

— INVITED REVIEW —

Evolutionary cytogenetics in Heteroptera

ALBA GRACIELA PAPESCHI* and MARÍA JOSÉ BRESSA

*Laboratorio de Citogenética y Evolución, Departamento de Ecología, Genética y Evolución,
Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina*

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In this review, the principal mechanisms of karyotype evolution in bugs (Heteroptera) are discussed. Bugs possess holokinetic chromosomes, i.e. chromosomes without primary constriction, the centromere; a pre-reductional type of meiosis for autosomes and m-chromosomes, i.e. they segregate reductionally at meiosis I; and an equational division of sex chromosomes at anaphase I. Diploid numbers range from $2n = 4$ to $2n = 80$, but about 70% of the species have 12 to 34 chromosomes. The chromosome mechanism of sex determination is of the XY/XX type (males/females), but derived variants such as an X0/XX system or multiple sex chromosome systems are common. On the other hand, neo-sex chromosomes are rare. Our results in heteropteran species belonging to different families let us exemplify some of the principal chromosome changes that usually take place during the evolution of species: autosomal fusions, fusions between autosomes and sex chromosomes, fragmentation of sex chromosomes, and variation in heterochromatin content. Other chromosome rearrangements, such as translocations or inversions are almost absent. Molecular cytogenetic techniques, recently employed in bugs, represent promising tools to further clarify the mechanisms of karyotype evolution in Heteroptera.

Key words: holokinetic chromosomes, karyotype evolution, molecular cytogenetics.

INTRODUCTION

Cytogenetic studies in Heteroptera date from 1891 with Henking's morphological study on the spermatogenesis of the bug *Pyrrhocoris apterus* Linnaeus (Pyrrhocoridae). He described the presence of a chromatin body (the "X chromosome") that showed an unusual staining during meiotic prophase and a peculiar behaviour during meiosis. The observations of Henking and other cytologists, together with their own observations in males and females of different Heteroptera species, were finally interpreted by Mc Clung (1901) and Wilson (1909b). They suggested a direct relationship between sex determination and presence of either one or two "X chromosomes" in X0/XX systems, or an XY or XX chromosome pair in species with XY/XX systems.

Through a series of publications that appeared

between 1897 and 1932, Wilson and Montgomery settled the foundations on Heteroptera cytogenetics. Some years later, between the 1930s and the 1960s, Schrader and Hughes-Schrader contributed significantly to a better knowledge on the organization and function of heteropteran chromosomes and their behaviour during cell divisions (Ueshima, 1979; Manana, 1984).

At present, although approximately 1600 heteropteran species belonging to 46 families have been cytogenetically analyzed, they are not a representative sample of the group (4.2% of approximately 38,000 described species) (Table 1) (Schuh & Slater, 1995). Most studies have been made on male testes, because meiotic cells are more often encountered than mitotic ones, and the earliest reports referred to the male chromosome number and sex chromosome system. No detailed analysis of heteropteran chromosome morphology is possible, since chromosomes are holokinetic (a primary constriction, the centromere, is lacking) and the chromosomes are generally

* Corresponding author: tel.: +54 11 45763354, fax: +54 11 45763384, e-mail: alpape@ege.fcen.uba.ar

relatively small and of similar size. Although DNA measurement is the best means of testing fusion/fragmentation hypothesis in karyotypic evolution of taxa bearing holokinetic chromosomes, this technique has been rarely used in Heteroptera (Schrader & Hughes-Schrader, 1956, 1958; Maudlin, 1974; Papeschi, 1988, 1991; Panzera *et al.*, 1992, 1995; Papeschi *et al.*, 2001; Grozeva & Nokkala, 2003). Furthermore, cytogenetic studies at the population level in Heteroptera are still scarce. All these facts represent serious constraints in comparative and evolutionary cytogenetics of this insect group.

Recently, molecular approaches such as fluorescent banding and fluorescent *in situ* hybridization with telomeric and ribosomal DNA probes (18S and 28S rDNA), have been carried out in bugs (González-García *et al.*, 1996; Sahara *et al.*, 1999; Papeschi *et al.*, 2003; Rebagliati *et al.*, 2003; Cattani & Papeschi, 2004; Cattani *et al.*, 2004; Frydrychová *et al.*, 2004; Grozeva *et al.*, 2004; Hebsgaard *et al.*, 2004; Ituarte & Papeschi, 2004; Bressa *et al.*, 2005; Vítková *et al.*, 2005). These molecular techniques have substantially contributed to a better understanding of the chromatin organization and composition of these holokinetic chromosomes. However, there is still much to be learnt before the mechanisms of karyotype evolution and the role in the speciation of heteropterans is completely clarified.

CYTOGENETICS OF HETEROPTERA: GENERAL FEATURES

The genetic system of Heteroptera has many characteristics that make it unique among most insect groups: the possession of holokinetic chromosomes, a different meiotic behaviour for autosomes and sex chromosomes, a mean chiasma frequency of only one chiasma per bivalent, and a pair of "m chromosomes" in some families.

All heteropteran species possess holokinetic chromosomes (i.e. without a localized centromere). During mitosis, microtubules attach to the entire length of the sister chromatids and at anaphase, they migrate parallel to each other and perpendicular to the polar spindle (Hughes-Schrader & Schrader, 1961). At the ultrastructural level, kinetochore plates, to which spindle microtubules are attached, cover almost all the polar surface of the mitotic chromosomes (Buck, 1968; Comings & Okada, 1972). However, kinetic activity during meiosis is restricted to the telomeric regions and the chromosomes can be

regarded as telokinetic (Motzko & Ruthmann, 1984). Both chromosome ends can show kinetic activity during meiosis in such a way that the telomeric regions that were inactive during the first meiotic division become active during the second one (Camacho *et al.*, 1985; Nokkala, 1985; Pérez *et al.*, 1997; Cattani *et al.*, 2004). The holokinetic nature of heteropteran chromosomes has led to the hypothesis that fusions and fragmentations would be the most frequent mechanisms of karyotype evolution. The non-localized kinetic activity does not have the constraints imposed by a localized centromere in species with monocentric chromosomes. In the latter, acentric fragments or dicentrics are mitotically and meiotically unstable.

The meiotic behaviour of autosomal bivalents, sex chromosomes and m chromosomes is slightly different. As a rule, autosomal bivalents are chiasmatic, whereas sex chromosomes and m chromosomes are achiasmatic (Ueshima, 1979; Manna, 1984; González-García *et al.*, 1996; Suja *et al.*, 2000). When autosomal bivalents form only one chiasma terminally located, they orientate at metaphase I with their long axes parallel to the polar axis; they segregate reductionally during meiosis I and equationally during meiosis II. On the other hand, bivalents with two terminal chiasmata orientate equatorially and two different behaviours have been described: a) one chiasma releases first and an axial orientation is finally achieved or b) alternative sites of kinetic activity become functional and no telokinetic activity is observed (Mola & Papeschi, 1993; Papeschi *et al.*, 2003). This latter behaviour has been described in *Pachylis argentinus* Berg and *Nezara viridula* (Linnaeus); both species possess a pair of chromosomes carrying a secondary constriction, and when this particular pair presented two chiasmata, the alternative kinetic sites were located next to the secondary constrictions (Papeschi *et al.*, 2003). When chiasmata are medially located, the terms pre-reduction and post-reduction lose their meaning. The genetic information located at the chiasma to one pair of telomeric regions divides reductionally, while the information located at the other half of the chromosome does so equationally. We consider meiosis in Heteroptera as pre-reductional taking into account the behaviour of bivalents with one terminal or sub-terminal chiasma, in which most genetic information segregates reductionally at meiosis I; and the behaviour of fusion/fragmentation trivalents, in which the largest chromosome always segregates from the two smaller ones at meiosis I (Ueshima, 1963; Papeschi,

1994). A post-reductional meiosis has been described in other groups with holokinetic chromosomes (e.g. Juncaceae, Odonata) (Nordenskiöld, 1962; Mola, 1995).

