acetic-orcein. The meiotic first metaphase was drawn with the aid of a camera lucida. The bivalents of each species were arranged in a decreasing order of size and tentatively arranged in groups of large (L), medium size (M) and small bivalents (S). Two specimens of each species were used for the analysis of first metaphase chromosomes.

Results

Four groups of karyotypes were found in all five species studied, but all of them shared the X0(♂) / XX(♀) sex mechanism type. The X is submetacentric, heteropicnotic during the first prophase, the larger of the set, but rather variable in size among species (Table 1).

Diophanes scaberrimus (Fig 1) and *L. humaita* (Fig 2) have $2n(\♂)=35$ and $FN=36$, due to the morphology of the X element that is submetacentric, while the autosomes are acrocentric. In the first prophase, the bivalents can be arranged into three groups according to their size: three large (L), seven or eight of medium size (M) and six or seven of small size (S). While there is a sharp limit among the groups L and M, the same does not happen among the groups M and S. Two chiasmata are normally seen in two bivalents, one belongs to the L group and the second to the M. The others have invariably a single one.

Bliastes viridifrons (Fig 3) has $2n(\♂)=33$ and $FN=36$. Its karyotype show four bivalents in the group L, five in the M and seven in the S group. The L_1 is submetacentric, while

the others are acrocentric. Only a single pair of the M group has two chiasmata, the others have only a single one.

Leptotettix crassiceri (Fig 4) has $2n(\♂)=31$ and $FN=34$. Their bivalents and even the X chromosome exhibit larger size when compared with the remaining species studied. The division of the bivalents by groups is only a tentative approach since they gradually decrease in size. The L, M and S groups are formed by five pairs of bivalents each. The L_1 is metacentric, and shows three chiasmata. The L_2 , L_4 , M_2 and M_7 have two chiasmata, and the remaining a single one (Fig 5).

Diophanes amazonensis (Fig 5) has $2n(\♂)=29$ and $FN=34$. The L group is formed by four bivalents, the M by four or five and the S by five or six. The L_1 and L_2 bivalents are formed by metacentric chromosomes and have two chiasmata, whereas the remaining are acrocentric and have one chiasma, excepting L_4 and M_2 , which have two.

