KARYOTYPES OF SOME TROPICAL REDUVIIDS AND CYTOTAXONOMY OF REDUVIIDAE (HEMIPTERA : HETEROPTERA)

BY

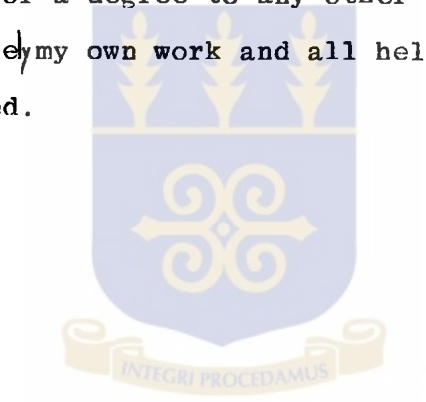
PETER G.O. KPORDUGBE, B.Sc. (HONOURS)

A thesis submitted for the degree of Master of Science at the University of Ghana, Legon.

September 1979.

ZOOLOGY DEPARTMENT
UNIVERSITY OF GHANA
LEGON, GHANA

This is to certify that this thesis has not been submitted for a degree to any other University. It is entirely my own work and all help has been acknowledged.



(P.G.O. IPORD[illegible])

This work is dedicated to my parents John, Mary, and my sisters Anthonia and Olivia for their ever present love and support.

A B S T R A C T

Data is presented on 2n-numbers of some forty-six (46) species of Tropical Reduviidae collected in Southern Ghana, West Africa. This information is combined with existing data and together analyzed and discussed. It was found that the recognised morphological plasticity of Reduviidae extends to the diploid numbers as well. However a level of cytological organization was found to exist within the family. Three autosomal-Chromosome groups: 20A, 24A and 28A are proposed. It has emerged that within the confines of these groups 2n-numbers are sufficiently restricted and consistent to be of definitive and therefore systematic value. These autosomal groups which bring together various related subfamilies have been found to have a close parallelism to earlier morphological groups suggested by Davis (1961, 1969), Kumar (1962) and Louis and Kumar (1972). With this strong support the dissolution of the present family Reduviidae is suggested; 3 new families based on the above groupings to replace it. These measures are all in aid of homogeneity of families within Heteroptera creation of tribal classification and reduction of unbalanced classification.

On the basis of biology, karyotype and genitalia morphology, the colour forms of Rhinocoris bicolor (Fab) have been re-identified recognizing R. bicolor, R. ghaurii, and R. louisii. Also (a) Karyotype evolution (direction and mechanisms)

(b) Origin of the multiple sex-chromosome mechanisms and

(c) Holokinetic theory, are discussed within the context of Reduviidae and Heteroptera in general.

ACKNOWLEDGEMENTS

I wish to express sincere gratitude to Professor R. Kumar my supervisor and current head of the department of Zoology, University of Ghana for suggesting this study, for his valuable suggestions and criticism and also for reading the manuscript.

The other members of the supervisory committee, Dr. S.E.A. Ntifo and Mr. B. Hughes also deserve special mention for their interest in my work.

I am indebted to Mr. K.I.N. Gavor, Mr. Chris Gordon, Ms A. Sutherland, Mr. N. Norman, Mr. A. Sebu, Mr. F. Agyei and Mr. J. Asare, for technical assistance.

My sincere thanks go to Dr. J.W. Knight and Mr. W.R. Dolling both of the British Museum of National History for giving me access to important museum material and to Professor J.K.M Bodasi, the former head of the department of Zoology, University of Ghana, for providing facilities during his tenure of office.

The numerous field trips which made this study possible were made on the Zoology department's Peugeot 504 car which is a gift from the Ghana Cocoa Growers Association, Birmingham. I am greatly indebted to the association.

TABLE OF CONTENTS

I GENERAL INTRODUCTION

1.1 Reduviidae; Importance

The Reduviidae is an important family of predatory bugs. The subfamily Triatominae is medically important since its members are vertebrate blood suckers. There is much focus on Triatoma and Rhodnius species. In Brazil and Argentina (South America), Triatoma spp. are being actively studied because they are vectors of the notorious Chagas disease. Most other reduviids belonging to over twenty-eight (28) subfamilies are agriculturally valuable predators.

The importance of Reduviidae in Ghana has been mentioned by many. Currently when chemical control of capsids on cocoa is receiving many setbacks (resistance of pests to chemicals, mammalian toxicity etc), possible alternative control measures are being seriously considered. Biological and integrated control, which come immediately into focus, both place emphasis on natural enemies including predators. William (1954) recognised that predators are a significant factor in the natural control of capsids. He indicated that reduviids and mantids together account for more than one and a half (1½) the capsid mortality attributed to ant predation. Although Leston (1970) considers this a misleading representation, it is however

clear that each predator - ants, mantids, reduviids - causes an appreciable amount of capsid mortality (Louis 1973). This constitutes a potent factor that can be manipulated for capsid control.

1.2 Systematics

More than 3,000 species of Reduviidae are known. These were grouped by Usinger (1943) into twenty (20) subfamilies. Miller (1956) regrouped Reduviidae into twenty nine (29) subfamilies. Since then, additional subfamilies have been proposed and added; the situation threatens to worsen. Already it seems abnormal and unbalanced enough with 29 families being recognized in the Reduviidae as compared to other large and diversified families such as Pentatomidae (11 subfamilies), Miridae (6 subfamilies), and Lygaeidae (14 subfamilies) - (Carayon et al. 1958).

Originally placed as a distinct Reduvoid family Phymatidae - Usinger (1943), Villiers (1948); the Phymatids were later brought down to subfamily status under Reduviidae (Carayon et al. 1958). Recently the group has been re-established as a family by China and Miller (1959). Davis (1959,1961,1969) however in trying to regroup Reduviids suggested (3) three major groups of reduviid subfamilies whose characteristics based on hind wing venation and certain other features re-introduce the

phymatids into the Reduviidae.

Emesinae (Amyot and Serville, 1843) and Triatominae (Jeannel, 1919) have on one occasion or the other been elevated to family ranks. Villiers (1948) etc insist that their features both internal and external do not justify these elevations. These therefore have been re-established as sub-families of Reduviidae - Carayon et al (1958), China and Miller (1959) Davis (1961).

There has been a stir over the creation of a new subfamily Eupheninae (Miller 1955) from Cetherinae (Jeannel, 1919) and the splitting of Harpactorinae (Amyot and Serville, 1843) recognizing Rhaphidosominae and Tegeinae (Villiers 1948).

Carayon et al. (1958) disagreed with these saying that the characters used are extremely derived - APOMORPHIC[1]. They felt that these authors allowed generic diversity to interfere with the naming of higher groups, thus ignoring basic Bauplane[2] characters.

---

1. After Hennig (1966); specialized or derived characters and barring convergence, indicate common descent.

2. Plesiomorphic characters relatively primitive or generalized characters indicative of common origin and of little value in showing a common descent.

China and Miller (1959) recognized Rhaphidosominae and Tegeinae and still maintained twenty-nine (29) subfamilies as Miller (1956). Davis (1961, 1969) suggests a complete reorganization of Harpactorinae Rhaphidosominae etc under a HARPACTOROID COMPLEX. Using evidence from wing-venation, genitalia etc Davis brought down Harpactorinae Villiers 1948) to tribal status together with Rhaphidosomini and Tegeini as one block, and Apiomerini, Diaspidini and Ectinoderini as another block of tribes all under a new broadbased subfamily Harpactorinae.

Louis and Kumar (1972) found evidence from the morphology of salivary glands and internal reproductive organs in favour of the reduction of Rhaphidosominae to tribal status.

These certainly are in line with the apparent want of tribal classification and balanced classification in the Reduviidae. Notwithstanding all this awareness to the tendency of an unbalanced classification, Davis (1969) recognized thirty-one (31) subfamilies in the Reduviidae.

The contradictions, disagreements, etc., even though they may not be conclusive, certainly show a conflict and therefore a need for further work to elaborate on the situation. Davis (1957, 1961, 1966, 1969);

Carayon et al. (1958); Kumar (1962) have tried to clarify the grouping of Reduviidae into subfamilies, but Louis and Kumar (1972) still think (together with others) that "the systematics of the family Reduviidae is in a confused state."

The situation in the Reduviidae is obviously a result of the recognized high plasticity in external characters. Recently there has been the increasing awareness that internal organs are less variable than external characters and may thus in some groups serve as valuable phylogenetic indicators.

Louis and Kumar (1972) tried to assess the utility of alimentary and reproductive organs along with available information on other characters in discussing the higher categories of the Reduviidae. They indicated that a systematic karyotypic study should be undertaken in judging the relationships of these categories.

1.3 Chromosome Cytology

Genetic forms and mechanisms are obviously of great significance in studies on population genetics and evolution. They are not merely morphological features commonly used in defining systematic categories, since they concern the whole of the genetic apparatus on which speciation, evolution and adaptive radiation depend (White 1956). This suggests that if we could decipher how

the major differences in genetic mechanisms had arisen in the course of evolution we might use this knowledge in establishing the relationships between 'higher' categories of insect orders on a firmer foundation.

Chromosome cytology is becoming of more and more importance in the clarification of evolutionary relationships among different taxa of organisms (Ueshima, 1963). Even though it has not proved to be the "final court of appeal" as its potentials earlier suggested, cytology as an additional tool in taxonomy has an undeniable value.

The Heteroptera have been undergoing extensive cytological investigation since Montgomery (1901, 1902) and Wilson (1911). The main investigations have been the use of cytological data along with morphological data to : (a) evaluate the broad mechanical principle underlying changes in karyotypes; (b) evaluate supergeneric, generic and specific classification and to construct phylogenetic trees based on such information.

From the contributions to the cytology of Reduviidae to date: Manna (1951, 1956), Ueshima (1966) etc. It is apparent that when karyotypes of large numbers of related species are examined, certain definite patterns usually emerge. The importance of studying closely related species before suggesting any meaningful compari-

sons among distantly related forms is more than obvious, and the need for the use of adequate data obtained in carefully planned studies in cytotaxonomic analysis cannot be over-emphasized.

Davis (1966) observed that the validity of generalizations regarding the morphology of the genitalia of a group so large and diverse as the Reduviidae depends largely on the breadth of the material studied. The principal weakness of earlier works has been their narrow representation, he pointed out. Davis' remarks apply very well to cytotaxonomy as well. Some authors have tried to propose type 2n numbers and phylogenetic relationship for families as well as subfamilies based on work on low numbers of unevenly distributed species within groups; obviously conclusions drawn this way are hasty unrepresentative and confusing. Also the works have been largely descriptive and without thoughtful appraisal of evolutionary implications, probably due to what Jackson (1971) calls 'lack of sophisticated understanding of basic cytogenetics'.

So far, apart from the comprehensive work on the Reduviidae subfamily Triatominae (Payne, 1909, 1912; Wigglesworth, 1936; Usinger, 1944; Manna, 1950; Schreider and Peliegrino 1950, 1951; Wygodzinsky, 1951; Barth, 1956, 1957; Ryckman, 1962; and Ueshima, 1966), efforts

to study Reduviidae cytologically have been spread too thin at the subfamily level. To be able to contribute to the total reassessment of the subfamily classification of the Reduviidae cytologically, each subfamily must be extensively studied.

The present study on the chromosomes of mainly tropical Reduviidae is intended to employ karyotypes in the clarification of the systematics of Reduviidae. Davis (1969) noted that a part of the difficulty with the higher systematics of Reduviidae stemmed from the fact that many species of Reduviids especially the rare forms occur in the tropics where practically no research on the subject was being carried out. It is hoped that the present study would be the beginning of work that would help in rectifying this deficiency.

2. MATERIALS AND METHODS

Adult male insects were collected from December 1976 to October 1978 in the South-eastern cocoa growing areas of Ghana, West Africa (Fig. 2.1). They were dissected for testes in tap water and the material was preserved in tubes of Carnoy's fixative Ueshima (1963).[1] The tubes were kept in an air conditioned room (Average Room Temp: 22°C) until squashing.

Lacto-aceto-orcein squashes (Warren et al. 1960) were made and the slides ringed with nail varnish.

Chromosome counts and other observations were made using a Reichert binocular optical compound microscope with X10 ocular, 40X and 100X (oil) objectives against a green filter.

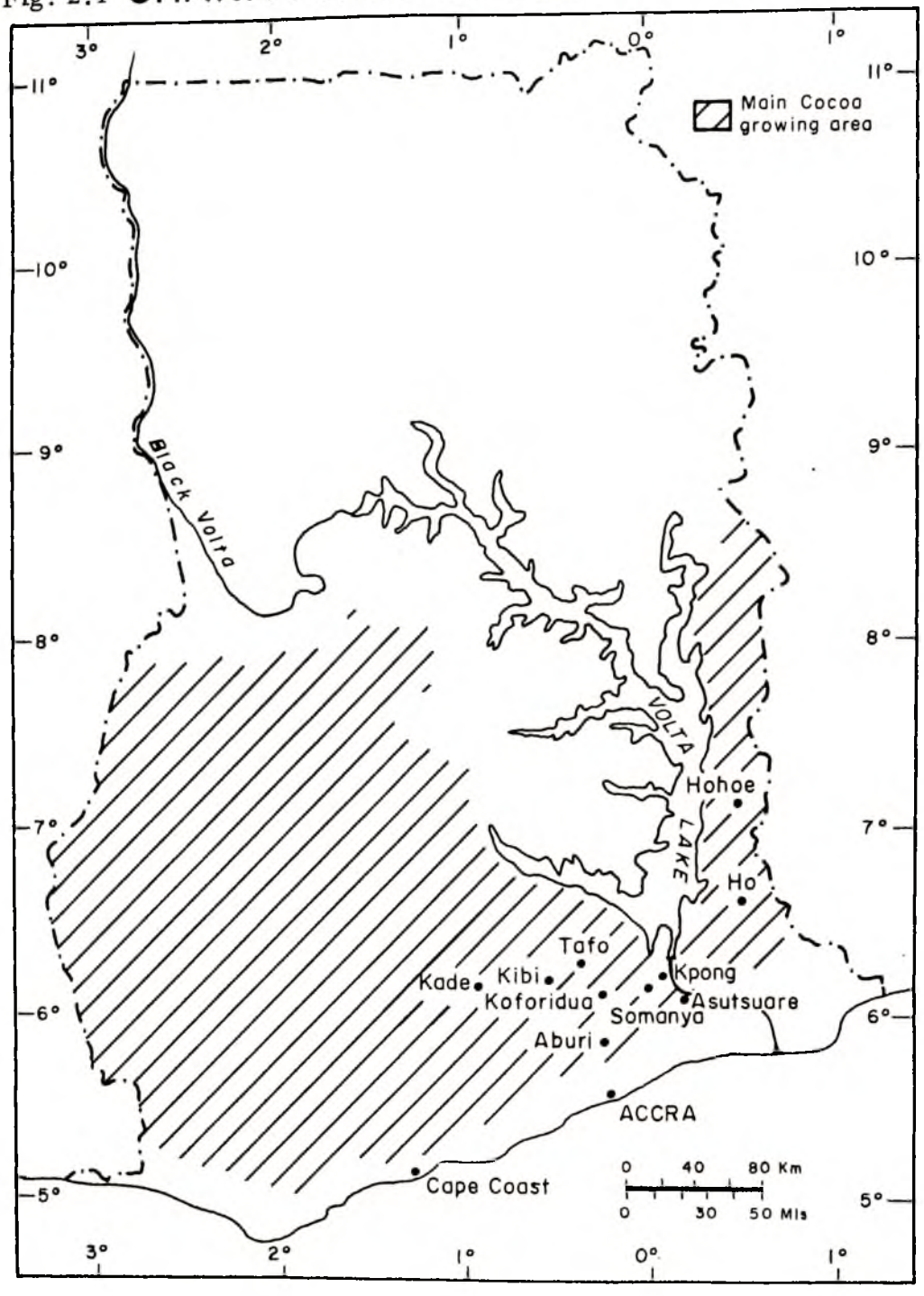
Unless stated otherwise, it should be taken that at least ten (10) male specimens of each species were dissected for testes material which was squashed and not less than one hundred (100) individual cells scanned. Photographs of meiotic stages were taken with a Kam VBX 35mm camera on a Reichert photomicroscope.

Drawings - which are tracings from photographs - were made where the original pictures are slightly obscured by extraneous material/artifacts on the lenses

---

1. 3 parts of pure Iso-propanol and 1 part of glacial acetic acid.

Fig. 2.1 GHANA : MAIN COLLECTION POINTS



(Refer Plate XXIV etc.). Magnifications are indicated by 10µ lines. N.T.S. on a picture/tracing scale indicates that the scale is an approximation.

The sources of material are indicated along with the description of meiosis for each species (3.3.1...etc).

2n numbers were determined for 46 species of male Reduviidae belonging to six (6) subfamilies. This brings to one hundred and twelve (112) species of reduviid bugs positively known cytologically.

Out of the forty-six (46) species of reduviids studied and for which 2n-numbers are recorded, pictures and tracings are presented for only forty-one (41) because of technical difficulties.

Attempts were made at studying chromosome behaviour during meiosis and at comparing karyo-types observed. No mention is made of female karyotypes.

On the basis of biology, genitalia morphology and karyotype, the colour forms of Rhinocoris bicolor (Fabr.) are distinguished into three (3) different species: R. bicolor (type designated) R. ghaurii sp. n and R. louisii sp. n.

2n numbers obtained in this study were pooled and analysed with those published to date. Possible complications due to the different localities from which results

in literature were collected - geographical variation - were ignored.

The student's t testwas used to compare the means of the distribution of diploid numbers in those subfamilies with more than ten recorded 2n-numbers (Appendix Tables III to IX; Appendix Tests I-VII). Where the t test gives no significant difference at the 5% significance level it is suggested that there is a close relationship between the two subfamilies concerned.

In applying the t test, two prerequisites for the test were however ignored: (a) That the variances of the two (2) samples being compared is equal or near so i.e. the samples are drawn from the same population; if we considered the family Reduviidae as the population from which the samples (subfamilies) were drawn, it could be assumed that since the samples were from the same population, the variances of these samples approach each other or are similar. This however is not the case (Appendix Tables VI to IX), due to the heterogeneity of the family Reduviidae as far as diploid numbers are concerned; (b) That the sizes of the samples (n_1 & n_2) being compared are equal ($n_1 = n_2$). This could not be satisfied because diploid numbers available for the various subfamilies differ in number.

Specimens used in my study were identified at both the British Museum of Natural History, London and Entomology Museum (Zoology Department), University of Ghana, Legon.

3. RESULTS AND OBSERVATIONS

3.1 Introduction

Heteroptera are a generally easy cytological material: deep staining chromosomes, heteropycnotic sex chromosomes; they have diffuse kinetic activity (that is, they are holokinetic[1]). Because of this property, chromosome number, relative size and chromosome behaviour, rather than arm length etc., indicate affinity and are therefore used to evaluate phylogenetic relationships (Manna 1951; White 1954; Ueshima 1963, 1965).