On the other hand, sex chromosomes are achiasmatic and behave as univalents in male meiosis I. They divide equationally at anaphase I and associate at meiosis II through the so-called “touch-and-go pairing”. Nevertheless, pre-reduction of the sex chromosomes has been described in three species of *Anisops* (*A. fieberi* Kirkaldy, *A. niveus* Fabricius, *A. sardea* Kirkaldy) (Notonectidae), two species of *Ectrychotes* (*E. abbreviatus* Reuter, *E. dispar* Reuter) (Reduviidae), two species of *Archimerus* (*A. alternatus* Say, *A. calcarator* Fabricius) and four species of *Pachylis* [*P. argentinus* Berg, *P. gigas* Barm., *P. laticornis* (Fabricius), *P. pharaonis* (Herbst)] (Coreidae) and in all the 29 species of Tingidae (Ueshima, 1979; Grozeva & Nokkala, 2001; Papeschi *et al.*, 2003). Finally, the m chromosomes are also achiasmatic, but associate at first meiotic division segregating pre-reductionally.

THE m CHROMOSOMES

Wilson (1905) introduced the term “m chromosomes” to describe the smallest chromosome pair in two species of Coreidae which behave differently from both the autosomes and the sex chromosomes during male meiosis. Until present, the m chromosomes have been reported in many heteropteran families (Table 1) (Ueshima, 1979). Although the m chromosomes are generally of small size, they are actually defined by their meiotic behaviour: they are usually unpaired and thus achiasmatic during early meiosis, and at late diakinesis they come close together. At metaphase I, they are always associated end-to-end (touch-and-go pairing) forming a pseudobivalent which segregates reductionally at anaphase I. The second meiotic division is equational for the m chromosomes.

One exception to this meiotic behaviour has been described in *Coreus marginatus* Linnaeus (Coreidae) by Nokkala (1986) and Suja *et al.* (2000), who reported that the m chromosomes were present as a bivalent in some cells.

The m chromosomes generally show alloreciprocity with respect to both the autosomes and the sex chromosomes during male meiosis, but the heterochromatin characterization in this chromosome pair showed that they are by no means completely het-

rochromatic. The different pycnotic cycle of the m chromosomes reflects differences in chromatin packaging, and this pattern of chromatin condensation is probably related to the regulation of gene expression (Bressa *et al.*, 2005). However, there is still no information on the genetic content of the m chromosomes.

Further studies are required in order to clarify the precise behaviour and function of the m chromosomes in different species. Are they always present as univalents or do they form a bivalent? Do they have different behaviour according to the genetic or environmental milieu? Furthermore, which are the mechanisms that guarantee their correct segregation when they are present as univalents? Do they represent some kind of selfish DNA? Nothing can still be said about their function in the genetic system of the heteropteran species possessing them.

SEX CHROMOSOME SYSTEMS

Sex chromosome systems described so far in Heteroptera are simple systems of the types XY/XX (71.4% of approximately 1600 species cytogenetically analyzed) and X0/XX (14.7%), and different multiple systems (X_nY/X_nX_n , X_n0/X_nX_n , XY_n/XX) (13.5%). Neo-sex chromosome systems are very rare and until present they have only been reported in seven species and subspecies (0.5%) (Table 1) (Ueshima, 1979; Bressa *et al.*, 1999; Nokkala & Nokkala, 1999; Jacobs, 2004).

Two hypotheses concerning the evolution of the sex-chromosome systems in Heteroptera have been proposed. Ueshima (1979) suggested that the XY system is derived from an ancestral X0 that is commonly encountered in primitive taxa and in phylogenetically related homopteran species (Halkka, 1959). By contrast, based on the presence of a Y chromosome in very primitive heteropteran species, Nokkala & Nokkala (1983, 1984) and Grozeva & Nokkala (1996) suggested that the X0 system is a derived condition from the ancestral XY that is present in the majority of the species cytogenetically analyzed.

Sex chromosome systems with multiple Xs or Ys most probably originated through fragmentation of the ancestral X or Y, respectively. The study of one population of *Belostoma orbiculatum* Estévez & Polhemus (Belostomatidae), polymorphic for the sex chromosome system, provided evidence that supports this hypothesis (Papeschi, 1996). The analysis of two samples from one population of Punta Lara (Buenos

TABLE 1. Number of species cytogenetically analyzed and principal cytogenetic features of heteropteran families

| Taxa | | Nº of species | 2n Range | Mode | m chromosomes | Sex Chromosome Systems |
|-----------------|--|-----------------|------------------|---------|------------------|------------------------|
| Dipsocoromorpha | | Dipsocoridae | 4 | (21-22) | present/absent | X0, XY, XnY |
| | | Schizopteridae | 2 | 30 | present | X0 |
| Gerrimorpha | | Hebroidea | Hebridae | 4 | (19-27) | absent |
| | | Hydrometroidea | Hydrometridae | 3 | (19-20) | absent |
| | | Gerroidea | Gerridae | 21 | (19-31) | absent |
| | | Veliidae | | 5 | (21-25) | absent |
| | | Mesoveloidae | Mesovelidiidae | 1 | 35 | absent |
| Nepomorpha | | Nepoidea | Belostomatidae | 27 | (4-30) | absent |
| | | | Nepidae | 11 | (22-46) | absent |
| | | Ochteroidea | Gelastocoridae | 1 | 35 | absent |
| | | | Ochteridae | 1 | 50 | ? |
| | | Corixoidea | Corixidae | 28 | (24-26) | present |
| | | | Micronectidae | 2 | (24-30) | absent |
| | | Naucoroidea | Naucoridae | 10 | (20-51) | present |
| | | Notonectoidea | Notonectidae | 14 | (24-26) | present |
| | | | Pleidae | 3 | 23 | present |
| Leptopodomorpha | | Saldoidea | Salidae | 9 | (19-36) | present |
| | | Leptopodoidea | Leptopodidae | 1 | 28 | absent |
| Cimicomorpha | | Reduviidea | Reduviidae | 125 | (12-34) | absent |
| | | Microphysioidea | Mycophysidae | 3 | 14 | absent |
| | | Joppeicoidea | Joppeicidae | 1 | 24 | absent |
| | | Miroidea | Miridae | 168 | (14-80) | absent |
| | | | Tingidae | 28 | (12-14) | absent |
| | | Naboidea | Nabidae | 30 | (18-40) | absent |
| | | Cimicoidea | Anthocoridae | 5 | (24-32) | absent |
| | | | Cimicidae | 44 | (10-44) | absent |
| | | | Polyctenidae | 3 | (6-12) | absent |
| Pentatomomorpha | | Aradoidea | Aradidae | 33 | (7-40) | absent |
| | | Pentatomoidea | Acanthosomatidae | 10 | (12-16) | absent |
| | | | Cydnidae | 12 | (12-31) | absent |
| | | | Dinidoridae | 7 | (14-21) | absent |
| | | | Pentatomidae | 303 | (6-27) | absent |
| | | | Plataspidae | 15 | (10-14) | absent |
| | | | Scutelleridae | 21 | (12-14) | absent |
| | | | Tessaratomidae | 1 | 12 | absent |
| | | | Urostylidae | 3 | (14-16) | absent |
| | | Lygaeoidea | Berytidae | 14 | (16-42) | absent |
| | | | Colobathristidae | 1 | 14 | present |
| | | | Lygaeidae | 402 | (10-30) | present/absent |
| | | | Piesmatidae | 4 | (22-24) | absent |
| | | Pyrrhocoroidea | Largidae | 11 | (11-17) | present/absent |
| | | | Pyrrhocoridae | 21 | (12-33) | absent |
| Coreoidea | | Alydidae | | 22 | (13-17) | present |
| | | Coreidae | | 108 | (13-28) | present |
| | | Rhopalidae | | 25 | (13-15) | present |
| | | Stenocephalidae | | 3 | 14 | present |

Aires province, Argentina) showed that 24 male individuals had the simple system XY, but five specimens from both samples had a multiple system X_1X_2Y . The comparison of area measurements of the sex chromosomes in individuals with $2n = 16$ and $2n = 17$ revealed that the relative size of the X_1 plus the X_2 did not differ significantly from the relative size of the single X. This pointed out that the X chromosome of the simple system has fragmented into two chromosomes of unequal size, one of them a little larger than the Y chromosome (Papeschi, 1996).