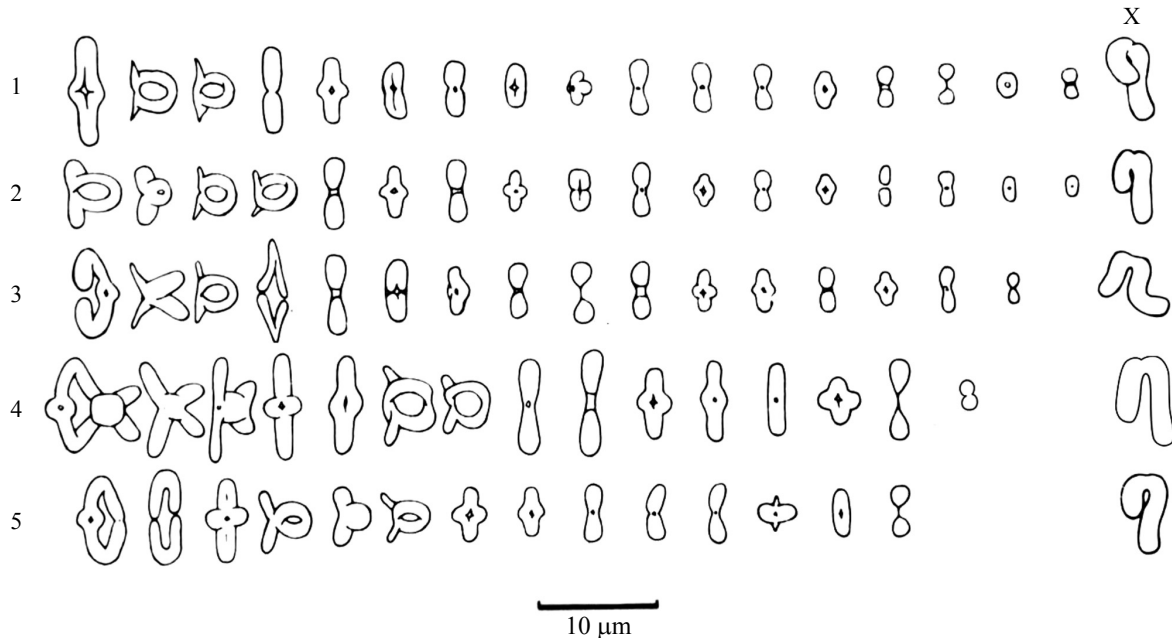
Discussion

From the twelve species of Pseudophyllinae known cytologically, six have $2n(\♂)=35$ and $FN=35$ or 36 depending of the morphology of the X chromosome that is biarmed in two. We are not considering *Phillozelus pectinatus* studied by Aswathanarayana & Aswath (1996), since this species was not formally described. This is the highest chromosome number found in the family and it is shared by 11 out of 17 species of Zaprochilinae, an endemic Australian subfamily (Rentz & Clyne 1983, Ueshima 1993). After Mesa & Ferreira (1977) reported a chromosome number of $2n(\♂)=37$ for a single male of *Platydecticus angustifrons* (Chopard), an extensive taxonomic revision was undertaken by Rentz & Guerney (1985) with the description of new genera and species of South American Tettigoniinae (former Decticinae).

Now that fourteen new species of the genus *Platydecticus* have been described, as well as several species of three others related genera, it is desirable to undertake cytological studies of these species. According to these authors, Australian Tettigoniinae are unrelated to those from Africa, but they show strong relationship with the South America genera and *Neduba* from North America. While Gorochoff (1988, 1995) places it in the subfamily Nedubinae, Rentz & Guerney (1985) and Rentz & Coless (1990) consider it belonging to the tribe Nedubini of the subfamily Tettigoniinae. The cytological data strengthen Rentz & Guerney (1985) and Rentz & Coless (1990) point of view since the family Tettigoniinae has a

Table 1 Chromosome number, morphology and sex determining mechanism in the five species of Tettigoniidae studied.

Taxa	$2n\♂$	NF	Sex	Morphology
<i>Diophanes scaberrimus</i>	35	36	XO	L_1 - S_{17} acroc; X subm.
<i>Leptotettix humaita</i>	35	36	XO	L_1 - S_{17} acroc; X subm.
<i>Bliastes viridifrons</i>	33	36	XO	L_1 met; L_2 - S_{16} acr; X subm.
<i>Leptotettix crassiceri</i>	31	34	XO	L_1 met; L_2 - S_{14} acr; X subm.
<i>Diophanes amazonensis</i>	29	34	XO	L_1 - L_2 met; L_3 - S_{12} acr ; X subm.



Figs 1-5 First metaphase of 1) *Diophanes scaberrimus*; 2) *Leptotettix humaita*; 3) *Bliastes viridifrons*; 4) *Leptotettix crassiceri*; and 5) *Diophanes amazonensis*. For each species, the chromosomes were organized in decreasing order of size from left to right, with the X at the right end. Scale bar = 10 μ m

wide numerical chromosomal variability that ranges from $2n(\sigma)=35$ to $2n(\sigma)=17$, according to Warchalowska-Śliwa (1998). In the six species of *Neduba* studied, the chromosome number varied from $2n(\sigma)=25$ to $2n(\sigma)=22$, and the FN from 28 to 23 (Ueshima & Rentz 1979).

The variability in chromosome number and morphology found among Pseudophyllinae species studied so far is not too large when compared to those seen in some subfamilies, especially in the Phaneropterinae, Tettigoniinae and Conocephalinae. It has nine karyotypes that ranged from $2n(\sigma)=35$ to $2n(\sigma)=29$. The basic and ancestral karyotypes were found in *J. flava* and *Sathrophyllia* sp. It is formed by $2n(\sigma)=35$ and FN=35. A centric inversion undergoes the X morphology from acrocentric to submetacentric, giving rise to a FN and an evolutionary branch with biarmed X, like the one found in *L. humaita* and *D. scaberrimus*. *Bliastes viridifrons* with a $2n(\sigma)=35$, FN=36, has one metacentric autosome pair surely originated by centric fusion involving acrocentric autosomes. In species with a low FN, the karyotypes could only be explained by the occurrence of tandem fusions followed by centric ones. This is the case of *L. crassiceri* - $2n(\sigma)=31$, FN=34 - and *D. amazonensis* $2n(\sigma)=29$, FN=34.

In the acrocentric X branch, the variability of the chromosomal number shows preponderance of tandem fusion in the origin of derived karyotypes. From seven species studied, three have karyotypes showing all the chromosomes acrocentric, but with number smaller than 35, as in the case of *J. unicolor*; *J. subguttata* - $2n(\sigma)=33$, FN=33 - and *S. rugosa*, $2n(\sigma)=31$, FN=31. The only exception is *M. intermedius* with $2n(\sigma)=31$, NF=35. The reduction in chromosomal number is associated with two pairs of metacentric autosomes, arisen surely by means of two independent centric fusions.