The morphology and behaviour of the chromosomes of the Reduviidae is typically Heteropteran. Karyotypically the Reduviidae seems to comprise a rather heterogenerous assemblage of insects. Sex-chromosomes, usually multiple, are the most variable among the Heteropterans (Manna 1958). The diploid number of chromosomes is revealed at the Spermatogonial metaphase, and the haploid numbers at the Spermatocytic metaphases. The usual

---

1. Holokinetic: discribes the activities of holocentric chromosomes, that is, those without single localized centromeres. The idea of this type of chromosome in Heteroptera is not clearly established.

course of meiosis is as follows: sex-chromosomes are positively heteropycnotic in the early prophase. In the confused stage the tendency is for the sex-elements to come together and have diverse interactions, forming different multi-valent units which persist in some cases into diakinesis. In the early diplotene stage the tetrad nature of each bivalent becomes evident. Much condensation of euchromatic portions take place through diplotene. Each pair of autosomes is usually associated with one terminal chiasma. Since the autosomal tetrads come to stain more intensely with continued condensation, the heteropycnotic knots of each tetrad become indisinguishable from the euchromatic portions at diakinesis. In prometaphase sex-chromosomes once more separate from each other and lose some of their heteropycnotic character. At this point sex-chromosomes can only be distinguished from the autosomes because they are composed of only two (2) instead of four (4) chromatids as in autosomal bivalents.

At the first spermatocyte metaphase (METAPHASE I), autosomal tetrads and sex dyads arrange themselves at the equator of the spindle. The inverted sequence of meiosis (Ris, 1942; Hughes-Schrader, 1944, 1948, 1955; La Cour, 1955; Nordenskjold 1961; Chandra 1962; Ueshima 1963 etc) found in holokinetic chromosomes operates here.

Autosomes co-orient and are reductional at the first meiosis and auto-orient and are equational during the second mieosis. The sex-chromosomes in contrast are equational at the first division and reductional at the second. This was confirmed by my own observations.

In the second spermatocyte metaphase (METAPHASE II) the sex-chromosomes lie in the centre of a ring formed by the autosomal dyads and undergo a characteristic "touch and go" pairing. The X-chromosomes segregate to one pole and the Y-chromosomes go to the other pole in Anaphase II, resulting in two kinds of spermatids.

In this study since chromosome complements were not determined for the females, (i), (ii), or all of the following proceedures rather than the comparison of male and female karyotypes were followed to distinguish the sex-chromosomes from the autosomes and to establish the sex mechanism.

(i) Diffuse stage of prophase I was studied and the sex-chromosomes which are positively heteropycnotic at this stage were noted (Plate I.2 etc).

(ii) Metaphase II feature of autosomes forming a ring around sex-chromosomes gives an easy way of separating these two components of the karyotype (Plates I,II,V, IX, XVIII etc).

(iii) Segregation patterns at Anaphase II normally result in two types of spermatids. The distribution of the chromosome elements in these two spermatids gives an indication of the mechanism of sex-determination (Plate XVIII 4,5 etc).

3.2 Summary of results

	Male 2n Number	Chromosome Formula
SUBFAMILY: HARPACTORINAE		
Rhinocoris loratus (Stål)	28	24A+XXXY
Rhinocoris carmelita (Stål)	28	24A+XXXY
Rhinocoris rapax (Stål)	28	24A+XXXY
Rhinocoris albopilosus (Signoret)	28	24A+XXXY
Rhinocoris nitidulus (Fab)	28	24A+XXXY
Rhinocoris bicolor (Fab)	28	24A+XXXY
Rhinocoris qhaurii sp.n	28	24A+XXXY
Rhinocoris louisii sp.n	28	24A+XXXY
Rhinocoris hutsebauti Schouteden	26	24A+XY
Sphedanolestes (Aula) leucocephalus (Fab)	28	24A+XXXY
Vestula lineaticeps (Signoret)	27	24A+XXY
Margasus impiger (Bergroth)	26	24A+XY
Pisilus tipuliformis (Fab)	28	26A+XY
Aprepolestes acutum (Stål)	28	24A+XXXY
Cosmolestes pictus Klug	28	24A+XXXY
Phonoctonus fasciatus Beauvois	28	24A+XXXY

Phonoctonus subimpictus Stål	28	24A+XXXY
Phonoctonus lutescens (Guerin & Percheron)	28	24A+XXXY
Harpagocoris nigroflavus Villiers	29	24A+XXXXY
Coranus pallidus (Reuter)	28	24A+XXXY
Dinocleptes torpidus (Miller)	26	24A+XY
Nagusta punctaticollis (Stål)	27	24A+XXY
Sphedanolestes keranderi Villiers	28	24A+XXXY
SUBFAMILY: RHAPHIDOSOMINAE		
Rhaphidosoma truncatum Jeannel	26	24A+XY
SUBFAMILY: TRIBELOCEPHALINAE		
Tribelocephala curticornis Villiers	30	28A+XY
SUBFAMILY: SALYAVATINAE		
Lisarda vandenplasi Schouteden	23	20A+XXY
Petalocheirus rubiginosus (Palisot de Beauvois)	22	20A+XY
SUBFAMILY: STENOPODINAE		
Oncocephalus subspinosus (Amyot & Serville)	24	20A+XXXY
Oncocephalus astridae Schouteden	23	20A+XXY
Oncocephalus posthi Villiers	23	20A+XXY
Ghesquierea dimorpha Schouteden	23	20A+XXY
Argolis calabarensis Stål	25	22A+XXY
Thodelmus addahensis Reuter	27	24A+XXY
Cachanocoris ivorensis	23	20A+XXY

SUBFAMILY: REDUVIINAE		
TRIBE: CETHERINI		
Cethera musiva (Germar)	23	20A+XXY
Cethera maculipennis (Breddin)	23	20A+XXY
TRIBE: REDUVIINI		
Leptacanthaspis decorsei Jeannel	29	26A+XXY
Acanthaspis petax (Stål)	24	22A+XY
Acanthaspis sulcipes Signoret	26	24A+XY
Acanthaspis bilineolata (Palisot de Beauvois)	26	24A+XY
Plynoides benoiti	23	20A+XXY
Plynoides pallidus	23	20A+XXY
Eriopreda feai Jeannel	24	22A+XY
Cerilocus inermipes (Stål)	18	16A+XY
Tetroxia nigrispinosa Villiers	22	20A+XY
Platymeris biguttata (Linne)	30	------

3.3 Description of karyotype and meiosis.

3.3.1 Rhinocoris loratus (Stål)

Locality: The species was collected from Kade, Tafo, Aburi and Hohoe; available all year round. They occur on the undergrowth of neglected cocoa-farms especially where coco-yam plants flourish. At least fifty (50) males were dissected for squashes and more than one hundred (100) individual cells were scanned.

Meiosis: Spermatogonial metaphase plates show 2n number as 28: twelve (12) pairs of autosomes and four (4) sex-chromosomes X_1 X_2 X_3 Y. At prophase, diffuse stage sex-chromosomes appear as heteropycnotic elements lying close together. Plates showing the sex-chromosomes in various associations were seen. The 3X's are of the same size and about half the size of the Y element.

First spermatocyte metaphase (Metaphase I) shows 16 elements: twelve (12) autosomal tetrads and 4 sex-chromosome dyads. The autosomes can be divided into three size categories. The smallest autosome is approximately twice the size of the Y sex-chromosome. No definite arrangement of elements is seen at this stage.

Second spermatocyte metaphase (Metaphase II) shows an autosomal ring of 12 elements (dyads) around the sex-chromosomes which lie close together.

Anaphase II the 3X's move to one pole and the Y and other resulting

in 2 kinds of spermatids:

(I) 12A + $X_1 X_2 X_3$.

(II) 12A + Y

No lagging chromosomes were observed during separation, there is therefore no indication of non-disjunction. The chromosome entities were indistinguishable in the telophase plates because they are closely packed.

Explanation of figures:

PLATE I

(1) Spermatogonial metaphase plate showing twenty-eight (28) chromosomes the diploid-number.

(2) Diffuse stage showing heteropycnotic sex chromosomes lying close together, the three small elements being X-chromosomes and the single largest element the Y-chromosome.

(3) Early metaphase I, shows highly condensed autosomes (12) and sex-chromosomes (4), Sixteen (16) elements can be seen in polar view, 3X-chromosomes are easily distinguishable due to their small size lie on the periphery of the chromosome congregation, Y-chromosome difficult to distinguish at this stage.

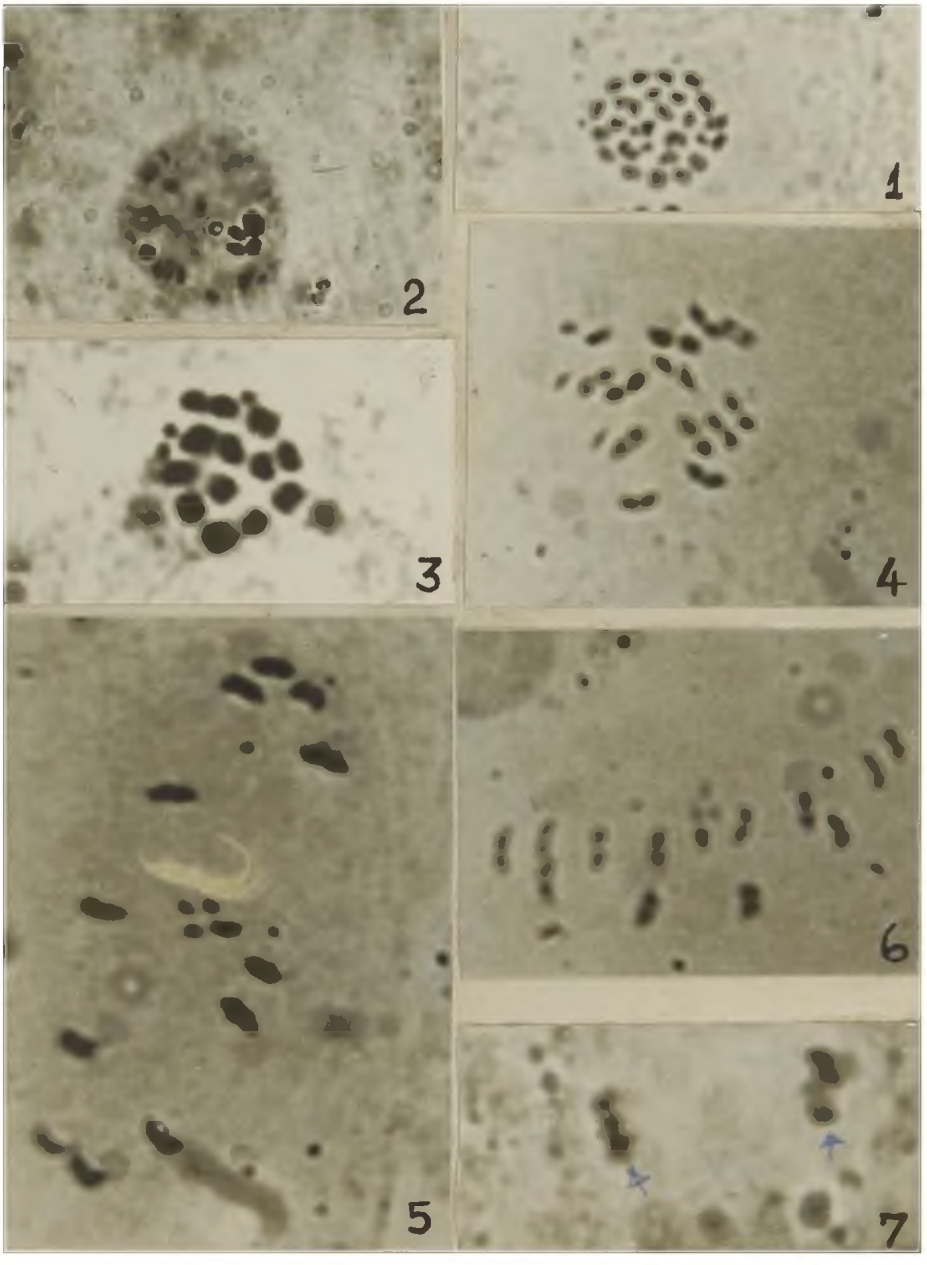
(4) Late metaphase I, arrangement of chromosomes as in (3), tetrad nature, dyad nature of autosomes and sex elements respectively more obvious at this stage, (16) elements clearly seen.

(5-6) Metaphase II plates, 12 autosomes present in a right arrangement around sex elements which lie close together as in (2). Notice that elements in (5) appear larger than their counterparts in (6) even though protographs were taken at similar magnifications, elements in (5) appear more condensed and larger because the slide from which the protograph was taken was slightly over heated

during preparation for squashing resulting in more uptake of the aceto-orcein dye.

(7) Telophase II

PLATE I



10 μ

RHINOCORIS LORATUS (STÅL)

3.3.2 Rhinocoris carmelita (Stål)

Locality: Insects were collected from Mampong, Aburi, Kade and Tafo.

Karyotype: Identical to that known in R. loratus. The course of meiosis is also identical with that of R. loratus.

Spermatogonial metaphase plates show 2n-number as 25, 26, 27 and 28, 25, 26 and 27 are most probably incomplete plates, probably the result of either overlapping of some elements by others or loss of element/s by bad squashing. The expected 2n-number (deducted from Metaphase I and II) is 28 elements: 12 pairs autosomes and four (4) sex-chromosomes, most likely $X_1 X_2 X_3 Y$. One point not clear is the persistence of a rather odd large chromosome in the spermatogonial metaphase complements showing 25 elements.

First spermatocyte metaphase shows 16 elements in several arrangements. Three elements are definitely smaller in both polar and side views and are the 3X's. The Y is less distinguishable from the 12 autosomes.

Second spermatocyte metaphase: An autosomal ring of 12 elements is predominant. Even though most plates showed the sex-chromosomes as pseudotetravalents, a few appeared with separated sex-entities: 3 small elements and a large one (approx. 2X the smaller entities) in the centre of the ring formed by the 12

autosomal dyads. Telophase elements are indistinguishable.

Explanation of figures:

PLATE II

(1) Spermatogonial metaphase, 28 elements but not clearly shown in picture; 25 elements easily distinguishable; other 3 probably overlapped, covered or fused together. Note largest chromosome/chromosome aggregate in complement.

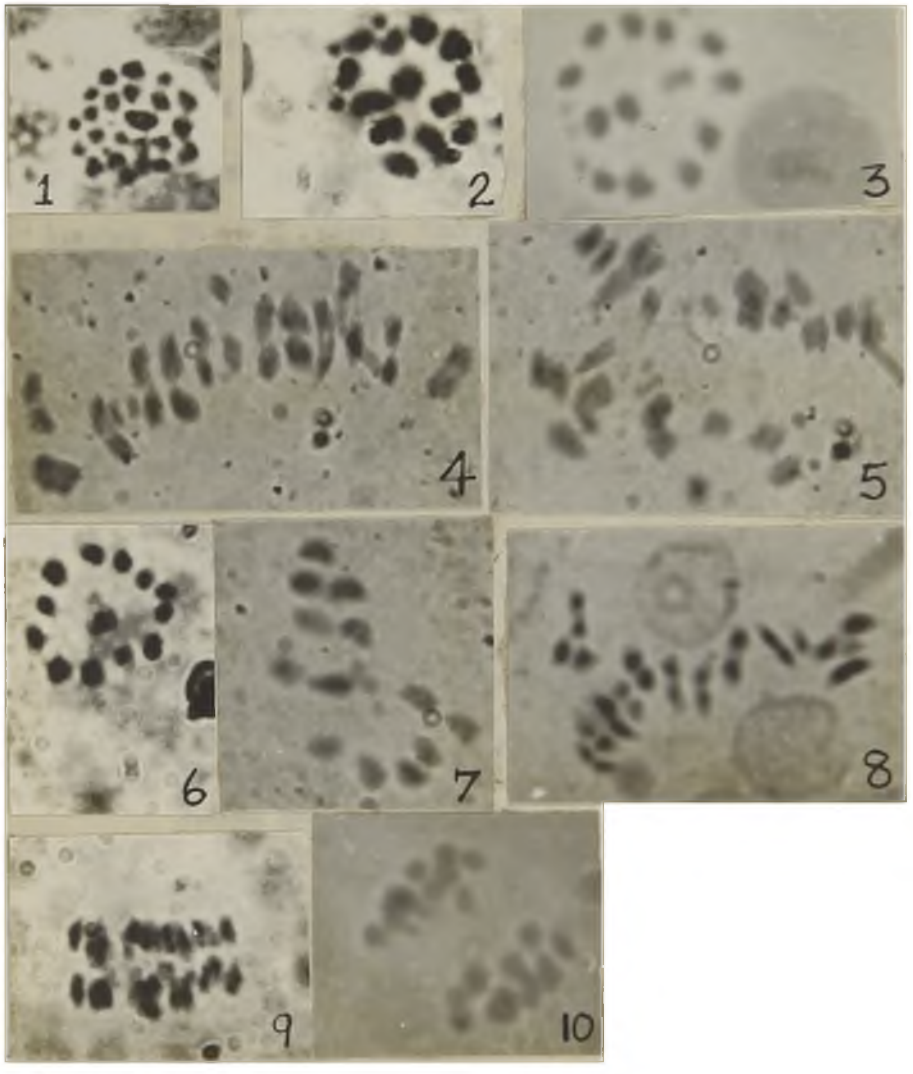
(2-4) Metaphase I; (2) and (3) show elements in polar view; note peripherial position of sex-elements in all these cases. (4) shows late Metaphase I in sideview.

(5) Anaphase I; first division complete, elements move towards different poles.

(6-7) Metaphase II; (6) and (7) in polar view show autosonal ring of 12 elements very clearly; in (7) sex-elements; 3 small X's and a slightly bigger Y, in centre of ring. (8) in side view shows cluster of sex-element towards right side end.

(9-10) Anaphase II; (9) early anaphase (10) later anaphase.

PLATE II



10μ

RHINOCORIS CARMELINA (STÅL)

3.3.3 Rhinocoris rapax (Stål) ♀

Locality: Insects were collected from Kade and Tafo.

Karyotype of Rhinocoris rapax (Stål) ♀ is identical to that of R. loratus and the course of meiosis being the same. 2n-number, 29 for R. rapax had been reported by Kumar and Louis (1972), with the chromosome compliment of 26 autosomes + X_1 X_2 Y. This study reviews this: 2n-number is 28 with a distribution of 24A + X_1 X_2 X_3 Y.