To date, neo-sex chromosomes in Heteroptera have been only found in two species of *Lethocerus* (*L. indicus* Lep. et Servielle, *Lethocerus* sp. Mayr) (Belostomatidae) (Chickering & Bacorn, 1933; Jande, 1959), and in *Rhytidolomia senilis* (Say) (Pentatomidae) (Schrader, 1940). In these species, both the ancestral X and Y chromosomes fused each with one chromosome of an autosomal pair, resulting in a neo-X/neo-Y system. The neo-system described in *Hebrus pusillus* Fallén (Hebridae) originated through the fusion of the ancestral X chromosome with one autosome (Nokkala & Nokkala, 1999); but the neo-sex chromosome systems of *Dysdercus albofasciatus* Berg (Pyrrhocoridae) (Bressa *et al.*, 1999) and of *Dundocoris nodulicarinus novenus* Jacobs and *D. nodulicarinus septeni* Jacobs (Aradidae) (Jacobs, 2004) have a more complex origin.

In *Dysdercus albofasciatus* the origin of the neo-XY system involved, most probably, a subterminal insertion of the ancestral X chromosome in an autosome followed by a large inversion, which included part of the original X chromosome (Bressa *et al.*, 1999). In *Dundocoris nodulicarinus novenus* the neo- XY_1Y_2 system probably originated by the fusion of a large autosome with the X chromosome (neo-X), while the homologue of the fused autosome formed a neo-Y (= Y_1) and the ancestral Y chromosome, the Y_2 . The neo-XY₁/neo-Y₂ sex chromosome system of *D. nodulicarinus septeni* probably originated by a later fusion of one pair of autosomes with the neo-X and the original Y chromosome (Y_2) (Jacobs, 2004).

HETEROCHROMATIN

Repeated DNA sequences in insect genomes are organized according to different patterns. They occur either as families of repeated elements interspersed throughout the genome or as large arrays usually representing satellite DNA sequences (Brutlag, 1980; Blanchelot, 1991). The current knowledge on the

organization of single copy and repeated sequences in insects comes mainly from extensive studies on *Drosophila* and early observations in other dipteran species (Blanchelot, 1991), and more recent studies in homopteran and lepidopteran species (Bizzaro *et al.*, 1996; Manicardi *et al.*, 1996; Spence *et al.*, 1998; Mandrioli *et al.*, 1999a, b, c; Mandrioli & Volpi, 2003; Mandrioli *et al.*, 2003).

Despite the general presumption that constitutive heterochromatin is an inert material, there is abundant and increasing evidence that constitutive heterochromatin can have important functions in chromosome pairing and segregation, position effect variegation and can even contain genes and other functional DNA sequences (Sumner, 2003).

Early reports on C positive heterochromatin in heteropterans showed that C bands are terminally located. This led to the suggestion that the principle of equilocal heterochromatin distribution of Heitz (1933, 1935) (i.e. the tendency of heterochromatin of non-homologous chromosomes to be located at similar positions) is also applied to Heteroptera (Solari & Agopian, 1987; Papeschi, 1991; Panzera *et al.*, 1995; Cattani *et al.*, 2004; Bressa *et al.*, 2005). However, recent reports describe a different distribution pattern in some species. In *Tenagobia fuscata* (Stål) (Corixidae), *Triatoma patagonica* Del Ponte (Reduviidae), *Petillia patullicollis* Walk. (Coreidae) and *Nezara viridula* (Linnaeus) (Pentatomidae), while most bands are terminally located, one autosomal pair presents a conspicuous C positive band in an interstitial position (corresponding at least in the latter to a nucleolus organizer region) (Camacho *et al.*, 1985; Dey & Wangdi, 1990; Panzera *et al.*, 1997; Papeschi *et al.*, 2003; Ituarte & Papeschi, 2004). The analysis of 13 species of Tingidae and four species of *Nabis* (Nabidae) using C banding revealed the presence of very scarce C positive heterochromatin located either at telomeric positions or, in some chromosomes, at interstitial ones (Grozeva & Nokkala, 2003; Grozeva *et al.*, 2004). Finally, a completely different pattern has been described in *Spartocera batatas* (Fabricius) (Coreidae), in which large heterochromatic blocks are located interstitially in all autosomal pairs (Franco, 2005).

Heterochromatin could be an active component of heteropteran chromosomes. Its accumulation in the karyotype of the species is not a random process and some constraints would regulate its acquisition and/or accumulation in different karyotypes.

There is still little information about heterochro-

matin base composition in Heteroptera, i.e. whether the heterochromatin is enriched in AT or GC bases as revealed by fluorescent banding techniques (DAPI and CMA₃ staining, respectively). Most reports referring to heterochromatin characterization describe C bands as DAPI-bright/CMA₃-dull. The presence of CMA₃ bright bands has been reported in a few species at interstitial or terminal position, either on autosomes or sex chromosomes, and they are generally associated to nucleolus organizer regions (González-García *et al.*, 1996; Papeschi *et al.*, 2001; Papeschi & Bressa, 2002; Papeschi *et al.*, 2003; Rebagliati *et al.*, 2003; Cattani *et al.*, 2004; Ituarte & Papeschi, 2004; Bressa *et al.*, 2005).

Sex chromosomes stain brightly with both fluorochromes, but their fluorescence probably represents differences in chromatin packaging between the autosomes and the sex chromosome rather than differences in base composition (Rebagliati *et al.*, 2003).

Very striking differences in the amount and distribution of C positive heterochromatin have been observed in species of *Triatoma* Laporte (Reduviidae). According to Panzera and colleagues (1995), despite the fact that heterochromatin variations represent the main source of karyological differentiation among and within species, they do not appear to affect homologous chromosome pairing and then they should not play a direct role in the speciation process (Panzera *et al.*, 1992; Pérez *et al.*, 1992; Panzera *et al.*, 1995).

CHROMOSOME NUMBER AND KARYOTYPE EVOLUTION

The male diploid chromosome number of Heteroptera ranges from 2n = 4 (*Lethocerus* sp., Belostomatidae) to 2n = 80 (four species of *Lopidea* Uhler, Miridae) (Fig. 1). However, the male diploid number of 14 is the most represented (460 species), followed by the diploid numbers 2n = 16 (186 species), 2n = 34 (92 species), 2n = 12 (89 species), 2n = 13 (80 species), 2n = 21 (70 species), 2n = 22 (76 species), and 2n = 24 (76 species). The Heteroptera comprise eight major groups, and cytogenetic reports are unequally distributed not only among these groups but also within them: Dipsocoromorpha (6 species), Gerromorpha (34 species), Nepomorpha (97 species), Lepidostomomorpha (10 species), Cimicomorpha (407 species) and Pentatomomorpha (1016 species) (Table 1). Within the Cimicomorpha, the families Miridae and Reduviidae are the more extensively studied (168 and 125 species, respectively) and within the Pen-

tatomorpha, the families Coreidae, Lygaeidae and Pentatomidae are the best represented (108, 402 and 303 species, respectively).

Most discussions on karyotype evolution in Heteroptera use the concept of modal chromosome number, that is, the commonest number present in a group. Sometimes this concept can be applied at a family level; more often, it is applicable to lower categories such as tribes or genera. Many times, the modal number is considered the ancestral one for the group under analysis (Ueshima, 1979).

Among the principal mechanisms of karyotype evolution, autosomal fusions and both autosomal and sex chromosome fragmentations can be included (Ueshima, 1979; Manna, 1984; Thomas, 1987; Papeschi, 1994, 1996). Other chromosome rearrangements, such as inversions and reciprocal translocations have been rarely reported (Papeschi & Mola, 1990; Bressa *et al.*, 1998; Pérez *et al.*, 2004). When analyzing karyotype evolution at the family level, some karyotypes are highly homogeneous, while others show intensive processes of karyotype alterations.

The Pentatomidae are one of the largest families of Heteroptera with approximately 760 genera and 4100 species. The family is worldwide in distribution and well represented in all of the major faunal regions (Schuh & Slater, 1995). Within this family, 303 species and subspecies belonging to 126 genera have been cytogenetically analyzed. The male diploid numbers are between 6 and 27 with a modal number of 14 chromosomes, which is present in 85% of the species. The sex chromosome system is XY/XX, except for only three species: *Macropygium reticulare* (Fabricius) (X₁X₂Y), *Rhytidolomia senilis* (neo-X/neo-Y), and *Thyanta calceata* (Say) (X₁X₂Y) (Rebagliati *et al.*, 2005). This family is cytogenetically highly homogeneous and karyotype changes probably played a minor role during speciation.