A similar scenario was found in Zaprochilinae (Rentz & Clyne, 1983, Ueshima 1993). From the 17 species cytologically known, 11 have $2n(\sigma)=35$ and FN=35, three have $2n(\sigma)=31$ and FN=31, two show $2n(\sigma)=31$ and FN=33 and one $2n(\sigma)=29$ and FN=36. Its basic and ancestral karyotype also has $2n(\sigma)=35$ and FN=35, while the remaining, as observed in the Pseudophyllinae, are the result of chromosomal rearrangement.

Karyotypes with $2n(\sigma)=33$ were also found in six species of Phaneropterinae (Pearson 1929, Cisneros-Barrios *et al* 1990), in 16 of Conocephalinae (King 1924, Hareyama 1939, Makino 1951, Warchalowska-Śliwa 1984, Ueshima & Rentz 1991) and in two of Meconomatinae (Kacker & Singh 1978). In the subfamilies Odonturinae and Austrosaginae the larger chromosome number is $2n(\sigma)=31$ (Ueshima 1993, Warchalowska-Śliwa 1998), whereas in Meconomatinae and Hetrodinae is $2n(\sigma)=29$ (Matthey 1948, Aswathanarayana & Aswath 1996).

Despite of these extreme numbers - $2n(\sigma)=35$ or $2n(\sigma)=33$ - and the wide range of numerical chromosomal variability found in Tettigoniidae (Warchalowska-Śliwa 1998) as a whole, the karyotype formed by $2n(\sigma)=31$ and FN=31 is found in the majority of the subfamilies and in 50% of the species studied so far. It is common in 12 subfamilies found all σ around the world and has not been observed in species of Mecopodinae and Hetrodinae (Warchalowska-Śliwa 1998) probably due to the few species studied so far. In Phaneropterinae, it is common to 50% of the species, where in Odonturini it appears in 83%, in Tettigoniinae in 37% and in 85% of the species of Austrosaginae.

Due to the prevalence of these karyotypes in terms of species, genera and its configuration, with all chromosomes being acrocentric, White (1973, 1973a, 1973b) suggested it

($2n(\♂)=31$ and $FN=31$) as the basic and ancestral character for the family Tettigoniidae. With the data now available, although still scarce and with gaps to be filled, the White suggestion does not have cytological support. To accept his hypothesis, it would be required to admit that during the process of chromosomal rearrangements that gave rise to the species with $2n(\♂)=33$ or 35 , there was an increase in chromosome arms. Only the conjunction of a centric inversion and a centric dissociation in the same, originally acrocentric chromosome, can be responsible by the increase in arm number. While both events are frequent in the evolutionary history of orthopterans, these conjunctions are very rare. Among the grasshoppers, there is a single case where an increase in chromosome number due to dissociation seems to have occurred (Mesa 1973, Mesa & Ferreira 1977). The majority of species belonging to the family Ommexechidae have two submetacentric autosomes originated in an ancient pericentric inversion. In the Chilean species *Conometopus sulcaticollis* (Blanchard), such chromosome has split into two independent acrocentric elements.

However, 48 out of nearly 300 species of grasshoppers were observed with one, two or three autosome centric fusions and almost the same number with X-autosome fusions, some of them even with Y-autosome fusions (Mesa *et al* 1982). Ferreira (1973) and Warchalowska-Sliwa (1998) also described the importance of these mechanisms in the chromosome number and arms reduction observed in the chromosomal variability found in the Phaneropterinae and Tettigoniinae. Therefore, the cytological data available show that the basic and ancestral karyotype of the family Tettigoniidae is $2n(\♂)=35$ and $NF=35$, and that its karyotypical reorganization has occurred in two steps. In the beginning of the evolutionary history of the family it has changed to $2n(\♂)=31$ and $FN=31$ and this karyotype was probably initially fixed in most of the subfamilies. The karyotypes with $2n(\♂)=35$ that are circumscribed specially in the subfamilies Pseudophyllinae and Zaprochilinae and those with $2n(\♂)=33$ found in several families would be therefore relict karyotypes of the evolutionary history of the family.

The karyotype with $2n(\♂)=31$ and $NF=31$ is the most successful in Tettigoniidae in terms of genera and species that have inherited it. However, in the last 250 million years, probably since the Permian, when tettigoniids arose as an independent lineage (Sharov 1968), several opportunities for the establishment of a great number of groups and a wide range of morphological and numerical chromosomal variability that is currently found in most of its subfamilies have occurred.

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