Explanation of figures:

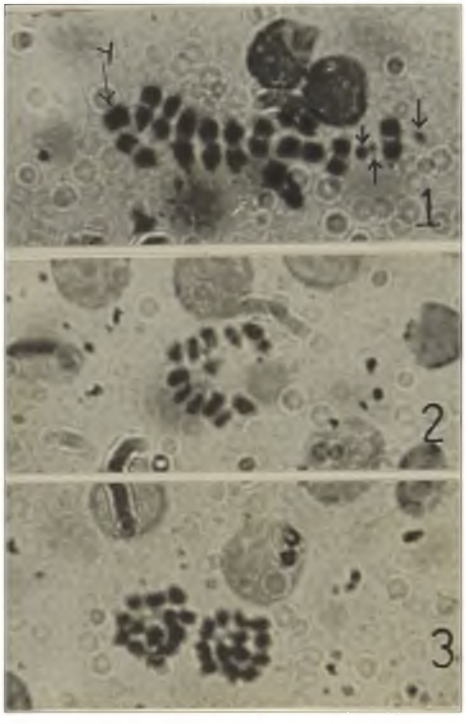
PLATE II

(1) Metaphase I (side-view) note 3 tiny X-chromosome elements, and Y-chromosome (arrowed)

(2) Metaphase II, with a broken autosomal ring with 12 elements; sex pseudo-tetravalent in centre of the ring rather indistinguishable.

(3) Anaphase II two spermatids, elements tightly packed making it difficult to count number of chromosomes per spermatid.

PLATE III



10μ

RHINOCORIS RAPAX (STÅL)

3.3.4 Rhinocoris albopilosus (Signoret)

Locality: Adult males were collected at Tafo, Kade and Aburi. Nymphs collected from Asutsuare were also reared to maturity.

Karyotype: 2n-number (28) = 24A + XXXY. Typical Rhinocoris karyotype as described for R. loratus (Stål)

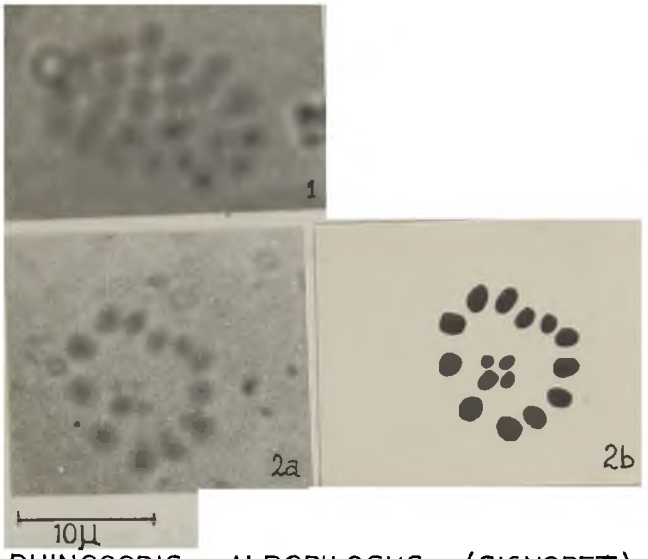
Explanation of figures:

PLATE IV

(1) Spermatogonial metaphase stage.

(2) a-picture; b-tracing of a; Metaphase II polar-view; twelve (12) membered autosomal ring clearly discernable. Sex-chromosomes at centre of ring. 3X's rather faintly displayed, however visible.

PLATE IV



RHINOCORIS ALBOPILOSUS (SIGNORET)

3.3.5 *Rhinocoris nitidulus* (Fab)

Locality: Insects were collected mainly from Wli near Hohoe in the Volta Region. A few were also collected from Aburi, Easter Region.

Karyotype: 2n number (28) = 24A + XXXY; even though the course of meiosis as well as the 2n number are identical with those of other members of the genus *Rhinocoris* described, karyotype differs slightly, autosomes are identical in size, or almost so with those of *R. loratus*; 3X-chromosomes are also identical. However the Y chromosome where its size is usually greater (approx 2X) than that of individual X-chromosomes but lesser or almost equal to size of smallest (size wise) group of autosomes in the other *Rhinocoris* species described, Y-chromosome is the largest single chromosome in the complement of *R. nitidulus*.

Explanation of figures:

PLATE VB

(1) Metaphase I, polar view. The sex-elements have taken the peripherial position as described for heteroptera.

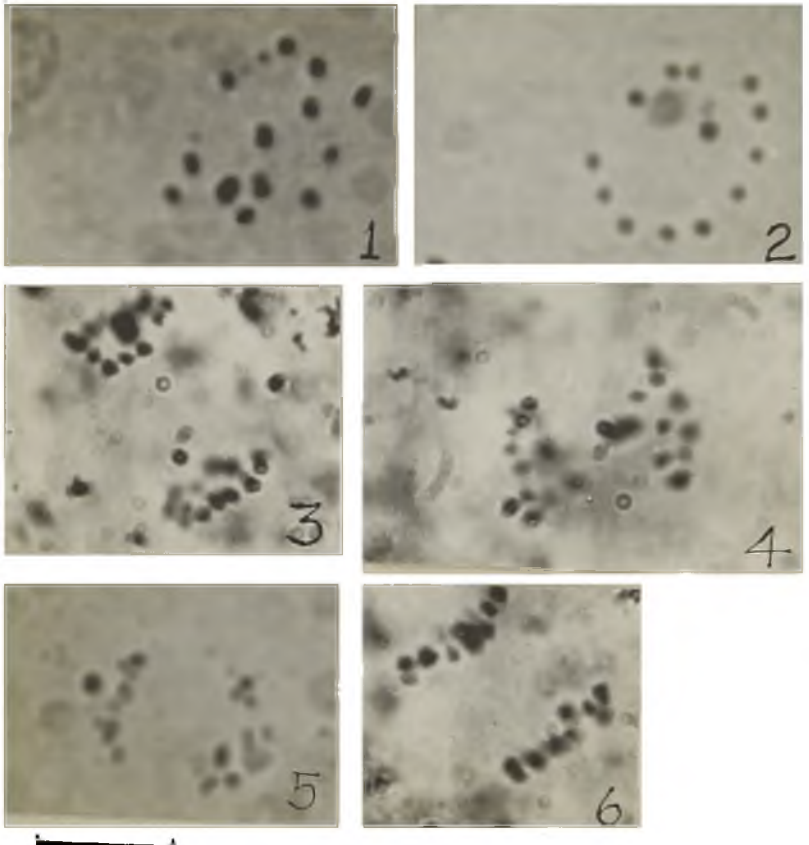
(2) Metaphase II, note the autosomal ring made up of 12 elements. The Y-chromosome but not all the 3X-chromosomes is clearly displayed in the centre of the ring.

(3,4,5,6) Anaphase II. The male spermatid in (3) clearly shows the Y-chomosome in the centre of an autosomal ring.

PLATE 5A

SHAPES & CONFIGURATIONS OF SEX - CHR. (XXXY)
DURING THE DIFFUSE STAGE; R. nitidulus

PLATE VB



10μ

RHINOCORIS NITIDULUS (FAB)

3.3.6 *Rhinocoris bicolor* (Fab)

3.3.6.1 THE IDENTITY OF THE COLOUR FORMS OF *RHINOCORIS BICOLOR* (FABRICIUS)

Rhinocoris bicolor (Fab.) one of the commonest reduviids in the cocoa-farms of West Africa, occurs in three distinct colour forms all associated with the low shrubs and grass on the periphery of the farms.

The pronotum, corium and connexiva differ in the three forms being dull red/orange, white and yellow respectively. During extensive studies on the biology and immature stages of cocoa-farms Reduviidae, Louis (1974a, 1974b) noted that the three colour forms, while occuring in the same ecological niche and living on similar food material, refused to interbreed. Detailed studies of the life cycle indicated that the three colour forms are indeed three distinct species (Louis, 1974 a&b). The genitalia as presented in this study confirm these conclusions. Even though evidence from karyotypes does not give any extra weight to separating these colour forms into distinct species, the karyotype evidence as presented here does not indicate the contrary.

I have examined the type: *Rhinocoris bicolor* (Fab).

This species is identical with the white colour form and its genitalia. Incidentally, the pygophore of genitalia presented as figure 103 by Villiers (1948) for Rhinocoris bicolor (Fab.) conforms with that of the white-form which is presented here as the type Rhinocoris bicolor (Fab).

Reduvius bicolor Fabricius Lectotype, O, Africa, 6847 here designated (examined) (Bank's collection in British Museum of Natural History); ♀ Paralectotype, 6847, here designated (examined) (in Bank's collection, BMNH). These are two specimens under the label of Redivius bicolor Fab. sp. Inst. n. 11 in Sir Joseph Banks collection and one of them is selected as a lectotype and the other as a paralectotype.

Description of R bicolor (Fab).

Colouration: Shiny black with posterior lobe of pronotum, corium of elytra, connexiva, white; lower part of all femora and under part of anterior femora yellow; pygophore of male genitalia yellow.

Body form: Posterior lobe of head very narrow, with parallel sides behind eyes; first segment of rostrum slightly shorter than second; anterior lobe of pronotum distinctly bituberculous dorsally, posterior lobe one and a half times longer than anterior one; lateral

angles rounded and barely wider than the elytra on lower part; sexual dimorphism not pronounced; females generally bigger more robust and have wider abdomen than males.

Male genitalia: Valves curved, very thin and wide apart; apophysis of ventral side of pygophore a flat blade, very short, very wide and bidentate underneath.

Dimensions (mm, n = 10, APPENDIX TABLE II)

body length: 14.00±1.20; head: length 2.79 ± 0.25, width 1.48 ± 0.10; eye: length 0.73 ± 0.07, width 0.36 ± 0.05; interocular width 0.83 ± 0.05; pronotal length 1.16 ± 0.08, pronotal width 1.99 ± 0.25; mesonotal length 1.82 ± 0.22; mesonotal width 3.54 ± 0.40; scutellum: length 0.90 ± 0.20; rostrum: 1.27 ± 0.20, 1.48 ± 0.13, 0.52 ± 0.03; antennae: 3.85 ± 0.22, 1.26 ± 0.07, 1.98 ± 0.07, 4.21 ± 0.42; forelegs: 4.63 ± 0.07, 4.90 ± 0.16, 0.46 ± 0.03, 0.63 ± 0.03; midlegs: 3.68 ± 0.05, 4.12 ± 0.33, 0.38 ± 0.03, 0.60 ± 0.05; hindlegs : 5.08 ± 0.13, 6.23 ± 0.17, 0.45 ± 0.05, 0.62 ± 0.03.

Karyotype: 2n number (28) = 24A + XXXY; karyotype resembles that of R. rapax.

Explanation of figures:

PLATE VI

Late metaphase I; side view; twelve (12) autosomes, some of which have started division, and Y-chromosome clearly visible; 3X-chromosome rather negatively heteropycnotic at this stage; two of them, arrowed discernable.

PLATE VI

10μ

RHINOCORIS BICOLOR (FAB)

3.3.7 *Rhinocoris ghaurii* n.sp.

The red colour form is here named in honour of Dr. M.S.K. Ghauri whose identification service for both Homoptera and Heteroptera has greatly helped entomologists in the Commonwealth.

Description of R. ghaurii.

Colouration: Shiny black with posterior lobe of pronotum, corium of elytra, connexiva, lower part of all femora and under part of anterior femora red/orange; pygophore of male genitalia pale yellow.

Body form: Posterior lobe of head very narrow, with parallel sides behind eyes; first segment of rostrum slightly shorter than second; anterior lobe of pronotum distinctly bituberculous dorsally, posterior lobe one and a hlaf times longer than anterior one; lateral angles rounded and barely wider than the elytra on lower part; sexual dimorphism not pronounced; females generally bigger more robust and have wider abdomen than males.

Male genitalia: Valves curved, very thin and wide apart; apophysis of ventral side of pygophore a flat, blade, very short, very wide and bidentate underneath.

Dimensions (mm. n = 10, APPENDIX TABLE II):

body length: 15.80 ± 2.00; head: length 2.87 ± 0.15

width 1.53 ± 1.00; eye: length 0.68 ± 0.08,

width 0.34 ± 0.03; interocular width 0.90 ± 0.10;

pronotal length: 1.23 ± 0.20; pronotal width 2.18 ± 0.35;

mesonotal length 2.09 ± 0.25; mesonotal width 3.95 ±

0.50; scutellum: length 1.11 ± 0.35; rostrum: 1.31 ± 0.15,

1.61 ± 0.25, 0.56 ± 0.07; antennae: 3.68 ± 0.30,

1.33 ± o.13, 2.53 ± 0.27, 4.07 ± 0.45; forelegs:

4.79 ± 0.07, 5.04 ± 0.15, 0.54 ± 0.15, 0.57 ± 0.07;

midlegs: 4.36 ± 0.75, 4.53 ± 0.50, 0.42 ± 0.03,

0.58 ± 0.07; hindlegs: 5.40 ± 0.33, 6.81 ± 0.40,

0.49 ± 0.05, 0.63 ± 0.10.

Karyotype: 2n number (28) = 24A + XXXY;

karyotype resembles that of R. rapax.

Explanation of figures:

PLATE VII

Late metaphase I, side view; 13 elements i.e. twelve autosomes and Y-chromosome at metaphase plate; some elements already dividing; 3X-chromosomes usually negatively heteropycnotic at this stage not discernable.

PLATE VII

10µ

RHINOCORIS GHAURII n. sp.

3.3.8 *Rhinocoris louisii* n. sp.

The yellow colour form is here named after Mr. D. Louis whose critical study of the biology and immature stages of Reduviidae led to the realization that the colour forms of *R. bicolour* (Fab) are three (3) distinct species.

Description of R. louisii

Colouration: Shiny black with posterior lobe of pronotum corium of elytra, connexiva, lower part of all femora and under part of anterior femora yellow; pygophore of male genitalia is similarly coloured-yellow.

Body form: Posterior lobe of head very narrow, with parallel sides behind eyes; first segment of rostrum slightly shorter than second; anterior lobe of pronotum distinctly bituberculous dorsally, posterior lobe one and a half times longer than anterior one; lateral angles rounded and barely wider than the elytra on lower part; sexual dimorphism not pronounced; females generally bigger more robust and have wider abdomen than males.

Male genitalia: Valves curved, very thin and wide apart; apophysis of ventral side of pygophore a flat blade, very short, very wide and bidentare underneath.

Dimensions (mm, n = 10, APPENDIX TABLE II).

body length 13.34 ± 2.10; head: length 2.80 ± 0.15 width 1.47 ± 0.07; eye: length 0.68 ± 0.03, width 0.35 ± 0.05; interocular width: 0.48 ± 0.05; pronotal length: 1.11 ± 0.12; pronotal width: 2.00 ± 0.33; mesonotal length: 1.84 ± 0.22; mesonotal width 3.58 ± 0.40; scutellum: length 0.98 ±0.37; rostrum: 1.27 ± 0.03, 1.39 ± 0.13, 0.48 ± 0.03; antennae: 3.87 ± 0.20, 1.23 ± 0.03, 2.33 ± 0.20, 4.68 ± 0.07; forelegs: 4.60 ± 0.40, 4.87 ± 0.03, 0.47 ± 0.03, 0.63 ± 0.07; midlegs: 3.97 ± 0.80, 4.37 ± 0.80, 0.44 ± 0.06, 0.63 ± 0.03; hindlegs 4.57 ± 0.35, 5.47 ± 0.33, 0.42 ± 0.03, 0.62 ± 0.07.

Karyotype: 2n number (28) = 24A + XXXY;

karyotype similar to that of R. rapax.

Explanation of figures:

PLATE VIII

Tracing; Metaphase II, side view; note central position of sex-chromosome cluster, arrowed; 12 autosomes clearly discernable.

PLATE VIII

10μ N.T.S

RHINOCORIS LOUISII n. sp.

In the three (3) species: R. bicolor, R. ghaurii, and R. louisii, apophysis of ventral side of pygophore is a flat blade as described earlier. Form of flat blade varies slightly with each of these species (Fig. 3.1).

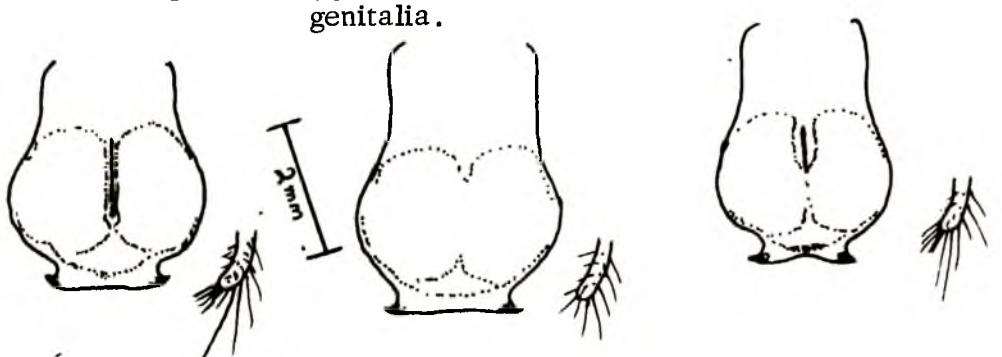
In R. bicolor, flat blade narrows in mid-portion; slight dome on outline (free end of blade) makes dentate ends appear curved forward. In R. louisii blade is similarly shaped but is uniformly long and wider than in R. bicolor; R. ghaurii differs from the other two species in the fact that the blade is indented at middle of free end, giving a pronounced bidentate form; further the blade is narrowest at mid-portion.

In R. biclor, the mid-ventral part of pygophore is domed with narrow, deep, approximately two (2) millimetre long groove on summit. The groove of R. ghaurii differs from that of R. bicolor being shorter, shallower and of less defined outline; no groove is present on the dome of pysophore of R. louisii.

Parameres are similarly shaped in all three species. R. ghaurii and R. bicolor have tuft of short bristles at tip of parameres, immediately on the upper portion of which a small group of rather longer bristles

are present; rest of paramere covered with mixed-length bristles, none as long as latter group; in R. louisii mixed length bristles present all over parameres; tuft of short bristles on tip absent.

Fig. 3.1 : Pygophore and parameres of male genitalia.



3.1.1 R. bicolor (Fab) 3.1.2 R. louisii n.sp 3.1.3 R. ghaurii n.sp

3.3.9 Rhinocoris hutsebauti Schouteden

Locality: The species is yet to be confirmed as R. hutsebauti Shouteden. A specimen (under label as Rhinocoris Sp.D) is available in the Entomology Museum, Zoology Dept., University of Ghana Legon. A single insect was collected at Tafo on the under-growth of a cocoa farm.

Karyotype: 2n-number 26 = 24A + XY. A careful look at the karyotype revealed that the autosomes are identical or almost so with those of R. loratus. R. nitidulus, R. rapax, R. carmelita. The sex-chromosomes are only two here however. The X and Y chromosomes are of the same size and the smallest in the complement. Course of meiosis is as in R. loratus (Stål) except that at Anaphase II, the resulting 2 spermatids are similar in number; 12 autosomes + Y (13 elements) go to one pole and other 12 autosomes + X (13 elements) to the other.