In Aradidae, at least 211 genera containing about 1800 species are currently classified in eight subfamilies. Aradids are represented in all major faunal regions with five out of the eight subfamilies being essentially cosmopolitan, but with three being restricted to the Australian-New Zealand-South American arc (Schuh & Slater, 1995). The known chromosome numbers of the Aradidae (33 taxa) range from 2n = 7 to 2n = 48 with two modal numbers of 27 and 14, and sex chromosome systems including XY, X₁X₂Y, X₁X₂X₃Y, X₁X₂X₃X₄Y and neo-sex chromo-

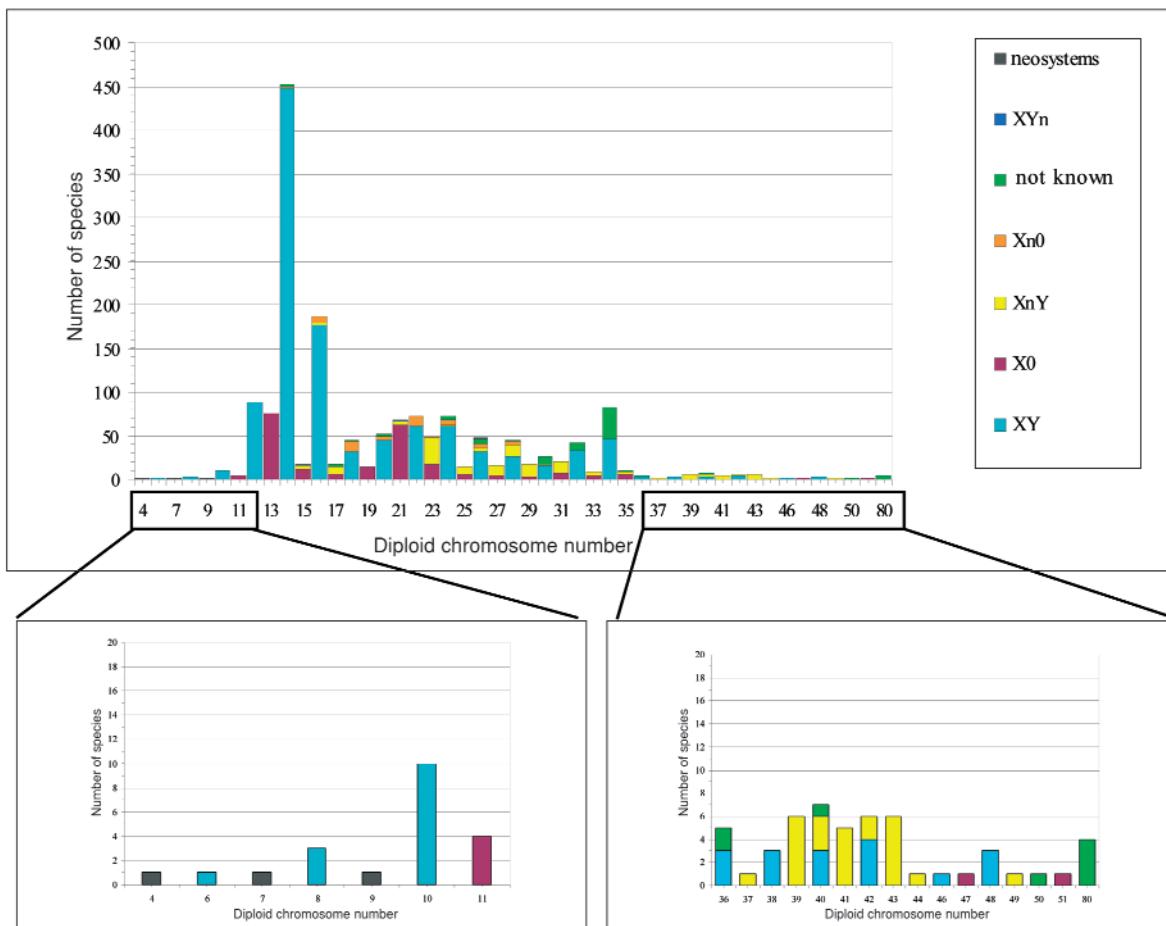


FIG. 1. Male diploid chromosome numbers and sex chromosome systems in Heteroptera.

somes (neo- XY_1Y_2 and neo- $XY_1/neo-Y_2$) (Jacobs & Groeneveld, 2002; Jacobs, 2004). The diversity in chromosome number and sex chromosome systems found in this family illustrates an intensive process of karyotype evolution. Although it is risky to speculate on the ancestral chromosome number of the Aradidae, Jacobs & Liebenberg (2001) suggested that since $2n = 12 + XY$ has been encountered in several genera in three of the six subfamilies thus far studied, it would probably represent the ancestral number of the family.

The Coreidae include at least 250 genera and 1800 species that are worldwide in distribution, but are more abundant in the tropics and subtropics (Schuh & Slater, 1995). The diploid number of the family ranges from 13 to 28, with a mode of 21, which is present in 47 out of the 108 species cytogenetically analyzed (43.5%). The Coreidae are also characterized by the possession of a pair of m chromosomes that has been described in 81.9% of the species

(Ueshima, 1979; Franco, 2005). The most common sex chromosome system of the family is $X0/XX$ (male/female) (64.3%) followed by the multiple system $X_1X_20/X_1X_1X_2X_2$ (32.1%). A multiple system $X_1X_2X_30$ in males has been ascribed to one population of *Coreus marginatus* Linnaeus (0.9%); and three species of *Acantocephala* (as *Metapodius*), namely *A. femorata* Fabricius, *A. granulosa* (Dallas), and *A. terminalis* (Dallas), have been reported as having an XY/XX system (2.7%). However, the three latter should be considered as a special situation, since the presence of a variable number of supernumeraries (B chromosomes) that associate with the X chromosome complicates the picture (Ueshima, 1979; Papeschi *et al.*, 2003; Cattani & Papeschi, 2004; Cattani *et al.*, 2004; Bressa *et al.*, 2005).

A striking feature of the X_n0 system in this family is that the X chromosomes are generally intimately associated during male meiosis, and in most species the tightly conjoined Xs were positioned outside the

ring of autosomes on both metaphase plates. Manna (1984) pointed out that in species with the X_n0 sex chromosome system the number of X chromosomes should be confirmed in the spermatogonial complement, because during meiosis the multiple Xs tend to fuse and then appear as a single element. Similar observations have been made by different authors (Manna, 1951; Dutt, 1957; Parshad, 1957; Fossey & Liebenberg, 1995).

Besides the coreids, similar multiple sex chromo-

some system has been described in several species of Pyrrhocoridae (10 out of 19 species), Notonectidae (3 out of 14 species), Miridae (1 out of 168 species) and Stenocephalidae (1 out of 3 species) (Ueshima, 1979; Manna, 1984; Grozeva & Nokkala, 1996; Grozeva, 1997; Bressa *et al.*, 1999; Nokkala & Nokkala, 1999; Bressa *et al.*, 2003; Angus *et al.*, 2004).