Explanation of figures:

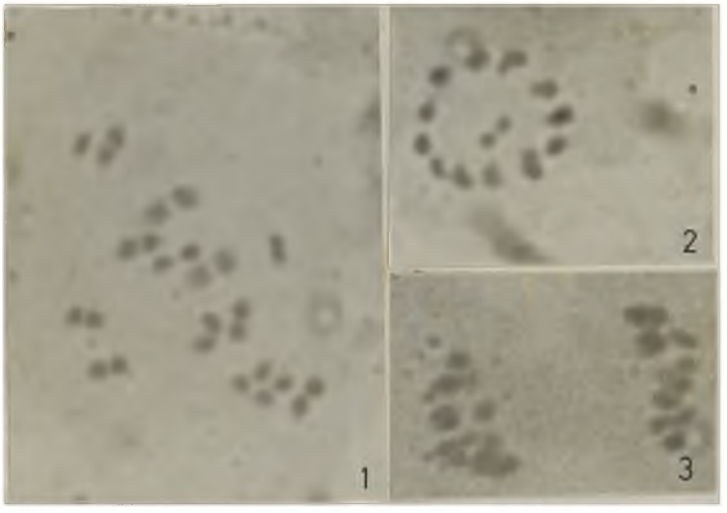
PLATE IX

(1) Metaphase I side view

(2) Metaphase II, polar view; note autosomal ring with 12 elements; X and Y chromosomes in centre of ring.

(3) Anaphase II.

PLATE IX



10μ

RHINOCORIS HUTSEBAUTI (SCHOUTEDEN).

3.3.10 Sphedanolestes (Aulacosphodrus) leucocephalus (Fabricius)

Locality: Adult males collected at Tafo, Aburi and Dodowa on the peripherial undergrowth of cocoa farms.

Karyotype: 2n-number (28) = 24A + XXXY; karyotype as described for R. loratus (Fab)

Explanation of figures:

PLATE X

(1) Spermatogonial metaphase, showing diploid complements, 28 elements; note artifacts obscuring elements.

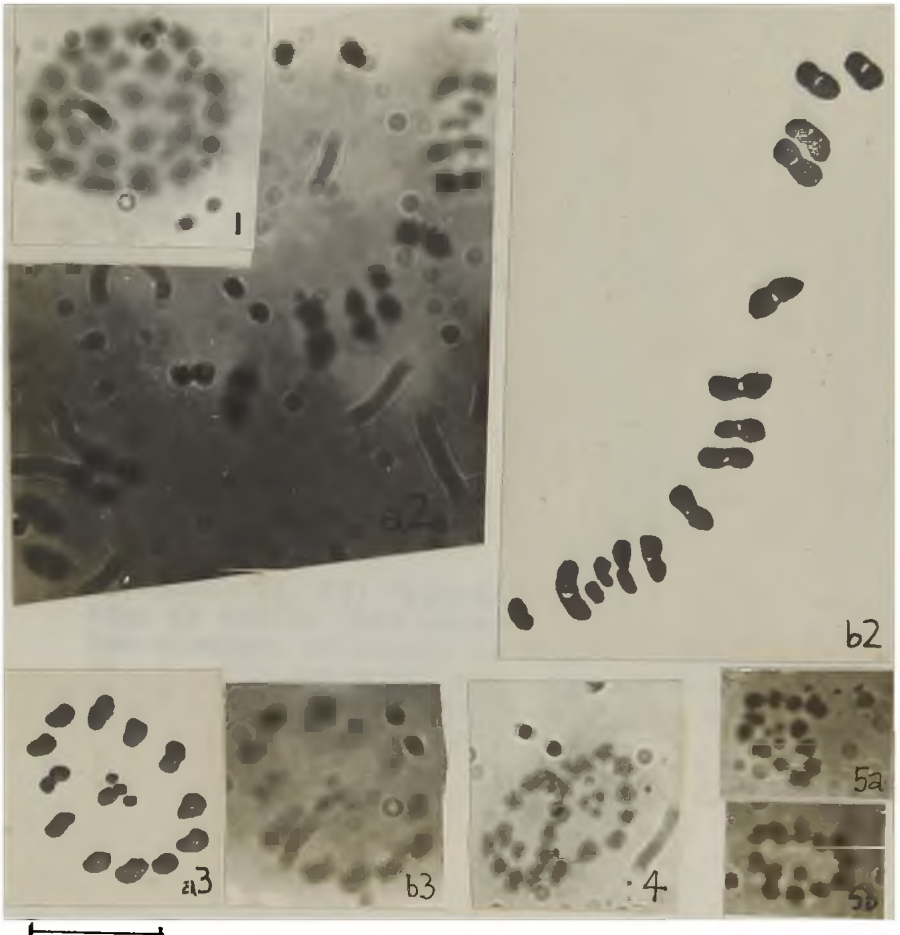
(2a,b) a-picture; b-tracing; Metaphase I. Haploid complement of sixteen (16) elements, one sex-element overlapped - giving impression of 15 member complement.

(3a,b) a-tracing; b-picture; Metaphase II. Twelve membered autosomal ring with four sex-element of centre. 3X-chromosomes smallest in karyotype. Y approximately twice the size of X-chromosomes.

(4) Anaphase II; Partially separated spermatids. Separation of sex-elements distinctly shown. 3X-chromosomes to one side (female spermatid) and Y-chromosome to other side (male spermatid).

(5a,b) Anaphase II shows male and female spermatids clearly; male spermatid with thirteen (13) elements i.e. twelve (12) autosomes and Y; female spermatid fifteen (15) elements i.e. twelve (12) autosomes and 3X's; autosomal ring prominent at this stage.

PLATE X



SPHEDANOLESTES (AULA) LEUCOCEPHALUS (FAB.)

3.3.11 *Vestula lineaticeps* (Signoret)

Locality: Commonest species of Reduviid in the cocoa farms of Ghana; appears in several colour varieties. Adults available all year round in all the cocoa growing areas.

Karyotype: 2n number (27) = 24A + XXY

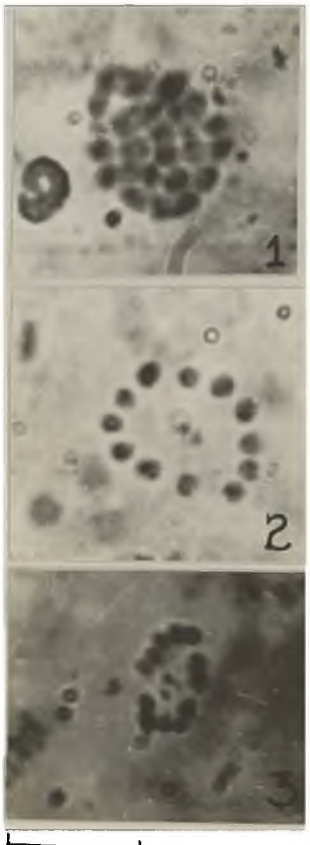
Explanation of figures:

PLATE XI

(1) Spermatogonial metaphase showing diploid complement of twenty-seven

(2,3) Metaphase II; (2) Typical harpactorine autosomal ring of twelve (12) elements clearly shown. Sex-elements at centre of ring not clearly shown. (3) Autosomal ring compact but elements discernable. Sex-elements - three - at centre of ring clearer than in (2).

PLATE XI



10μ

VESTULA LINEATICEPS (SIGNORET)

3.3.12 Margasus impiger (Bergroth)

Locality: Two (2) adult males were caught during sweeping at Tafo.

Karyotype: 2n-number revealed by five (5) spermatogonial metaphase plates is 26. Diffuse stage showed two (2) heteropycnotic sex elements most likely XY ; 24A + XY = 26

Explanation of figures:

PLATE XII

(1) Spermatogonial metaphase: Twenty-six elements, diploid complement discernable.

PLATE XII

10μ

MARGASUS IMPIGER (BERGROTH)

3.3.13 Pisilus tipuliformis (Fabricius)

Locality: Adult males were collected at Tafo, Fade, Aburi, Apedwa and Dodowa.

Karyotype: 2n-number (28) = 26 + XY Course of meiosis typically heteropteran.

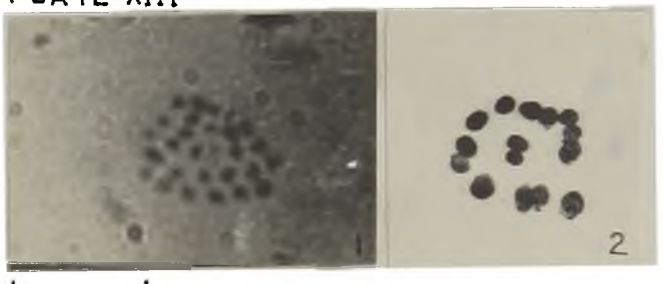
Explanation of figures:

PLATE XIII

(1) Spermatogonial metaphase showing diploid complement of 28 elements.

(2) Tracing; Metaphase II: disturbed 12 membered autosomal ring with XY towards centre of ring.

PLATE XIII



10μ

PISILUS TIPULIFORMIS (FAB)

3.3.14 Aprepolestes acutum (Stål)

Locality: Adult insects collected from Tafo, Kade and Legon.

Karyotype: Course of meiosis as described for R. loratus;

2n number (28)= 24A + X_1 X_2 X_3 Y

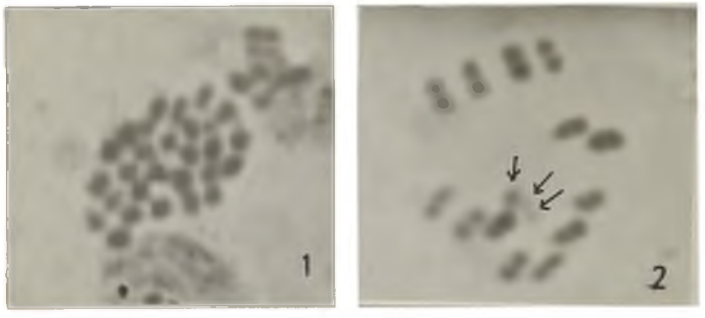
Explanation of figures:

PLATE XIV

(1) Spermatogonial metaphase clearly showing 2n complement of 28 elements.

(2) Metaphase II: an autosomal ring around sex-elements; note almost symmetrical autosomal complement, and small 3X chromosomes (arrowed) clustered above the Y-chromosome.

PLATE XIV



10μ

APREPOLESTES ACUTUM (STÅL)

3.3.15 Cosmolestes pictus Klug

Locality: Males were collected at Kade.

Karyotype: 2n-number (28) = 24 + XXXY; karyotype as described for R. loratus (Stål)

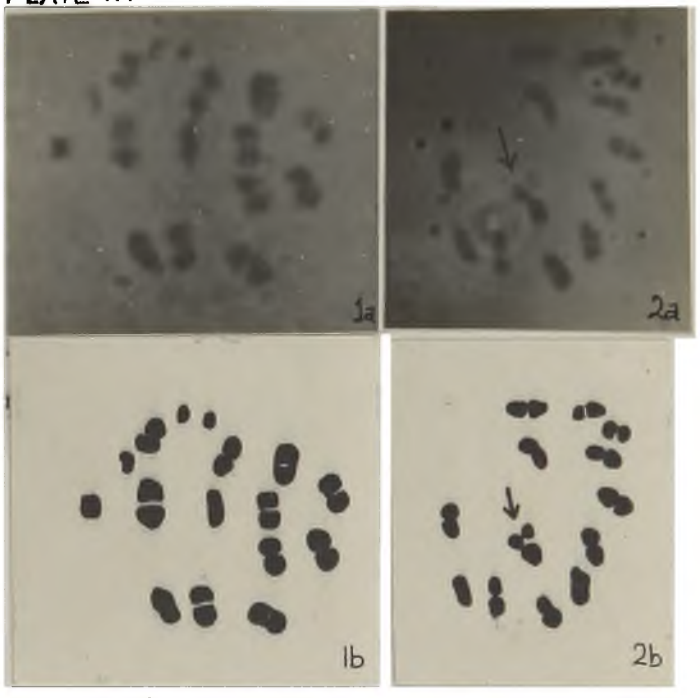
Explanation of figures:

PLATE XV

(1) a-picture; b-tracing of a; Metaphase I: side view with slightly over squashed elements, haploid complement of 16 elements clearly discernable; note usual peripherial position of sex-chromosomes at this stage.

(2) a-picture; b-tracing of a; Metaphase II: autosomal ring slightly displaced, elements in side view. Sex-elements at centre of ring 2X's and Y-elements visible, one X out of plane and therefore overlapped; cluster of sex-elements arrowed.

PLATE XV



COSMOLESTES PICTUS KLUG

3.3.16 Phonoctonus fasciatus Beauvois

Locality: Insects were collected from the under-growth of silk-cotton trees, Botanical garden, Legon.

Karyotype: 2n-number (28) = 24A + XXXY.

Explanation of figures:

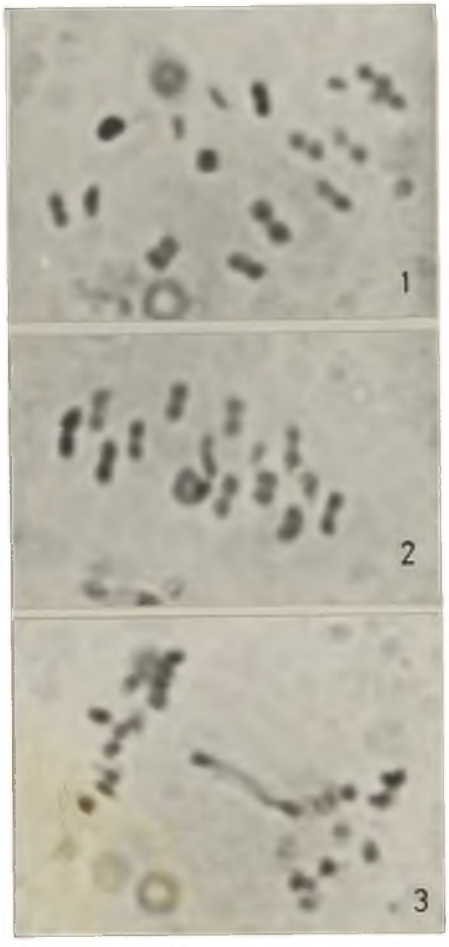
PLATE XVI

(1) Metaphase I. Karyotype resembles that of Rhinocoris loratus (Stål), note sixteen elements, autosomes almost symmetrical except for one rather large element.

(2) Metaphase II (side view) autosomal ring not very distinct.

(3) Anaphase II. Note chromosomal-bridge, possibly a result of non-disjunction.

PLATE XVI



PHONOCTONUS FASCIATUS (BEAUVOIS)

3.3.17 Phonoctonus subimpictus (Stål)

Locality: Males were collected from Tafo, Kade, Aburi, Legon and Somanya.

Karyotype: 2n number (28) = 24A + XXXY.

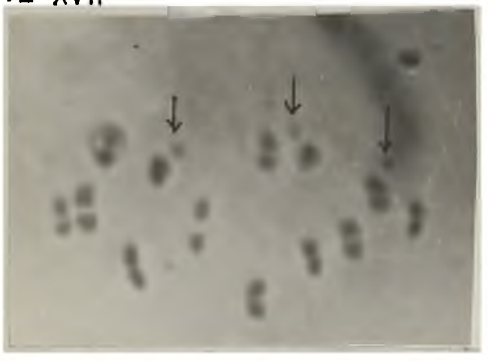
Karyotype similar to that of R. loratus

Explanation of figures:

PLATE XVII

(1) Metaphase I shows sixteen (16) elements. Sex-elements smallest of group and peripherally placed. As usual with Harpactorine karyotypes Y-chromosomes approximate four times size of X-chromosomes 3X-chromosomes arrowed.

PLATE XVII



10μ

PHONOCTONUS SUBIMPICTUS STÅL

3.3.18 Phonoctonus lutescens (Guerin and Percheron)

Locality: as for P fasciatus

Explanation of figures:

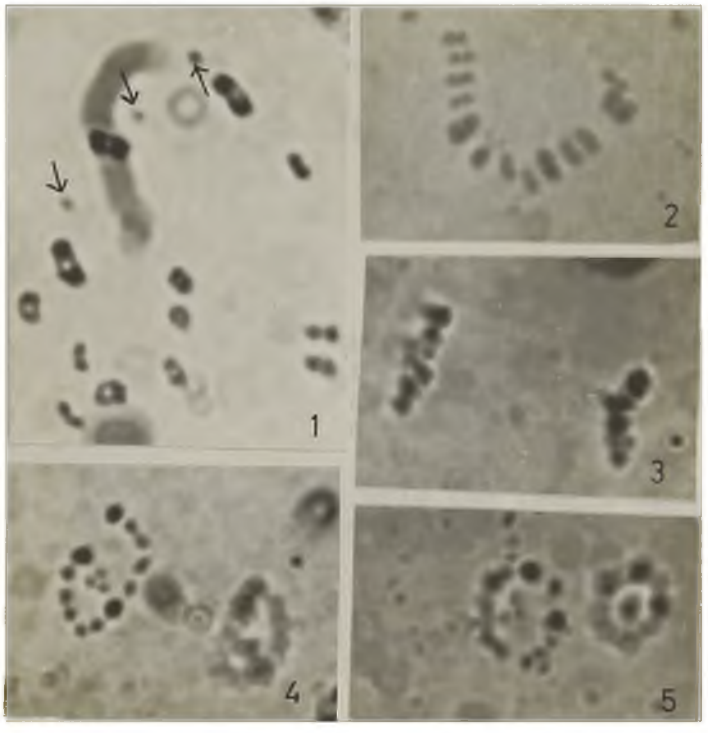
PLATE XVIII

(1) Metaphase I; note the haploid complement of 16 elements, karyotype differs slightly from that of P. fasciatus and P. subimpictus; autosomes acutely assymmetrical three (3) elements are of the size of the single biggest element of both P. fasciatus and P. subimpictus. The second group (size wise) of elements are slightly smaller than those of other members of the genus studied, and comprises nine (9) elements as opposed to eleven (11) in the haploid complements of other species; the sex-complements are identical; 3X-chromosomes arrowed.

(2) Metaphase II (side view); note central position of the sex-elements; the Y-element slightly smaller in size than the smallest autosome is in the same plane as the autosomal ring but the tiny 3X-elements are slightly removed from this plane.

(3-5) Anaphase II; (3) in side view and others in polar; note complements of the two (2) different spermatids (4 and 5); the 3X chromosomes go to one pole with an autosomal ring of twelve elements and Y chromosome to the other with its complement of autosomes.

PLATE XVIII



10μ

PHONOCTONUS LUTESCENS (GUERIN & PERCHERON)

3.3.19 Harpagocoris nigroflavus Villiers

Locality: Adult insects collected from Tafo.

Karyotype: 2n-number (29) = 24A + XXXXY

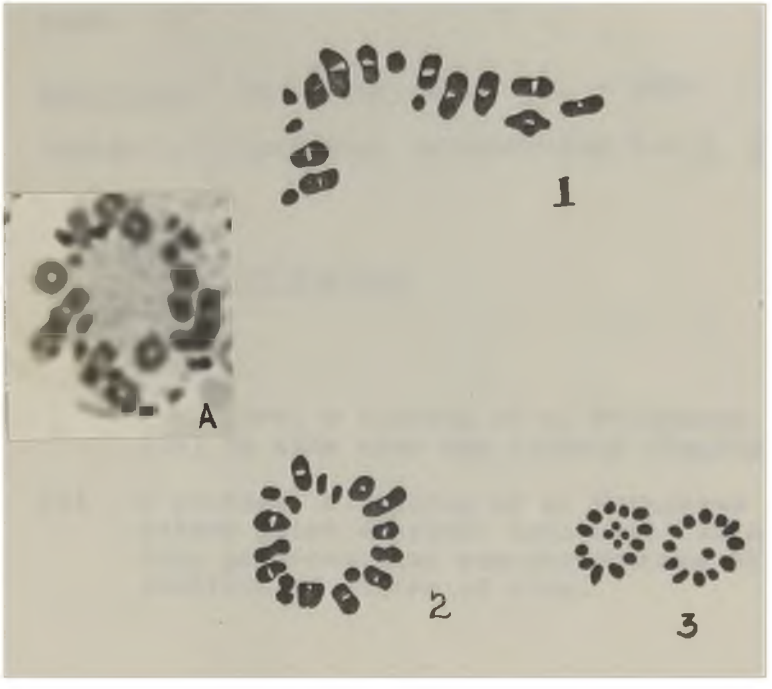
Explanation of figures:

PLATE XIX

(1), (2), (A): Late diakinesis, sex-elements seperated; (1) Elements 16, i.e. one short of expected number probably due to bad squashing; (2) expected complement, 17 elements.

(3) Anaphase II, note male and female spermatids. Autosomal ring distinct with 12 elements.

PLATE XIX



N.T.S
10μ

HARPAGOCORIS NIGROFLAVUS VILLIERS.

3.3.20 Coranus pallidus (Reuter)

Locality: Adult insects collected at Weja, Winneba road.

Karyotype: 2n-number (28) = 24A + XXXY; karyotype typically harpactorine as described for R. loratus (Stål).

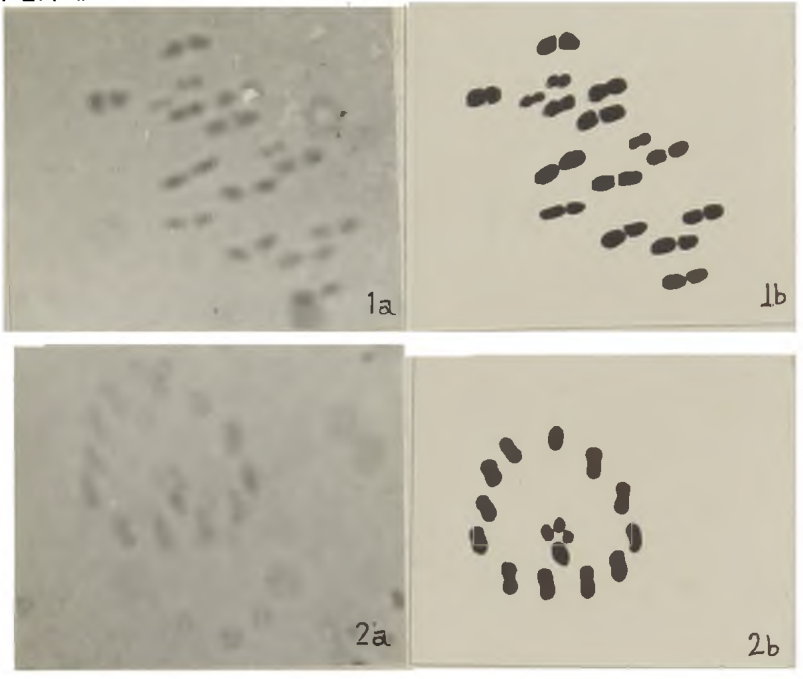
Explanation of figures:

PLATE XX

(1) a picture; b tracing of a; Metaphase I elements (16) in side view and clearly displayed.

(2) a picture; b tracing of a; Metaphase II in rather faint display; autosomal (12 membered) ring prominent and sex-chromosomes XXXY in position at centre of ring.

PLATE XX



10μ

CORANUS PALLIDUS (REUTER)

3.3.21 *Dinocleptes torpidus* (Miller)

Locality: Two adult males were captured in the Botanical garden of the University of Ghana, Legon.

Karyotype: 2n-number (26) = 24A + XY; course of meiosis typically heteropteran

Explanation of pictures:

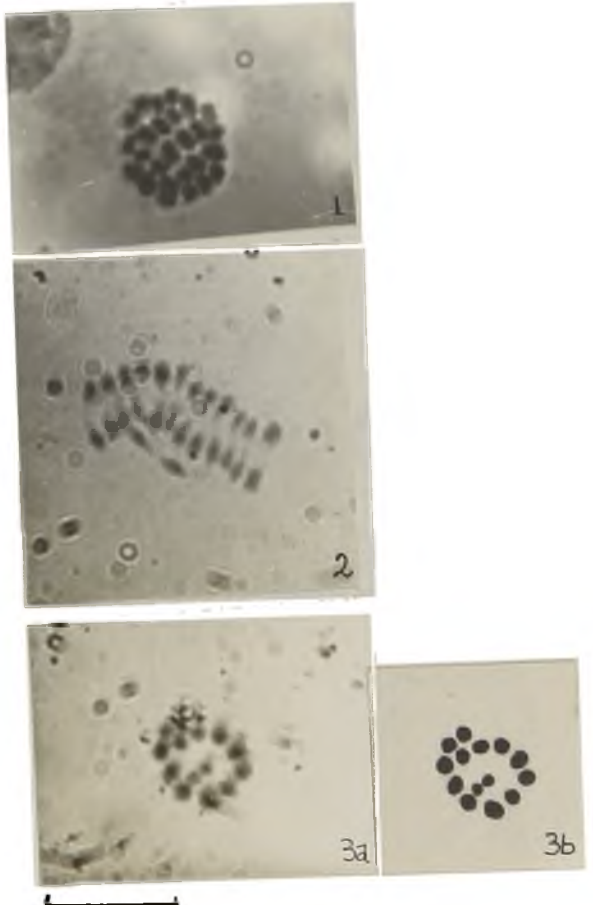
PLATE XXI

(1) Spermatogonial metaphase shows diploid complement of twenty-six (26) elements.

(2) Anaphase I: metaphase I elements at metaphase plate completely divided, movement started towards poles.

(3) a picture; b-tracing of a; Metaphase II, partially collapsed autosomal ring (12) elements; eleven autosomes clearly visible, 12th obscured by artifacts. X and Y chromosomes at centre of ring. Note similar size of sex-elements.

PLATE XXI



10μ

DINOCLEPTES TORPIDUS (MILLER)

3.3.22 Nagusta punctaticollis (Stål)

Locality: Adult males were collected from Weja, Winneba road and Tafo.

Karyotype: 2n-number (27) = 24A + XXY; karyotype is identical to that of R. loratus (Stål) except for the rather small sex-elements (2X-chromosomes) and a Y-chromosome approximately thrice (3X) the size of each X-chromosome.

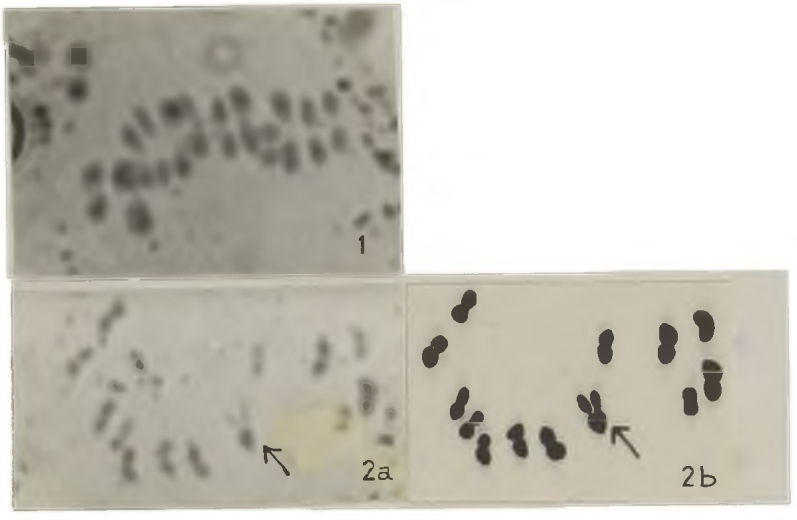
Explanation of pictures:

PLATE XXII

(1) Early Anaphase I: Metaphase I elements at metaphase plate partially divided, movement towards poles started.

(2) a picture; b, tracing of a; Metaphase II note displaced autosomal ring of twelve elements in side-view, sex-elements in pseudotrivalent arrowed.

PLATE XXII



10μ

NAGUSTA PUNCTATICOLLIS (STÅL)

3.3.23 Rhaphidosoma truncatum Jeannel

Locality: Two (2) adult males collected in light trap at Legon.

Karyotype: 2n number (26) = 24A + XY. Course of meiosis typically heteropteran.

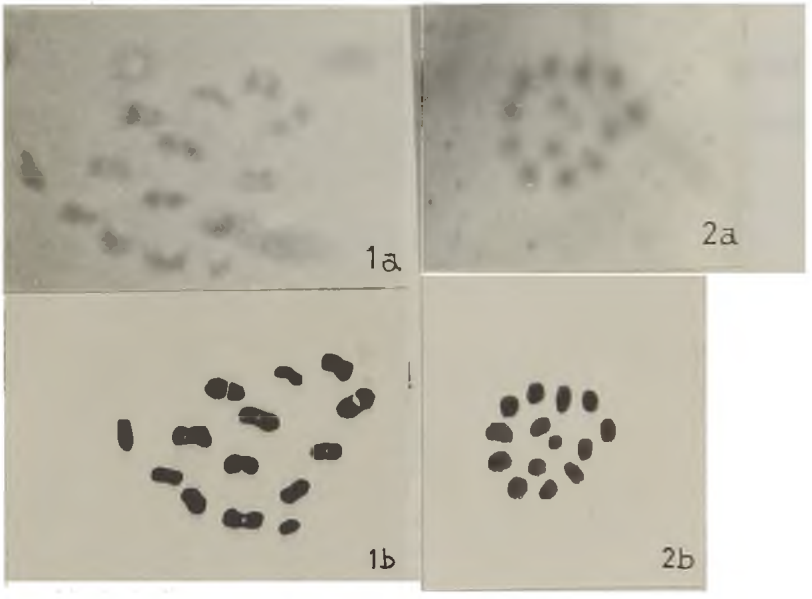
Explanation of pictures:

PLATE XXIII

(1) a-picture; b-tracing of a; Metaphase I, shows haploid complement of 14 elements. Slightly over-squashed.

(2) a-picture; b-tracing of a; Metaphase II, note autosomal ring of 12 elements, one element displaced inwards joining two sex-elements, XY in the ring.

PLATE XXIII



RHAPHIDOSOMA TRUNCATUM JEANNEL

3.1.24 Tribelocephala curticornis Villiers

Locality: Adults insects collected on walls near lights at Legon, Tafo and Kade.

Karyotype: 2n-number (30) = 28A + XY This species is the only one of the small subfamily Tribelocephalinae studied.

Explanation of figures:

PLATE XXIV

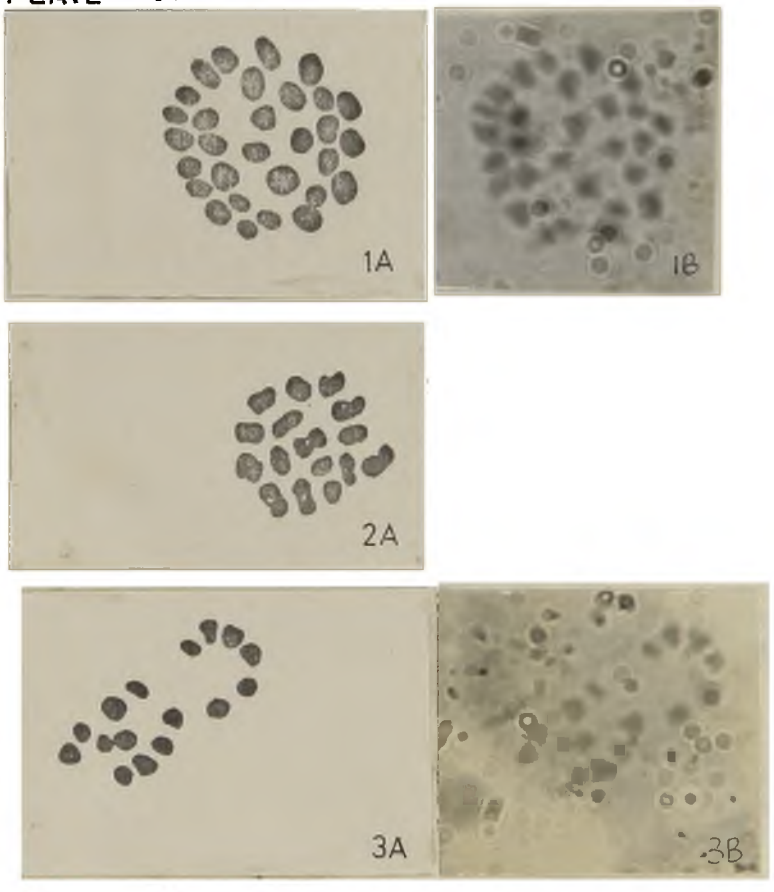
PICTURE 1B, 2B & 3B; Tracing: 1A, 2A, 3A

(1A and B: Spermatogonial metaphase showing thirty (30) elements.

(2A and B: Metaphase I. 16 elements, 14 autosomal tetrads and X and Y. Autosomes almost symmetrical, X and Y rather small in size and difference between two negligible.

(3A and B: Metaphase II autosomal ring of 14 chromosomes with X and Y in centre.

PLATE XXIV



10μ

TRIBELOCEPHALA CURTICORNIS VILLIERS

Sub family: SALYAVATINAE

Course of meiosis in two species of Salyavatinae studied is typically heteropteran. Species of Lisarda vandenplasi were collected at light trap at Somanya and Legon. Petalocheirus rubiginosus specimens were collected by searching and sweeping at Apedwa near Tafo.

3,3.25 Lisarda vandenplasi Schouteden

Karyotype: 2n-number (23) = 20A + XXY;

Explanation of figures:

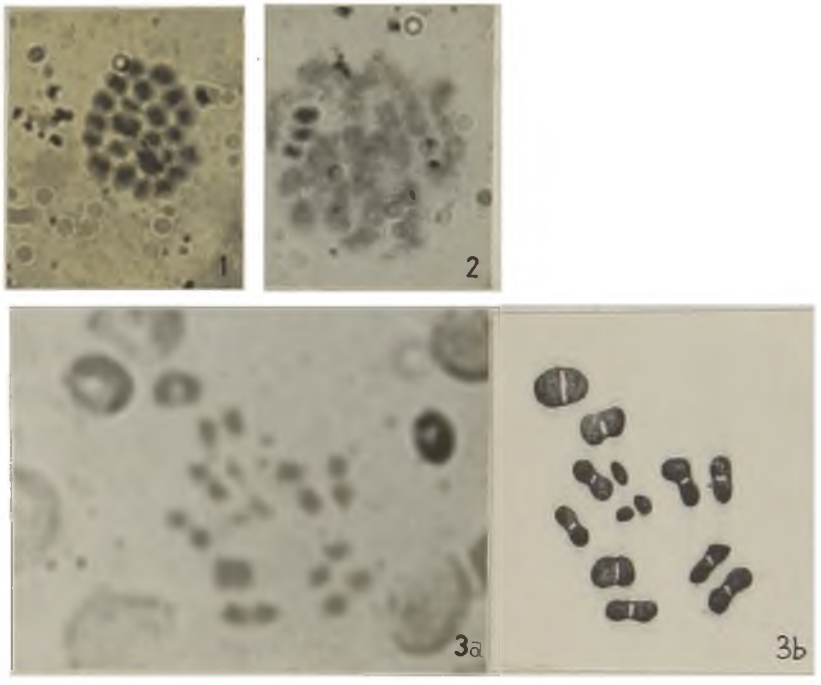
PLATE XXV

(1) Spermatogonial metaphase, 23 elements representing 2n-number visible.

(2) Diffuse stage of Prophase I, note three heteropycnotic elements ; sex chromosomes X X Y; one element slightly larger in size and most likely the Y chromosome.

(3) a-picture; b-tracing of a: Metaphase I: showing ten (10) autosomes including two rather large elements and 3 sex-elements.

PLATE XXV



10µ

LISARDA VANDENPLASI SCHOUTEDEN

3.3.26 Petalocheirus rubiginosus (Palisot de Beauvois)

Karyotype: 2n-number (22) = 20A + XY. Course of meiosis typically heteropteran.

Explanation of figures:

PLATE XXVI

(a) - picture; (b) tracing of (a); Metaphase II showing ten (10) membered autosomal ring; two (2) autosomal elements slightly displaced. Sex-elements at centre of ring arrowed.

PLATE XXVI

PETALOCHEIRUS RUBIGINOSUS (PALISOT de BEAUVOIS)

3.3.27 Oncocephalus subspinosus (Amyot and Seville)

Locality: Males were collected at lights and in lights traps at Kpong and Somanya.

Karyotype: 2n-number (24) = 20A + XXXY (or XXYY) i.e. the sex-determining mechanism for this species is not clear.

Explanation of figures:

PLATE XXVII

(1) Spermatogonial metaphase stage, diploid complement (24) shwn.

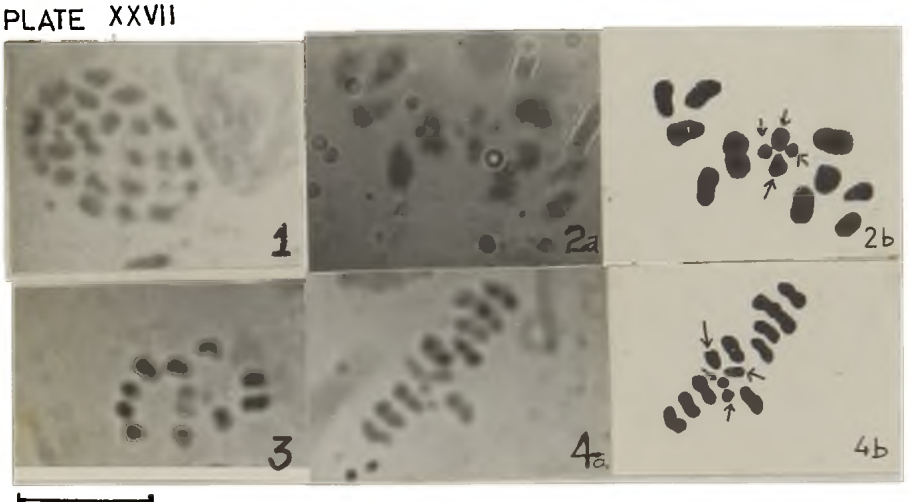
(2,3,4) Metaphase II all in side view;

(2) Over-squashed and heavily artifacted, but shows sex-complement of two very small elements and two slightly larger ones.