Two heteropteran families are included in the superfamily Pyrrhocoroidea: Largidae and Pyrrhocoridae. The former is represented in all major zoo-

TABLE 2. Diploid chromosome numbers in species of Pyrrhocoroidea

| Taxa | | 2n | 2n (male) | References |
|----------------------|--|----|--|--|
| Largidae | | | | |
| Larginae | <i>Largus cinctus</i> (Herrick-Schaeffer) | 11 | 10+X0 | (Wilson, 1909a) |
| | <i>L. fasciatus</i> Blanchard | 13 | 12+X0 | (Vidal & Lacau, 1985) |
| | <i>L. humilis</i> (Drury) | 13 | 12+X0 | (Piza, 1953) |
| | <i>L. rufipennis</i> Laporte | 13 | 12+X0 | (Piza, 1946; Mola & Papeschi, 1993; Bressa <i>et al.</i> , 1998) |
| | <i>L. succintus</i> Herrich-Schaeffer | 13 | 12+X0 | (Wilson, 1909a) |
| | <i>Macrocheraia grandis</i> Gray [= <i>Lohita grandis</i> (Gray)] | 15 | 14+X0 | (Banerjee, 1958; Banerjee, 1959; Manna & Deb-Mallick, 1981) |
| Physopeltinae | <i>Physopelta cincticollis</i> Stål | 15 | 12+2m+X0 | (Ueshima, 1979; Manna <i>et al.</i> , 1985) |
| | <i>P. gutta</i> Burmeister | 17 | 12+2m+X ₁ X ₂ Y | (Manna <i>et al.</i> , 1985) |
| | <i>P. quadrigutta</i> Bergs. | 17 | 12+2m+X ₁ X ₂ Y | (Manna <i>et al.</i> , 1985) |
| | <i>P. schlanbuschi</i> (Fabricius) | 17 | 14+X ₁ X ₂ Y | (Ray-Chaudhuri & Manna, 1955) |
| Pyrrhocoridae | | | | |
| | <i>Antilocus conqueberti</i> (Fabricius) | 27 | 26+X0 | (Parshad, 1957; Banerjee, 1958) |
| | <i>Cenaeus abortivus</i> Gerstäcker | 33 | 32+X0 | (Ueshima, 1979) |
| | <i>Dysdercus albofasciatus</i> Berg | 12 | 10+neo-XY | (Bressa <i>et al.</i> , 1999) |
| | <i>D. chaquensis</i> Freiberg | 13 | 12+X0 | (Mola & Papeschi, 1997) |
| | <i>D. cingulatus</i> (Fabricius) | 16 | 14+X ₁ X ₂ 0 | (Sharma <i>et al.</i> , 1957; Banerjee, 1958; Manna & Deb-Mallick, 1981) |
| | <i>D. evanescens</i> Distant | 16 | 14+X ₁ X ₂ 0 | (Manna & Deb-Mallick, 1981) |
| | <i>D. fasciatus</i> Signoret | 16 | 14+X ₁ X ₂ 0 | (Banerjee, 1958) |
| | <i>D. honestus</i> Bloete | 15 | 14+X0 | (Piza, 1947b) |
| | <i>D. imitator</i> Bloete | 13 | 12+X0 | (Bressa, 2003) |
| | <i>D. intermedius</i> Distant | 16 | 14+X ₁ X ₂ 0 | (Ruthmann & Dahlberg, 1976) |
| | <i>D. koenigii</i> (Fabricius) | 16 | 14+X ₁ X ₂ 0 | (Ray-Chaudhuri & Banerjee, 1959) |
| | <i>D. peruvianus</i> Guérin-Menéville | 16 | 14+X ₁ X ₂ 0 | (Mendes, 1949; Piza, 1951) |
| | <i>D. ruficollis</i> Linnaeus | 13 | 12+X0 | (Piza, 1947b) |
| | <i>Dysdercus</i> sp. | 16 | 14+X ₁ X ₂ 0 | (Manna, 1951) |
| | <i>D. supersticiosus</i> (Fabricius) | 16 | 14+X ₁ X ₂ 0 | (Banerjee, 1958; Kuznetsova, 1988) |
| | <i>Iphita limbata</i> Stål | 20 | 14+X ₁ X ₂ X ₃ X ₄ X ₅ X ₆ 0 | (Banerjee, 1958) |
| | <i>Odontopus sexpunctatus</i> Laporte | 27 | 26+X0 | (Banerjee, 1958) |
| | <i>Pyrrhocoris apterus</i> (Linnaeus) | 23 | 22+X0 | (Henking, 1891; Wilson, 1909b) |
| | <i>P. tibialis</i> Stål | 23 | 22+X0 | (Takenouchi & Muramoto, 1967; Ueshima, 1979) |
| | <i>Pyrrhopeplus posthumus</i> Horvath | 24 | 22+X ₁ X ₂ 0 | (Parshad, 1957) |
| | <i>Scantius volucris</i> (Gerstäcker) | 19 | 18+X0 | (Parshad, 1957) |

geographic regions, but is most abundant and diverse in the tropics and subtropics. Approximately 15 genera and over 100 species are known. The Pyrrhocoridae are chiefly tropical and subtropical, with only a very few species reaching into temperate Holarctic. However, they are found in all major zoogeographic regions. Approximately 30 genera and 300 species are known (Schuh & Slater, 1995).

From the cytogenetic point of view, 10 species of Largidae and 21 species of Pyrrhocoridae are known (Table 2). Six species of the subfamily Larginae lack

m chromosomes and have an X0/XX sex chromosome mechanism. The number of autosomes varies between 10 and 14. All the studied species that belong to the other subfamily (Physopeltinae) possess 12 autosomes plus two m chromosomes, but different sex chromosome mechanisms (X0 or X_1X_2Y).

Cytologically, Pyrrhocoridae are a heterogeneous family and 21 species belonging to eight genera have been cytogenetically analyzed. Chromosome numbers range from 12 to 33. *Dysdercus* Guérin-Ménéville, the most studied genus within this family, is present both