(3) a-picture; b tracing of a; Shows ten (10) membered autosomal ring distinctly all sex-chromosomes (arrowed) visible except one of smaller two most likely out of plane.

(4) a-picture; b tracing of a. Complete side view of elements at metaphase II, all components distinctly displayed; sex chromosomes arrowed.

PLATE XXVII



10μ

ONCOCEPHALUS SUBSPINOSUS (AMYOT & SERVILLE)

3.3.28 Argolis calabarensis (Stål)

Locality: Specimens were collected from light-traps at Asutsuare, Kpong, Somanya and Legon.

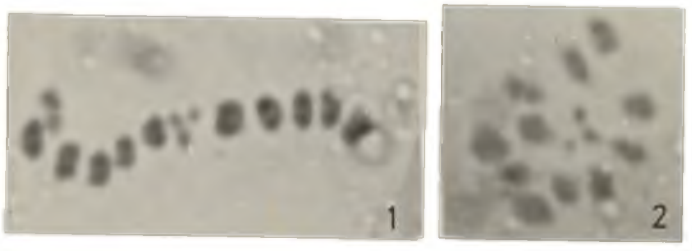
Karyotype: 2n-number (25)=22A : X_1 X_2 Y.

Explanation of figures:

PLATE XXVIII

(1 & 2) Metaphase II, (1) shows side view with autosomal ring of eleven (11) dyads, broken. Sex-chromosomes retain central position, (2) shows autosomal ring distinctly; 3 sex-chromosomes in both cases distinctly smaller in size (approx. ½ size of autosomes); note near symmetrical karyotype as far as autosomes are concerned; sex-elements are of same size.

PLATE XXVIII



10μ

ARGOLIS CALABARENSIS (STÅL)

3.3.29 *Thodelmus addahensis* Reuter

Locality: Adult males were collected from light-traps at Legon, Somanya, Kpong and Asutsuare.

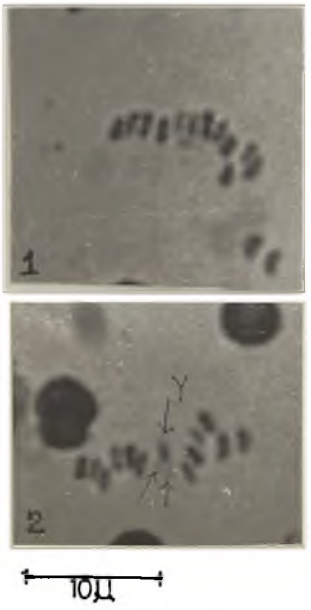
Karyotype: 2n-number (27) = 24A + XXY, course of meiosis typically heteropteran.

Explanation of pictures:

PLATE XXIX

(1) & (2) Metaphase II, both in side view; how haploid complement of fifteen (15) elements; sex-elements slightly negatively heteropycnotic; note central position of sex-elements, arrowed in (2)

PLATE XXIX



THODELMUS ADDAHENSIS REUTER

3.3.30 Oncocephalus posthi Villiers

Locality: Most adult males were collected at Somanya and Kpong.

Karyotype: 2n-number (23) = 20A + XXY Course of meiosis typical heteropteran.

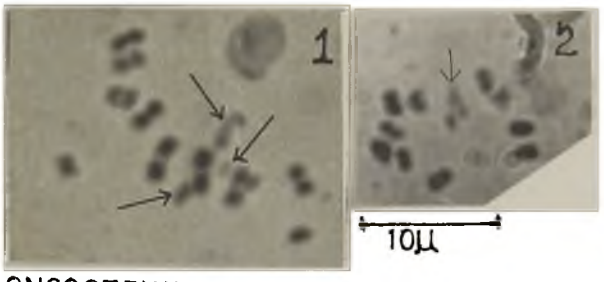
Explanation of pictures:

PLATE XXX

(1) & (2) Metaphase II: (1) Elements and autosomal ring in sideview, note central position of sex-elements all arrowed; sex-elements slightly out of plane with autosomes.

(2) Ten (10) membered autosomal ring discernable; 3 sex-elements in pseudo-trivalent arrowed, each element of trivalent however recognizable.

PLATE XXX



ONCOCEPHALUS POSTHI VILLIERS

3.3.31 Cethera musiva (Germar)

Locality: Adult insects collected from Kade, Somanya and Tafo.

Karyotype: 2n number 23 = 20A + XXY; Course of meiosis typically heteropteran.

Explanation of figures:

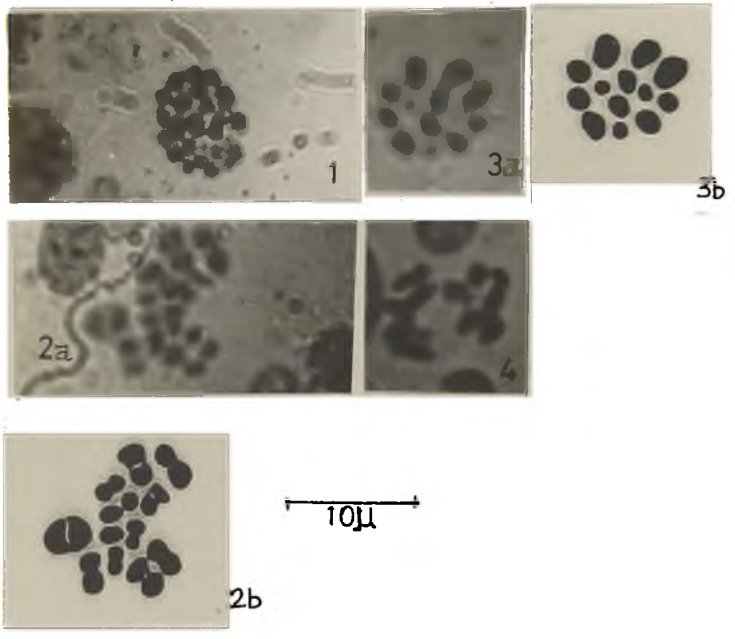
PLATE XXXI

(1) Spermatogonial metaphase showing 23 elements.

(2 and 3) a-picture; b-tracing of a; Metaphase I, (2) side view, (3) polar view, haploid complement of 13 elements showing rather assymmetric karyotype, note largest element in complement clearly shown in (2).

(4) Anaphase II.

PLATE XXXI



CETHERA MUSIVA (GERMAR)

3.3.32 Cethera maculipennis (Breddin)

Locality: Adults collected at Somanya, Kpong and Legon.

Karyotype: 2n-number (23) = 20A + XXY

Explanation of figures:

PLATE XXXI

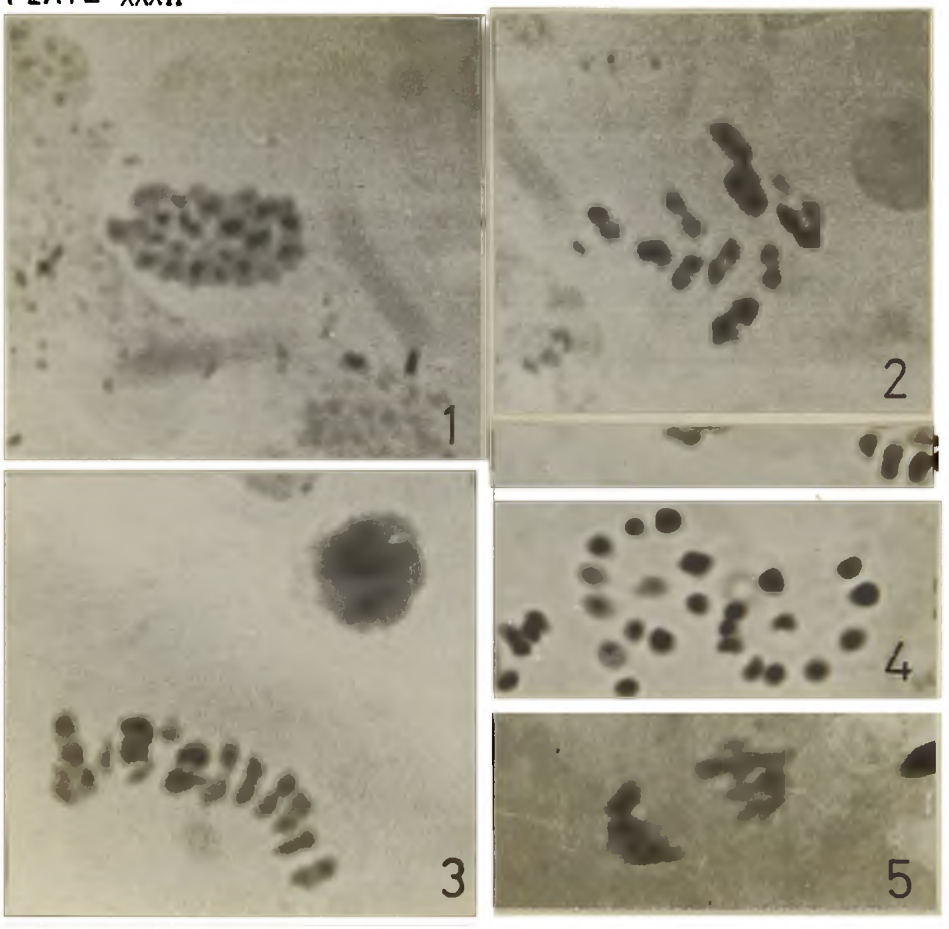
(1) Spermatogonial metaphase, elements not easily distinguishable

(2,3) Spermatocyte Metaphase I. Not assymmetry of karyotype; smallest elements (3) of almost equal size (sex-elements), autosomes distinguishable into two categories: one group comprising four (4) comparatively larger autosomes, remaining six (6) smaller.

(4) Metaphase II: autosomal rings formed by ten autosomes clearly visible in each cell, sex-chromosomes in centre of rings are pseudo-trivalents at the "touch and go" phase.

(5) Late anaphase II.

PLATE XXXII



CETHERA MACULIPENNIS (BREDDIN)

3.3.33 Leptacanthaspis decorsei Jeannel

Locality: Specimens from light traps at Somanya, Kpong, Legon and Tafo.

Karyotype: 2n-number (29) = 26A + X_1 X_2 Y.

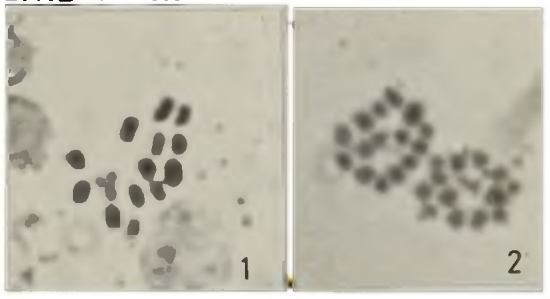
Explanation of figures:

PLATE XXXIII

(1) Metaphase II autosomal ring appears collapsed, result of over-squashing. 3 sex-chromosomes however shown in 'touch' condition. 13 autosomal dyads clearly visible.

(2) Anaphase II showing two spermatids.

PLATE XXXIII



10μ

LEPTACANTHASPIS DECORSEI (JEANNEL)

3.3.34 Acanthaspis petax (Stål)

Locality: Adult males collected from Legon, Kade and Tafo.

Karyotype: 2n-number (24) = 11A + XY; Karyotype differs from other two members of genus Acanthapis studied It appears there is a fusion between 2 original autosomes as shown for A. bilineolata and A. sulcipes bringing the autosome complement down from twelve (12) to eleven (11)

Explanation of pictures:

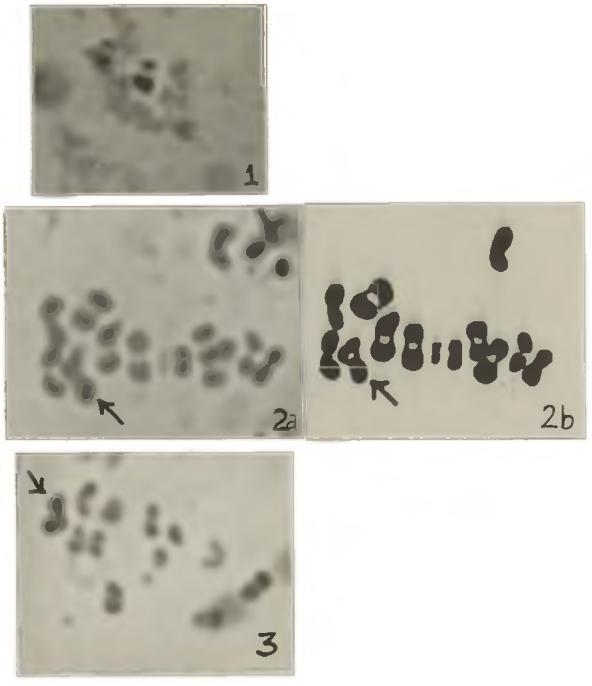
PLATE XXXIV

(1) Diffuse stage of prophase. Shows heteropycnotic sex-elements.

(2) a-picture; b tracing of a: Metaphase I; note 13 elements, arrowed elements represents 2 fused autosomes?

(3) a-picture; b tracing of a: Metaphase II; eleven elements in autosomal ring around two sex-elements, arrowed element represents 2 fused autosomes?

PLATE XXXIV



10μ

ACANTHASPIS PETAX (STÅL)

3.3.35 Acanthaspis sulcipes Signoret

Locality: Adult males were reared out of nymphs collected on cocoa shade trees at Kade and Tafo.

Karyotype: 2n number (26) = 24A + XY; Course of meiosis typically heteropteran.

Explanation of figures:

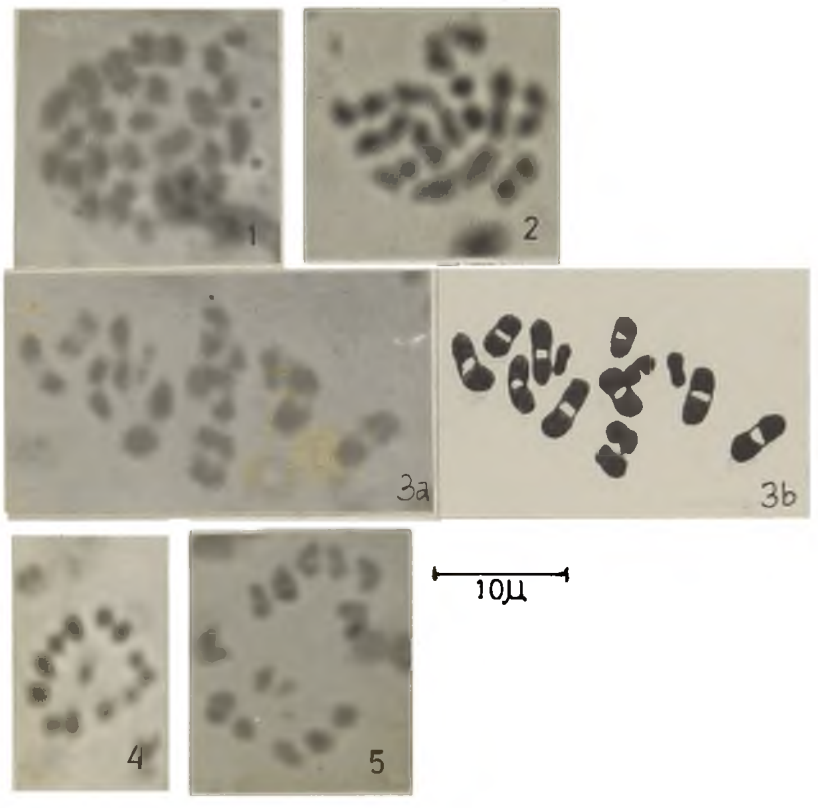
PLATE XXXV

(1) Spermatogonial metaphase showing the diploid complement of 26 elements = 24A + XY.

(2, 3a & b) 3b-tracing of 3a: Metaphase I (side view) 12 tetrads and 2 sex-dyads are visible. The assymmetry of the karyotype is evident.

(4,5) All show Metaphase II. (4) is a polar view and (5) is side view; note the 12 autosomes in the autosomal ring around X and Y.

PLATE XXXV



ACANTHASPIS SULCIPES SIGNORET

3.3.36 Acanthaspis bilineolata (Palisot de Beauvois)

Locality: Males collected from under barks of cocoa shade trees at Kade.

Karyotype: 2n number (26) = 24A +XY

Explanation figures:

PLATE XXXVI

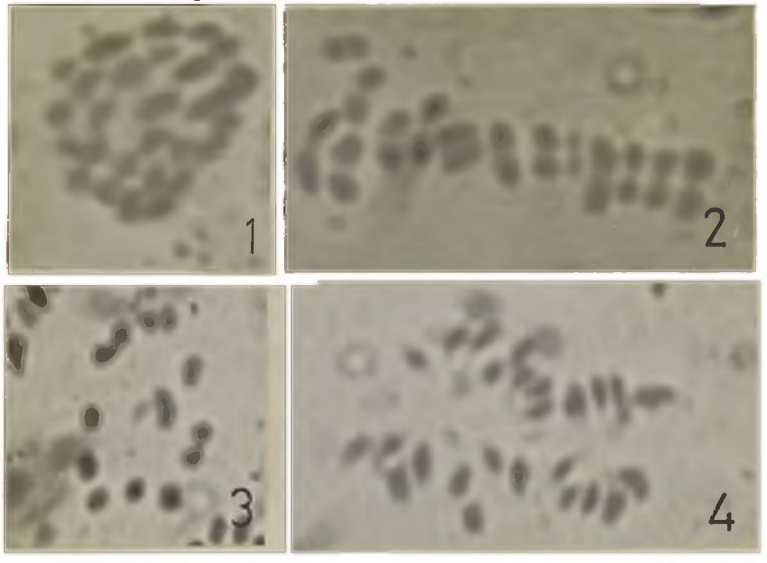
(1) Spermatogonial metaphase with 26 elements.

(2) Metaphase I. 12 autosomal tetrads and 2 sex-dyads seen in side view; assymmetry of karyotype clear.

(3) Metaphase II. An autosomal ring of 12 elements with two (2) sex-chromosomes in centre. One element larger than the other; bigger sex-element differs in karyotype of A. bilineolata, A. sulcipes and A. petax.

(4) Anaphase. I.