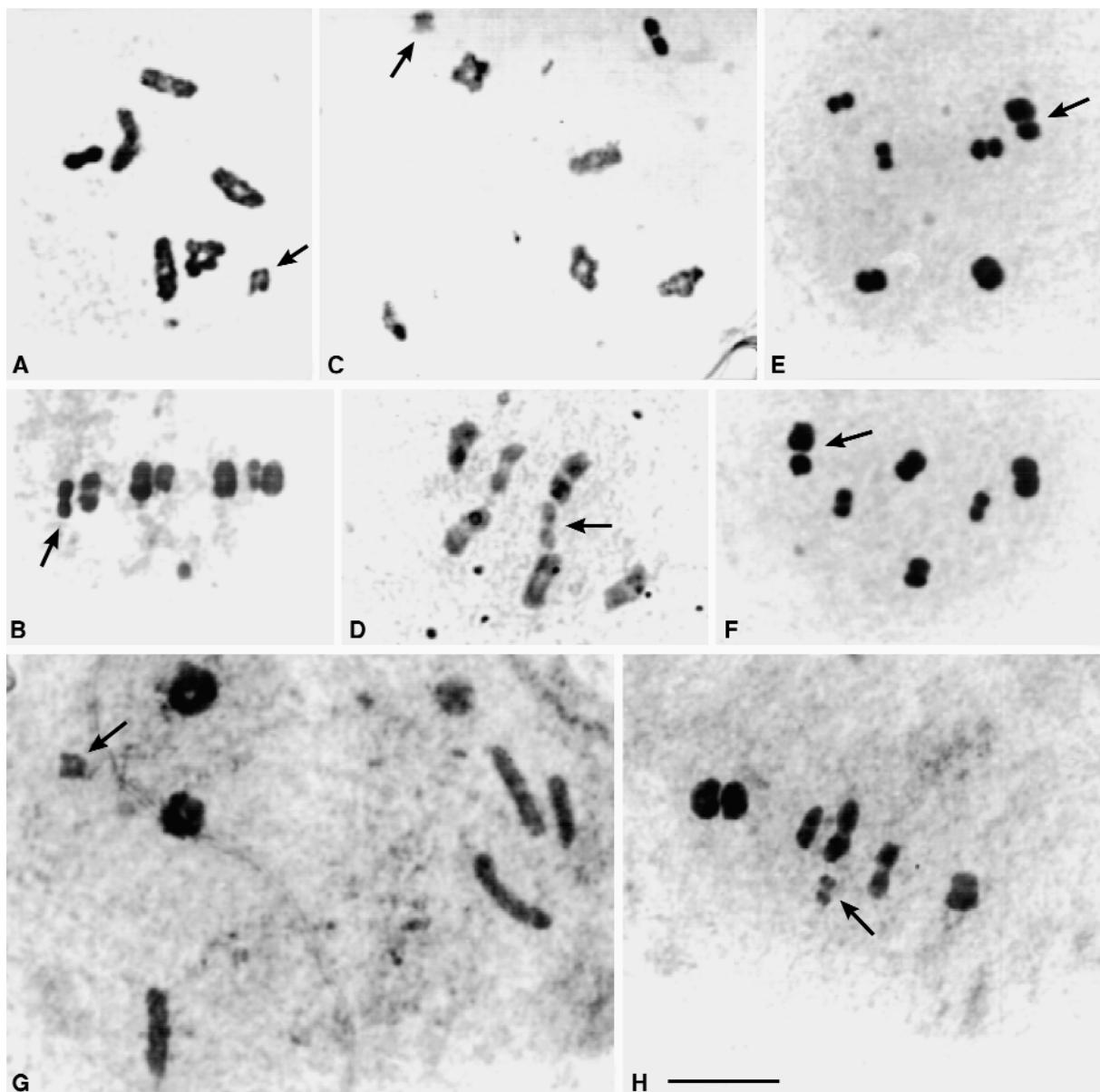


FIG. 2. *Dysdercus chaquensis*: cells at diakinesis (A) and metaphase I (B); *D. ruficollis*: cells at diakinesis (C) and metaphase I (D); *D. albofasciatus*: cells at diakinesis (E) and metaphase I (F); *D. imitator*: cells at diakinesis (G) and metaphase I (H). Arrows point sex chromosome in A-D, G, H and neo-XY bivalent in E, F. Bar = 10 µm. Haematoxylin staining.

in the Old and the New Worlds. So far, from the 13 cytogenetically analyzed species, seven belong to the Old World, while the remaining six are American species (Ueshima, 1979; Manna & Deb-Mallick, 1981; Mola & Papeschi, 1997; Bressa *et al.*, 1999, 2002, 2003). The Old World species [(*Dysdercus cingulatus* (Fabricius), *D. evanescens* Distant, *D. fasciatus* Signoret, *D. intermedius* Distant, *D. koenigii* (Fabricius)], *Dysdercus* sp. and *D. superstitiosus* (Fabricius) share a common male diploid chromosome number of 16 and an $X_1X_20/X_1X_1X_2X_2$ sex chromosome system (Table 2) (Manna, 1951; Banerjee, 1958; Ray-Chaudhuri & Banerjee, 1959; Ruthmann & Dahlberg, 1976; Ueshima, 1979; Manna & Deb-Mallick, 1981; Kuznetsova, 1988). The six neotropical species are much more distinct not only in the male diploid chromosome number, i.e. from 12 to 16, but also in the sex chromosome system ($X0$, X_1X_20 and neo-XY, males) (Table 2) (Ueshima, 1979; Mola & Papeschi, 1997; Bressa *et al.*, 1999, 2003). Considering $2n = 15 = 14 + X0$ (male) as the ancestral chromosome complement from *Dysdercus*, the multiple sex chromosome system should have originated through fragmentation of the original X chromosome giving rise to a diploid chromosome number $2n = 16 = 14 + X_1X_20$. Both situations are found in *Dysdercus honestus* (Mendes, 1947, 1949; Piza, 1947b, 1951) and *D. peruvianus* (Piza, 1947a, 1951; Mendes, 1949), respectively. On the other hand, an autosomal fusion between two non-homologous chromosomes could have led to a reduction in the diploid number ($2n = 13 = 12 + X0$), which has been reported in *D. chaquensis* (Mola & Papeschi, 1997) and *D. ruficollis* (Piza, 1947b), as well as in *D. imitator* (Bressa *et al.*, 2003). Finally, a later fusion between the original X chromosome and an autosome took place during karyotype evolution, resulting in the neo-XY sex chromosome system in *D. albofasciatus*, which possesses the lowest diploid chromosome number of the genus reported so far ($2n = 12 = 10 + \text{neo-XY}$) (Fig. 2) (Bressa *et al.*, 1999).

The Belostomatidae, often referred to as giant water bugs, are distributed worldwide, although their greatest diversity is in the tropics. According to Lauck & Menke (1961), the 146 species of the family can be grouped into three subfamilies: Lethocerinae (including the cosmopolitan genus *Lethocerus* Mayr), Horvathininae (represented only by the genus *Horvathinia* Montandon), and Belostomatinae (with the genera *Belostoma* Latreille, *Diplonychus* Laporte,

Hydrocyrius Spinola, and *Limnogeton* Mayr). Cytogenetic reports on Belostomatidae refer to the male chromosome complement and meiosis of seventeen *Belostoma* species, three *Diplonychus* species and seven *Lethocerus* species (Table 3). The modal diploid chromosome number is $2n = 26 + X_1X_2Y$ (present in 11 species of *Belostoma*), although in both subfamilies Belostomatinae and Lethocerinae, species with a noticeable reduction in diploid number are encountered: $2n = 14 + XY$ (three species of *Belostoma*), $2n = 6 + XY$ [*B. oxyurum* (Dufour) and *L. americanus* Leidy], and $2n = 2 + \text{neo-X}/\text{neo-Y}$ (*Lethocerus* sp.) (Chickering, 1927b; Chickering & Baicorn, 1933; Papeschi, 1992; Papeschi & Bressa, 2002). Our results, together with previous cytogenetic information on the family, led us to propose an ancestral karyotype $2n = 26 + XY$, from which the present karyotypes $2n = 26 + X_1X_2Y$ should have derived through the fragmentation of the ancestral X chromosome. The analysis of a population of *Belostoma orbiculatum*, polymorphic for the sex chromosome system, lend support to this hypothesis (Papeschi, 1996). The DNA content has been determined in nine Argentine species of *Belostoma* and there are significant differences in the DNA content among them (Table 3). Heterochromatic C positive bands are terminally located, and since they are DAPI-bright and CMA₃-dull, they probably represent AT-rich DNA sequences (Figs 3, 4). The comparison of the DNA and heterochromatin content among the species suggests that both the amount of C positive heterochromatin and C negative chromatin changed during evolution. The species with reduced chromosome complements are also characterized by a low DNA content and very scarce C positive heterochromatin. We have suggested that these karyotypes probably originated from the ancestral chromosome complement through chromosome fusions. Besides, the scarce C positive heterochromatin implies either that the ancestral karyotype was devoid of this kind of heterochromatin, or else, that it became lost during the fusion events.

Finally, fluorescence *in situ* hybridization with an rDNA probe (Fig. 5) and DAPI and CMA₃ banding (Fig. 4) in *B. oxyurum* ($2n = 6 + XY$), *B. micantulum* (Stål) ($2n = 14 + XY$), and *B. elegans* (Mayr) ($2n = 26 + X_1X_2Y$) revealed the presence of a NOR at the telomeric region of the X and Y chromosomes in the first two species, but at the telomeric region of an autosomal pair in the latter. In the three species, the

TABLE 3. Diploid chromosome numbers, DNA and heterochromatin content in Belostomatidae

| Taxa | 2n | 2n (male) | DNA (1C) (pg) | % Het. | References |
|---|--------|------------------------------------|------------------|--------|--|
| <i>Belostomatinae</i> | | | | | |
| <i>Belostoma bifoveolatum</i> Spinola | 29 | 26+X ₁ X ₂ Y | 1.21 | 60 | (Papeschi, 1991) |
| <i>B. bergi</i> (Montandon) | 29 | 26+X ₁ X ₂ Y | — | — | (Papeschi & Bressa, 2004) |
| <i>B. cummingsi</i> De Carlo | 29 | 26+X ₁ X ₂ Y | — | — | (Papeschi & Bidau, 1985) |
| <i>B. dentatum</i> (Mayr) | 29 | 26+X ₁ X ₂ Y | 1.93 | 58 | (Papeschi & Bidau, 1985; Papeschi, 1991) |
| <i>B. dilatatum</i> (Dufour) | 29 | 26+X ₁ X ₂ Y | — | — | (Papeschi, 1992) |
| <i>B. discretum</i> Montandon | 29 | 26+X ₁ X ₂ Y | 1.02 | 38 | (Papeschi, 1992) |
| <i>B. elegans</i> (Mayr) | 29 | 26+X ₁ X ₂ Y | 1.55 | 60 | (Papeschi & Bidau, 1985; Papeschi, 1988, 1991) |
| <i>B. elongatum</i> Montandon | 29 | 26+X ₁ X ₂ Y | 1.74 | 59 | (Papeschi, 1992) |
| <i>B. gestroi</i> Montandon | 29 | 26+X ₁ X ₂ Y | 1.13 | 37 | (Papeschi, 1992) |
| <i>B. martini</i> (Montandon) | 29 | 26+X ₁ X ₂ Y | 1.11 | 25 | (Papeschi, 1991) |
| <i>B. micantulum</i> (Stål) | 16 | 14+XY | 0.88 | 15 | (Papeschi, 1988) |
| <i>B. orbiculatum</i> Estévez & Polhemus | 16 | 14+XY | — | — | (Papeschi, 1996) |
| <i>B. plebeium</i> (Stål) | 16 | 14+XY | — | — | (Papeschi, 1994) |
| <i>B. oxyurum</i> (Dufour) | 8 | 6+XY | 0.53 | 30 | (Papeschi & Bidau, 1985; Papeschi, 1988) |
| <i>B. indentatum</i> (Haldeman) | 29 | 26+X ₁ X ₂ Y | — | — | (Ueshima, 1979) |
| <i>B. fluminense</i> (Say) | 24 | 22+XY | — | — | (Chickering, 1916, 1927a) |
| <i>Belostoma</i> sp. | 24 | 22+XY | — | — | (Mongomery, 1901, 1906) |
| <i>Diplonychus annulatus</i> (Fabricius) | 28 | 26+XY | — | — | (Jande, 1959) |
| <i>D. rusticus</i> (Fabricius) | 28 | 26+XY | — | — | (Bawa, 1953; Jande 1959) |
| <i>D. subhombeus</i> (Mayr) | 28 | 26+XY | — | — | (Jande, 1959) |
| <i>Lethocerinae</i> | | | | | |
| <i>Lethocerus annulipes</i> (Herrick-Schaeffer) | 28 | 26+XY | — | — | (Papeschi, 1992) |
| <i>Lethocerus americanus</i> Leidy | 8 | 6+XY | — | — | (Chickering, 1927b) |
| <i>L. griseus</i> (Say) | 28 | 26+XY | — | — | (Chickering, 1927b) |
| <i>L. indicum</i> Lep. et Ser. | 26 | 24+neoX-neoY | — | — | (Banerjee, 1958; Bagga, 1959; Jande, 1959) |
| <i>L. melloitaioi</i> De Carlo | 28 | 26+XY | — | — | (Papeschi & Bressa, 2004) |
| <i>Lethocerus</i> sp. | 4 | 2+neoX-neoY | — | — | (Chickering, 1927a, 1932; Chickering & Bacorn, 1933) |
| <i>L. uhleri</i> (Montandon) | ca. 30 | — | — | — | (Chickering, 1932) |

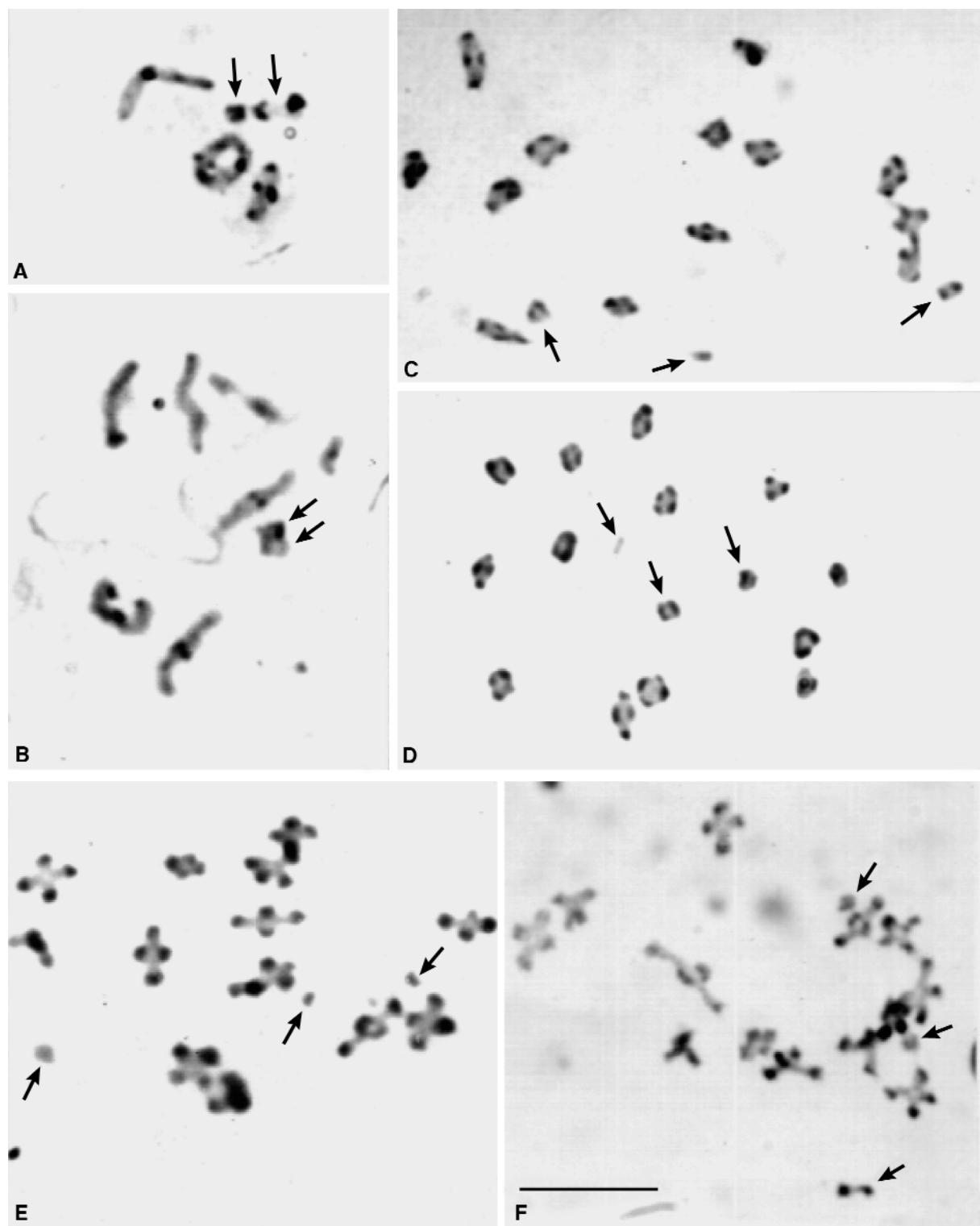


FIG. 3. C-banding of cells at diakinesis of *Belostoma oxyurum* (A), *B. micantulum* (B), *B. elegans* (C), *B. dilatatum* (D), *B. elongatum* (E), and *B. dentatum* (F). Arrows point sex chromosomes. Bar = 10 μ m.