PLATE XXXVI



10μ

ACANTHASPIS BILINEOLATA (PALISOT de BEAUVOIS)

3.3.37 Plynoides benoiti

Locality: One adult male was captured during sweeping at Apedwa.

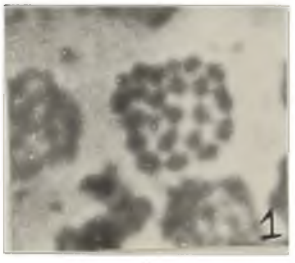
Karyotype: 2n number (23) = 20A + XXY.

Explanation of figures:

PLATE XXXVII

(1) Spermatogonial metaphase showing diploid complement (23)

PLATE XXXVII



PLYNOIDES BENOITI

3.3.38 Plynoides pallidus

Locality: Specimens collected at Somanya from light traps

Karyotype: 2n-number 23 = 20A + XXY, course of meiosis heteropteran

Explanation of figures:

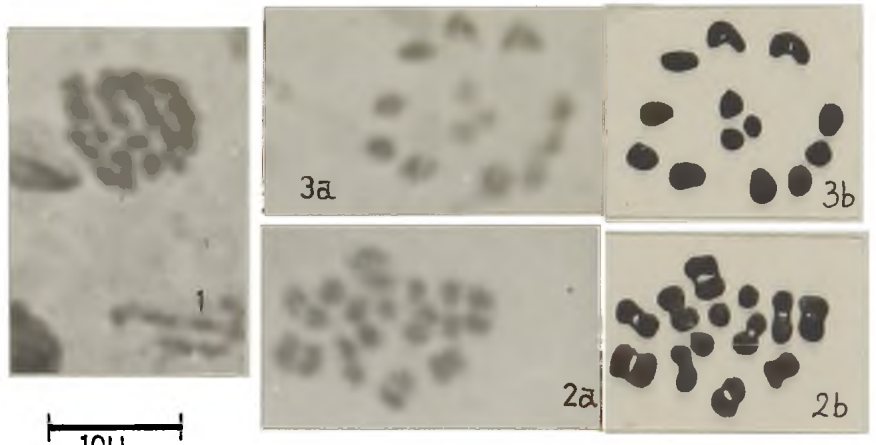
PLATE XXXVIII

(1) Spermatogonial metaphase. Careful check gives a count of twenty three (23) elements.

(2) a-picture; b tracing of a; Metaphase I: Ten autosomal tetrads similar to that of C. maculipennis (Breddin)

(3) a - picture; b tracing of a; Metaphase II. Autosomal ring of ten (10) elements around three (3) sex-chrosomes. Note sex-elements are of same size.

PLATE XXXVIII



PLYNOIDES PALLIDUS

3.3.39 Eriopreda feai Jeannel

Locality: Adult males collected from Kade on Spatodia sp. (shade plants).

Karyotype: 2n-number 24 = 22A + XY.

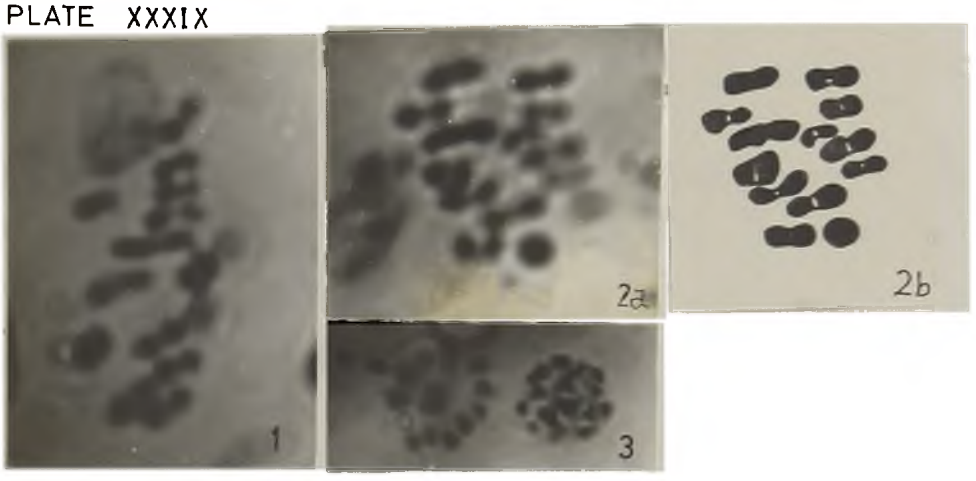
Explanation of figures:

PLATE XXXIX

(1),(2) 2a picture; 2b tracing of 2a: Metaphase I: shows haploid complement of thirteen (13). Note acute asymmetry of karyotype, note long and large, short and large and round and large chromosome-elements, standing out.

(3) Metaphase II (left of print); note autosomal ring of eleven (11) elements, sex-elements at centre as pseudobivalent.

PLATE XXXIX



10μ

ERIOPREDA FEAI JEANNEL

3.3.40 Cerilochus inermipes (Stål)

Locality: 2 specimens were collected from Kade under the corky bark of a shade tree, Spatodia sp.

Karyotype: 2n-number was found to be (18) = 16A + XY. This is the lowest among the 12 species of Reduviinae studies for this work.

Explanation of figures:

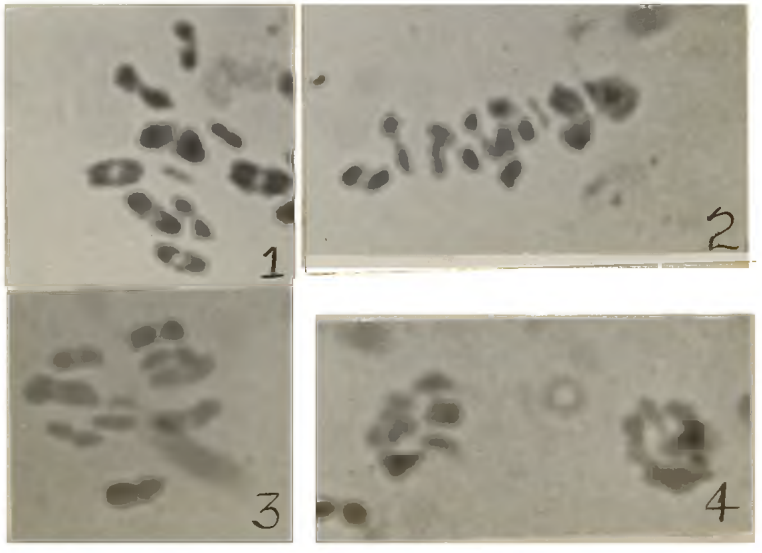
PLATE XXXX

(1) and (2) Metaphase I (side view). Elements distinctly large except X and Y which are easily distinguishable from rest of karyotype because of small size. Size difference between sex-chromosomes: one approximately 2X size of other. Smaller of two slightly negatively heteropycnotic at this stage.

(3) Metaphase II. Note central position of X and Y chromosomes.

(4) Anaphase II. Two spermatids separated.

PLATE XXXX



10μ

CERILOCHUS INERMIPES (STÄL)

3.3.41 Tetroxia nigrospinosa Villiers

Locality: Adult insects were collected from under the bark of shade trees at Tafo, Kade and Apedwa. Some nymphs were also collected at the same points and reared to maturity in the laboratory at Legon.

Karyotype: 2n-number (22) = 20A + XY (?). The behaviour of chromosomes and course of meiosis in this species is not clear. The karyotype is rather unique. It appears as if there has been two recent fusions between four (4) autosomes resulting in two (2) rather large chromosomes. The karyotype is quite assymmetrical. In some cases e.g. Plate XXXXI 2, 3, 4, the elements at metaphase I are arranged as to give an impression of a separation of spermatids at Anaphase II. In these cases the 2n of 12 i.e. 10A + XXO seems more appropriate. A re-investigation of the karyotype of this species is necessary.

Explanation of figures:

PLATE XXXXI

(1) Diffuse stage of prophase 1,2 heteropycnotic sex elements visible, either XY or XX.

(2) Metaphase I,(?). Twelve (12) elements discernable. Note largest single element. Possibly result of recent fusion. Spatial distribution of 12 elements gives impression of two different entities of seven (7) and five (5) elements.

(3) Metaphase I (?) 12 elements, separation of 5 and 7 entities more prominent. Distribution of single-elements in two entities different from (2); note largest element now in group of seven (7). Two negatively heteropycnotic elements side by side in seven element unit, most likely two sex-elements of (1); (3) suggests 10A + XXO system, at 'normal' Anaphase II.

(4) Gives strength to 10A + XXO idea. Note distinct separation of two entities.

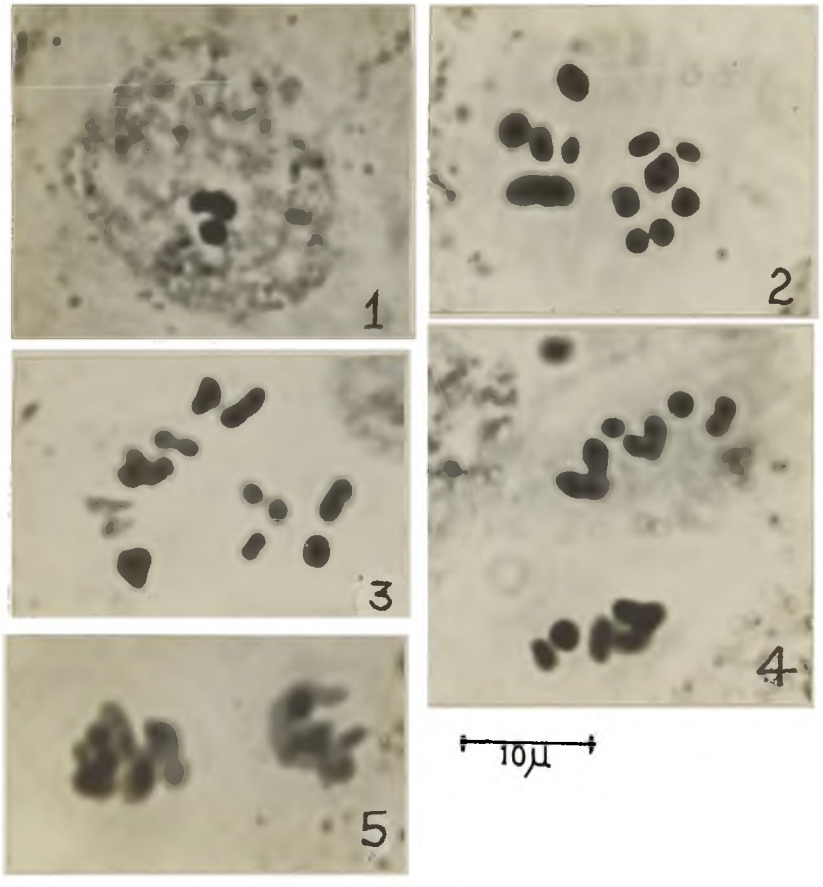
(5) Telophase II elements not distinguishable.

3.3.42 Platymeris biguttata (Linne)

Locality: 2 adult males were caught under bark of spatodia sp. in Kade.

Karyotype: 2n-number as displayed by spermetogonial metaphase plates is 30; chromosome formula not worked out due to lack of further information.

PLATE XXXXI



TETROXIA NIGROSPINOSA VILLIERS

4. DISCUSSION AND CONCLUSIONS

4.1 Introduction

The information available on reduviid karyotypes, and cytotaxonomy, even though more extensive now than before, is hardly exhaustive or representative of the family as a whole. In the limited circumstances of this study it was impossible to investigate enough subfamilies and to spread out equally into the ones that are reported here since only available species were investigated. Therefore it is not within the scope of this study to tackle all the problems of Reduviid systematics outlined in the general introduction.

4.2 Karyotypes and subfamilies

The subfamily Reduviinae (chapter 3.2; Fig. 4.1 - 4.2; Appendix Table III) shows the greatest spread of diploid numbers (18-30) in the Reduviidae known cytologically. The modal number of 23 however stands out among the fourteen (14) members so far investigated. This low modal 2n-number links the Reduviinae with Stenopodiinae (chapter 3.2; Fig. 4.3 - 4.4; Appendix Table III) which also has a modal 2n-number of 23 for the 12 members known; Triatominae (Appendix Tables I and III; Ueshima 1966) which exhibits a modal 2n-number of 22 for 29 members; and Salyavatinae

ig 4.1 REDUVIINAE: DISTRIBUTION OF 2N-NUMBER, SEX-CHROMOSOME, AND AUTOSOMAL-CHROMOSOME TYPES.

LITERATURE (2 SPECIES)

2N-NO.	22	29
FREQ	1	1

4.1.1

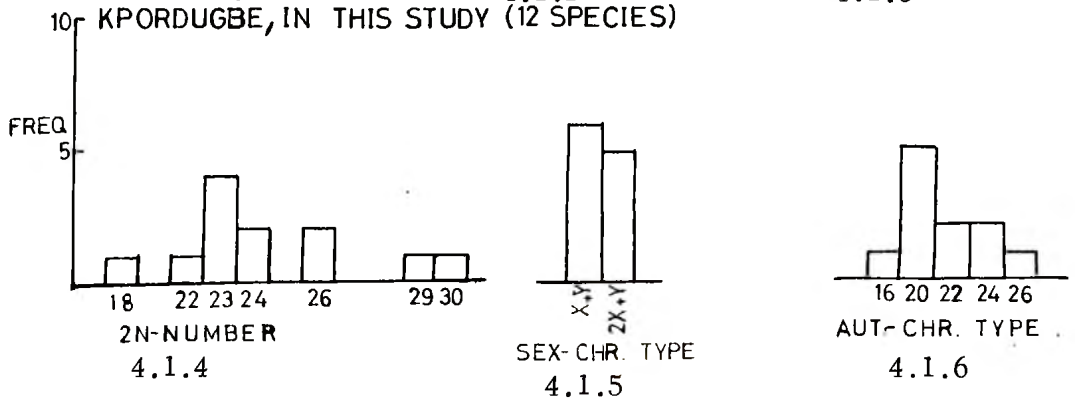
SEX-CHR.	X+Y	4X+Y
FREQ.	1	1

4.1.2

AUT-CHR.	20	24
FREQ.	1	1

4.1.3

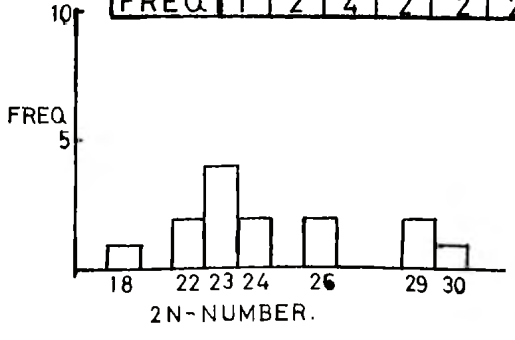
KPORDUGBE, IN THIS STUDY (12 SPECIES)



4.1.4 4.1.5 4.1.6

Fig 4.2 DISTRIBUTION OF 2N-NUMBER IN THE 14 SPECIES OF REDUVIINAE STUDIED CYTOLOGICALLY TO DATE.

2N-NO.	18	22	23	24	26	29	30
FREQ	1	2	4	2	2	2	1

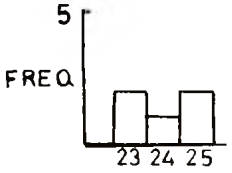


(chapter 3.2; Appendix Table I) for which the 2 species, Lisarda vandenplasi and Petalocheirus rubiginosus so far investigated show diploid numbers of 23=20A + XXY and 22 = 20A + XY respectively. Actually the differences between the two diploid numbers for Salyavatinae are due to the multiple sex-chromosomes.

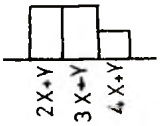
In his review of the cytotaxonomy of Triatominae, Ueshima (1966) recorded a male diploid chromosome range of 20-25 (Appendix Table III). He mentioned that 22 = 20A + XY is the most common (51.7%) for 29 species investigated. The majority of deviations from this modal number (22) are due to compound sex-chromosomes. This shows an apparent stability of the autosome complement in Triatominae. The more variable sex-chromosome mechanism ranges from XY to XXXY. Ueshima (1966) presented 20A + XY as the type number and the diploid complement of the ancestral stock of Triatominae. This he supports by accepting the earlier evolution of the XY sex-mechanism as compared to that of the multiple mechanisms and the other arguments as advanced by Xavier (1945), Manna (1951), White (1954) and Schrader and Hughes-Schrader (1956) when they presented 12A + XY as the type number for family Pentatomidae. Ueshima (1966) went further to suggest direct or indirect fragmentations and

Fig 4.3 STENOPODIINAE: DISTRIBUTION OF 2N-NUMBER SEX-CHROMOSOME AND AUTOSOMAL-CHROMOSOME TYPES.

LIT. (5 SPECIES)

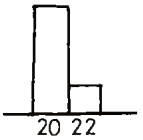


4.3.1



SEX-TYPES

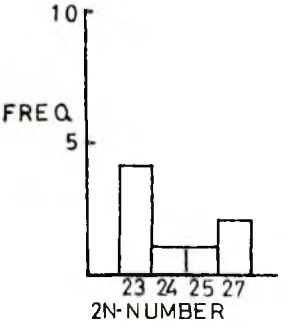
4.3.2



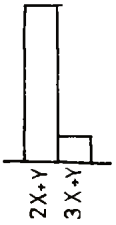
AUTOSOME-TYPES

4.3.3

DETERMINED BY KPORDUGBE IN THIS STUDY (7 SPECIES)

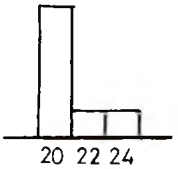


4.3.4



SEX-TYPES

4.3.5



AUTOSOME TYPES

4.3.6

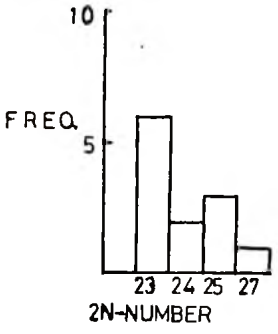
duplications as the mechanism by which the other karyotypes evolved from the ancestral type.

The Salyavatinae resembles Triatominae by having a stable 20A complement and variations due to sex-mechanism. In Reduviinae chromosome mechanism ranges from XY to 4X + Y for the 14 species so far recorded. In the present investigation only two (2) types were found: XY and XXY for 12 species of tropical Reduviinae; XXXY is not represented at all in the subfamily.

There seems to be more stability in the sex-mechanism in the Reduviinae than in Triatominae while the opposite seems to be the case for the autosomes: Reduviinae autosomes range from 16 to 26. However the most common autosome group is 20A (35.7%). Even though the 2n-number 23 = 20A + XXY comes out as the modal 2n-number (Fig. 4.2), the breakdown into autosomes and sex-chromosomes (figs. 4.1.1 - 4.1.6) shows that among the sex-mechanisms encountered in Reduviinae, the XY is clearly dominant and that the karyotype in this subfamily is closely related to that of Triatominae and Salyavatinae. Even though 23 = 20A + XXY is the modal number of the collection of karyotypes in Reduviinae, it is not sufficiently widespread (28.6%) in the subfamily to be regarded as the type number.