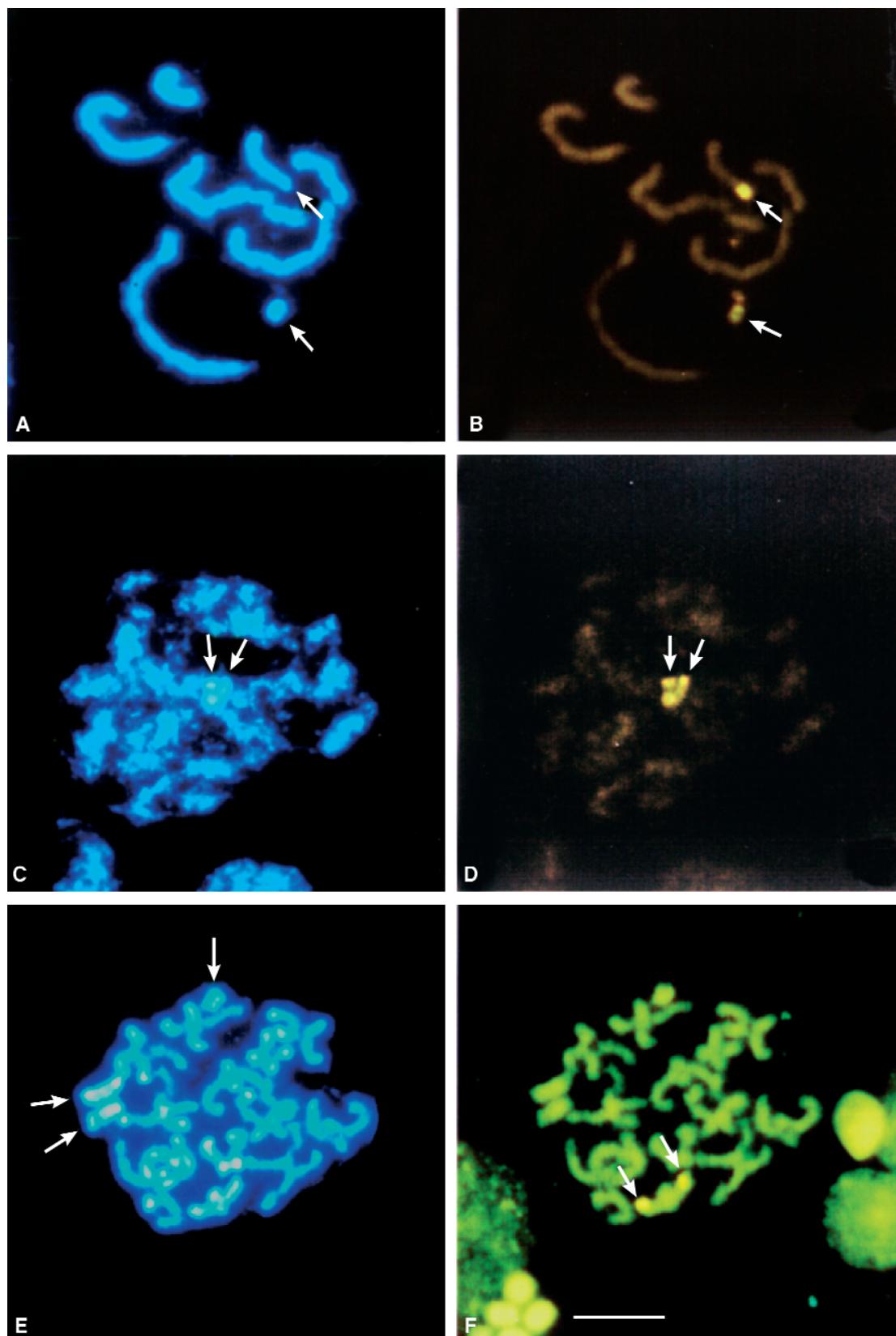


FIG. 4. DAPI (A, C, E) and CMA (B, D, F) banding in: spermatogonial prometaphase (A, B) of *Belostoma oxyurum*; diffuse stage (C, D) of *B. micantulum*; diakinesis (E, F) of *B. elegans*. Arrowheads point CMA₃-bright bands corresponding to NOR regions. Arrows point sex chromosomes. Bar = 10 µm.

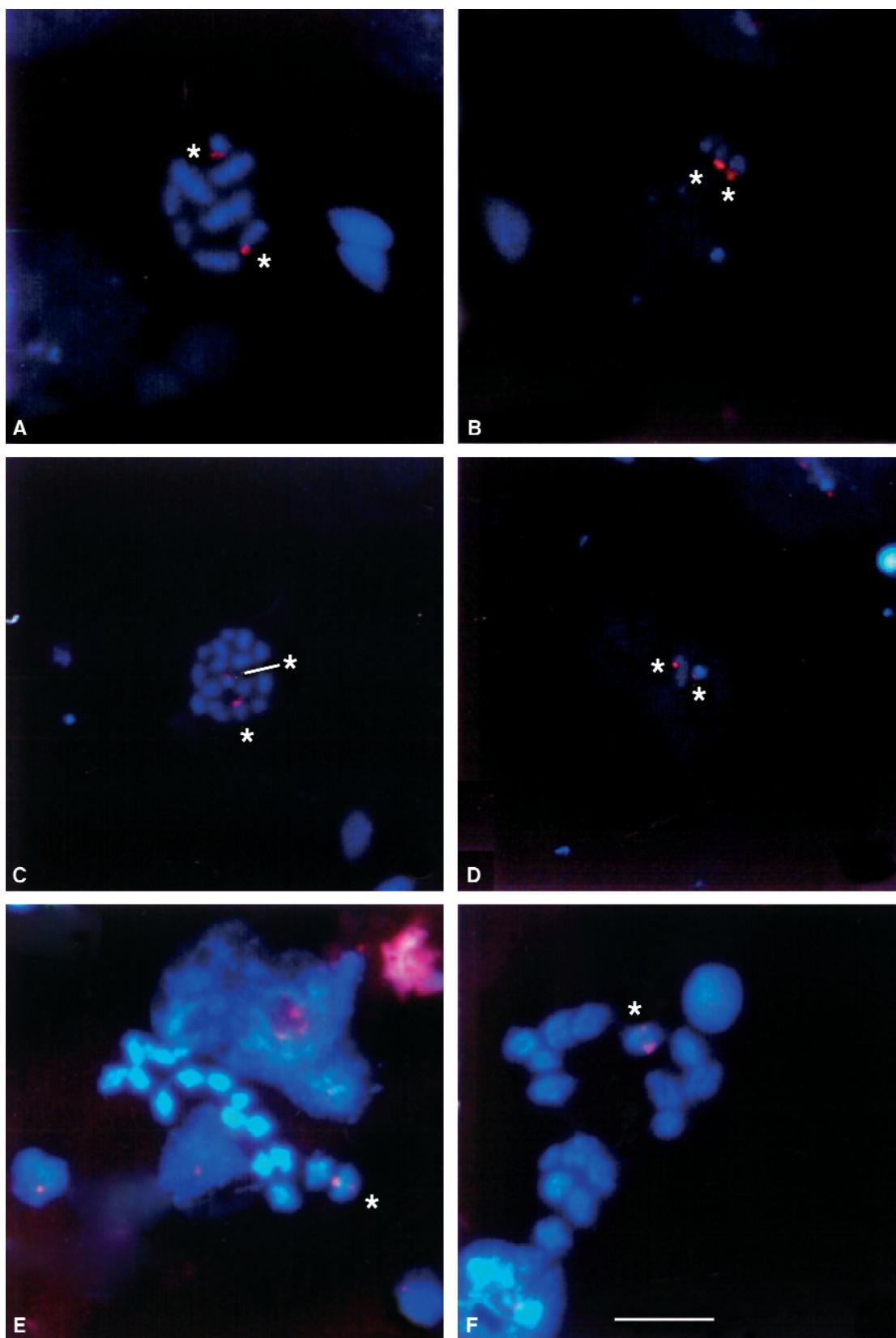


FIG. 5. Fluorescence *in situ* hybridization with an 808 bp 18S rDNA probe in: spermatogonial prometaphase (A) and diffuse stage (B) of *Belostoma oxyurum*; spermatogonial prometaphase (C) and diffuse stage (D) of *B. micantulum*; diakinesis (E, F) of *B. elegans*. Asterisks point rDNA regions. Bar = 10 μ m.

NOR region is also detected as a CMA₃-bright/DAPI-dull band. These observations suggest that the reduction in the diploid number probably involved the fusion of the ancestral sex chromosome pair with the autosomes carrying the NOR. Alternatively, the rDNA gene cluster could have been translocated from an autosomal location (as in *B. elegans*) to the X and Y chromosomes (as detected in *B. micantulum* and *B. oxyurum*). Further studies in other species of *Belostoma* will shed light on the karyotype evolution within the genus.

CONCLUDING REMARKS

More than a hundred years have gone since Henking's first report on *Pyrrhocoris apterus*, but chromosome organization, function and evolution in Heteroptera is far from being fully understood. Molecular cytogenetic techniques are promising tools that will help uncover the mechanisms governing chromatin organization of holokinetic chromosomes, their behaviour during mitosis and meiosis, and the importance of chromosome change during the speciation of heteropterans.

Fusions and fragmentations, along with variations in the amount of heterochromatin, location and constitution are the principal mechanisms of karyotype evolution so far reported in Heteroptera. However, different genera and even families are karyotypically more variable than others, a fact that probably reflects differences in the biology of the species, and their environmental relationships. The coming years will probably outline some answers, but also bring about more new questions.

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