Akingbohungbe (1974) suggested that in

Fig 4.4 DISTRIBUTION OF 2N-NUMBER IN THE 12 SPECIES OF STENOPODINAE STUDIED CYTOLOGICALLY TO DATE.



2N-NO.	23	24	25	27
FREQ.	6	2	3	1

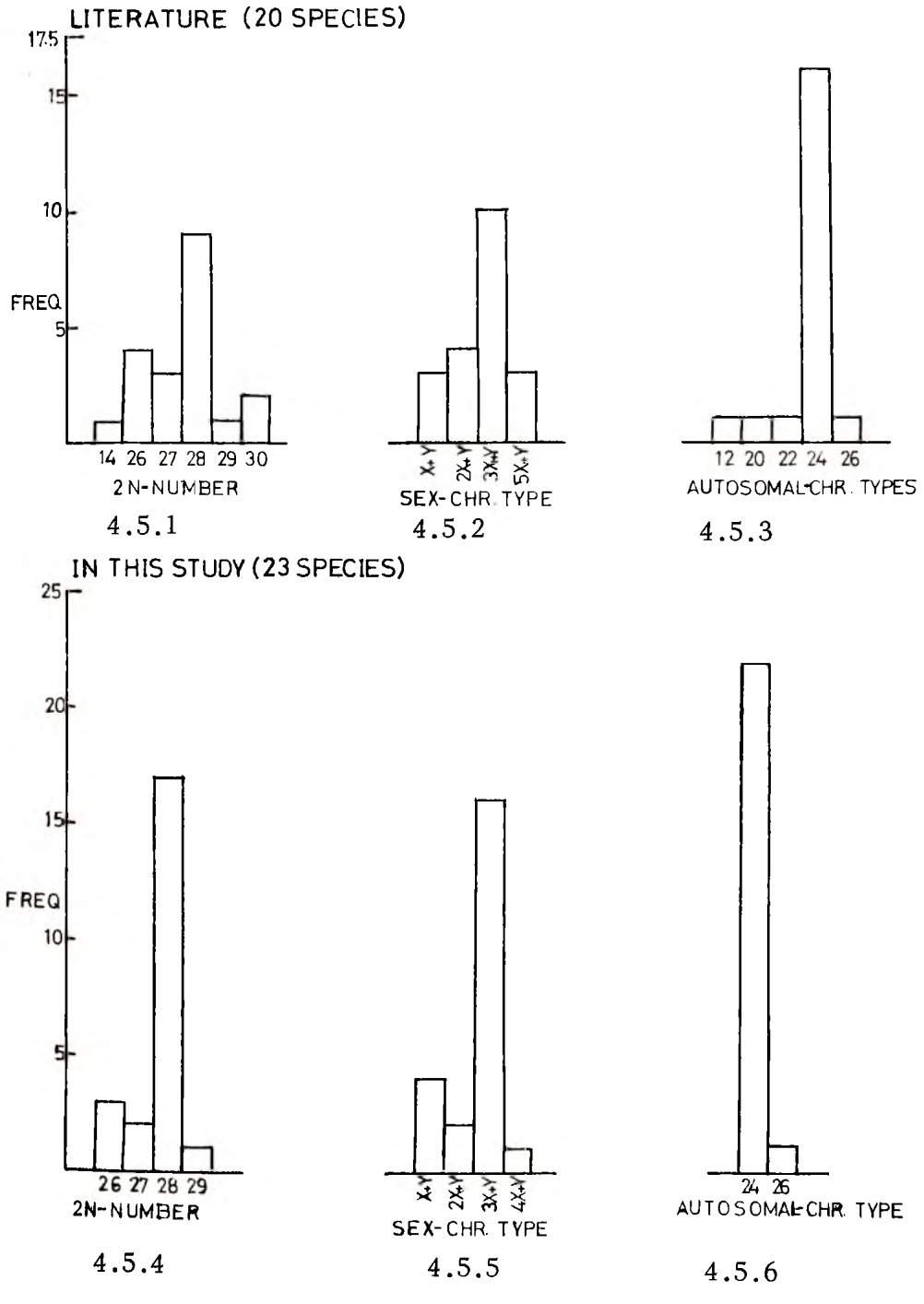
postulating a basic or type karyotype for any group, care should be taken to ensure that such a karyotype recurs in the different components of the group with a reasonable degree of stability and frequency. He illustrated the importance of this by drawing attention to the effect of his contribution of additional eighty (80) mirid karyotypes on the type number 32A + XY suggested by Leston (1957) for Miridae based on a limited and skew karyotype data.

Stenopodinae shows a sex-chromosome mechanism range of XXY to XXXXY and autosome numbers ranging from 20A to 24A. The dominant diploid number is clearly 23 = 20A + XXY (Fig. 4.3 - 4.4).

The Piratinae (Appendix Table I) shows clear affinity for the 20A group. All five (5) species investigated by Jande (1959) and Banerjee (1959) have twenty autosomes differing only in sex-chromosome mechanism which ranges from XY to XXY.

Emesinae represented by two (2) species so far (Ueshima, 1963), appears to be a group with low diploid numbers. Barce fraferna (Baker) is 20 = 18A + XY and Empicoris rubromaculatus (Blackburn) is 16 = 14A + XY (Appendix Table I).

Fig 4.5 HARPACTORINAE: DISTRIBUTION OF 2N-NUMBER SEX-CHROMOSOME AND AUTOSOMAL-CHROMOSOME TYPES.

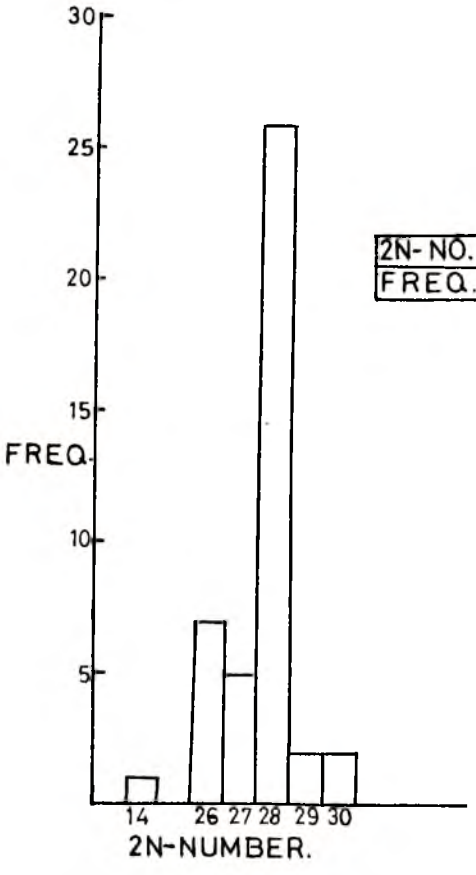


The subfamily Harpactorinae is the most extensively investigated in the Reduviidae. Presently karyotypes of 43 species are known. Of this number, twenty-three (23) are from this study. This is obviously the result of the availability and wide distribution of this successful group. The genus Rhinocoris is clearly the largest single one known in the Harpactorinae.

Sex-chromosome mechanism in Harpactorinae is diverse, ranging from XY to 5X + Y; XXXY dominates the group (chapter 3.2; Fig. 4.5 - 4.6; Appendix Table III). The autosomes range from 12 to 26 with 24A easily the commonest here. Species with 28 = 24A + XXXY dominate the Hapactorinae (60.5%).

Here as in Triatominae, the majority of deviations from this modal number are due to compound sex-chromosome mechanisms. Unlike in Triatominae however, the modal number and clearly the type number for Harpactorinae (28 = 24A + XXXY) does not seem to be the karyotype of the ancestral stock. Polididus armatissimus has been mentioned by Jande (1960) as a primitive survivor carrying a 14 = 12A + XY karyotype. Within the genus Rhinocoris it appears that R. hutsebauti Schouteden carries the ancestral Rhinocoris karyotype, 26 = 24A + XY

Fig 4.6 DISTRIBUTION OF 2N-NUMBERS IN THE 43 SPECIES OF HARPACTORINAE STUDIED CYTOLOGICALLY TO DATE.



2N-NO.	14	26	27	28	29	30
FREQ.	1	7	5	26	2	2

because it is the only one carrying the supposedly primitive sex-determining mechanism (XY) identical to that of P. armatissimus and Tribelocephala curticornis Villier. The X and Y are almost equal in size. Tribelocephalinae are considered close to the basal stock of Reduviidae (Davis 1966, 1969; Kumar 1962; Louis and Kumar 1973). Jande (1960) discussed the primitive nature of the more or less equal size of X and Y.

The obviously higher chromosome numbers remove the Harpactorinae from the 20A group of Triatominae etc. The 24A group that has emerged includes Rhaphidosominae where two (2) species described so far have 24 autosomes differing only in their multiple sex configurations (chapter 3.2; Appendix Table I).

Another karyotype group appears to bring together Ectrichodinae, Tribelocephalinae and Phymatinae. These groups represented so far by one species each (chapter 3.2; Appendix Table I) have 28 autosomes (28A). Ectrichodinae and Phymatinae possess the primitive X + O sex-chromosome mechanism (Manna 1951; Montgomery 1906) and Tribelocephalinae the XY type.

The Apiomerinae (2 species investigated, Appendix Table I) appears intermediate between the 20A and 24A groups with 24 = 22A + XY. However Davis (1961, 1969) grouped them with Rhaphidosominae, Harpactorinae and Tegeinae (all 24A group members except Tegeinae where no work has been reported) under his Harpactorine complex based on external morphology.

The apparent rarity of differences in autosome number between related species as compared to that of sex-chromosome number, suggests the greater importance of the former. The groupings based on autosome numbers, rather than conventional 2n-number groupings are on firmer grounds at least as far as the reduviids are concerned.

The comparison of means of distribution of 2n-number within subfamilies (Appendix Tests II-VII) strenghthens the argument that on the basis of karyotype numbers the Reduviinae and Stenopodinae are very close and different from Harpactorinae and related groups; also that the Triatominae is closer to the former than latter group. It appears that within the confines of autosome groups that have emerged, 2n-numbers are sufficiently restricted

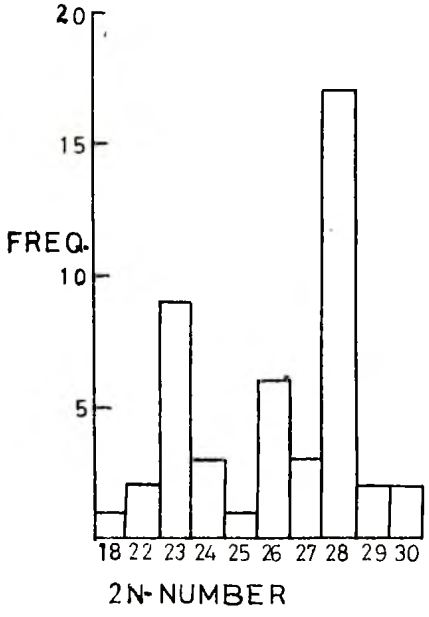
and consistent to be of definitive and systematic value (see later).

4.3 Heterogeneity of Reduviidae and the problem of unbalanced classification.

The distribution of 2n-numbers at family level (Reduviidae current composition) is multi-modal (Figs. 4.7 - 4.9); a comparison between means of diploid numbers from the present investigations and those from literature (two independent samples of Reduviidae), gave a significant difference at the 5% significance level. These clearly demonstrate the diversity of the group and suggest that the recognised morphological plasticity of Reduviidae extends to diploid numbers as well. The 2n-number/autosome groups discussed in 4.2 (above) however indicate a definite level of cytological modality or organisation within the family. The interesting point is that these groups as proposed here are not new.

Davis (1961, 1966, 1969) in his morpho-taxonomic review on Reduviidae suggested, on available morphological information, the grouping of Piratinae, Salyavatinae, Reduviinae, Stenopodinae, Emesinae, Vescilinae, Cetherinae, Chryxinae, Saicinae and

Fig 4.7 DISTRIBUTION OF 2N-NUMBERS IN THE SPECIES OF TROPICAL REDUVIIDAE WORKED ON IN THIS STUDY

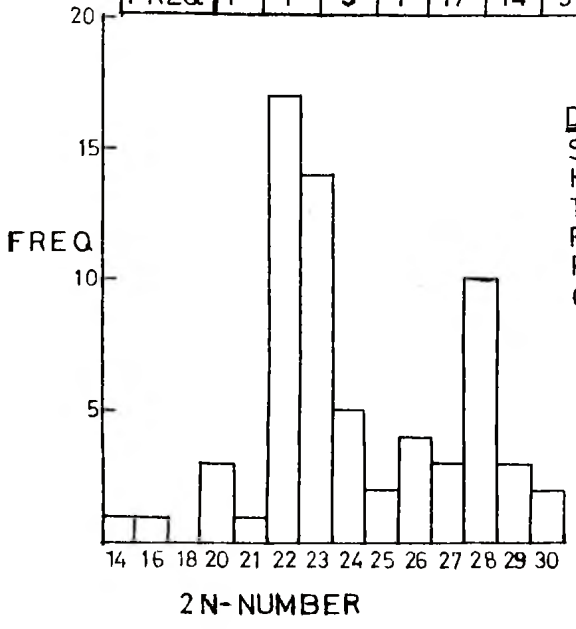


2N-NO.	18	22	23	24	25	26	27	28	29	30
FREQ.	1	2	9	3	1	6	3	17	2	2

DATA	%
STENOPODINAE	15.2
REDUVIINAE	26.1
HARPACTORINAE	52.2
OTHERS	6.5

Fig. 4.8 DISTRIBUTION OF 2N-NUMBERS IN 66 SPECIES OF REDUVIIDAE CYTOLOGICALLY STUDIED AND ALREADY PUBLISHED.

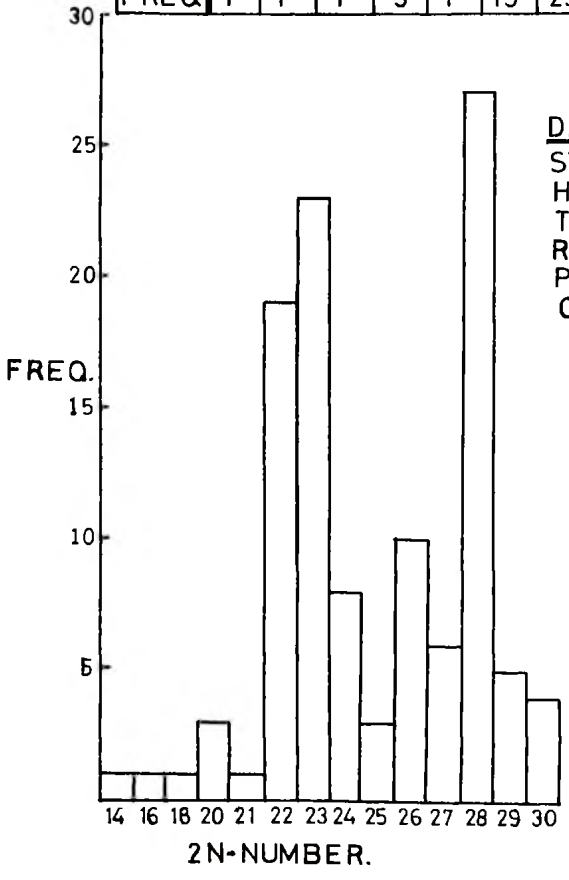
2N-NO.	14	16	20	21	22	23	24	25	26	27	28	29	30
FREQ.	1	1	3	1	17	14	5	2	4	3	10	3	2



DATA.	%
STENOPODINAE	7·6
HARPACTORINAE	30·3
TRIATOMINAE	42·4
REDUVIINAE	3·0
PIRATINAE	7·6
OTHERS	9·1

Fig. 4.9 DISTRIBUTION OF 2N-NUMBERS IN 112 SPECIES OF REDUVIIDAE CYTOLOGICALLY STUDIED TO DATE.

2N-NO.	14	16	18	20	21	22	23	24	25	26	27	28	29	30
FREQ.	1	1	1	3	1	19	23	8	3	10	6	27	5	4



DATA	%
STENOPODINAE	10.7
HARPACTORINAE	39.3
TRIATOMINAE	25.0
REDUVIINAE	12.5
PIRATINAE	4.5
OTHERS	8.0

Sphaeridopinae under a PIRATINE COMPLEX; those members of this group known cytologically(reported above) constitute the 20A - group of the present study. This however, excludes Emesinae as currently known. The affinities of Emesinae have not been much discussed and except for a casual mention of a close relationship of this subfamily to Saicinae (Wygodzinsky 1966), little else is known as far as affinities are concerned.

Davis also recognised the close relationship between Harpactorinae, Apiomerinae, Phaphidosominae, Tegeinae and suggested their re-organistion under a HARPACTORINE COMPLEX corresponding almost wholly to the 24A group of this study.

The above groupings have been supported by Kumar (1962) with work on genitalia and salivary glands of Cimicomorpha and by Louis and Kumar (1972) with investigations on alimentary and reproductive organs of Reduviidae.

Davis in his reviews (1961, 1966, 1969) commented on the close relationship between Ectrichodinae and Tribelocephalinae; and that of Phymatinae to Holoptilinae. Kumar (1962) linked these two groups by finding Tribelocephalinae closer

to Phymatinae especially its tribe Carcinocorini. These subfamilies (except Holoptilinae - no information available) constitute the 28A group referred to above.

From the foregoing discussion, a partial super-generic correspondence of morphology and karyotypes within Reduviidae is evident. With so much support to its credit, it seems opportune to effect this re-organization of the Reduviidae now. The benefits of such a re-organization to the subfamily as well as tribal classification in Reduviidae cannot be over-emphasized. However, to achieve homogeneity (morphological, cytological) at family level comparable to that of Pentatomidae, I suggest that the family Reduviidae be broken up and the 3 groups so far discussed constituted into three (3) new families:

a) PIRATIDAE to include Piratinae, Salyavatinae, Reduviinae Triatominae, Stenopodinae and probably Emesinae;

b) HARPACTORIDAE to include Harpactorinae, Rhaphidosominae and probably Apiomerinae;

c) PHYMATIDAE to include Phymatinae (Carayon et al. 1958), Tribelocephalinae and Ectrichodinae.

Further work is necessary to fit the remaining Reduviidae subfamilies into these groups.

Reduvoidea will then be made up of Piratidae, Phymatidae, Harpactoridae and Cimicidae.

4.4 Karyotype evolution; evidence from Reduviidae.

4.4.1 Origin of multiple sex-chromosomes:

It is assumed that whenever multiple sex-chromosomes are present, they have originated from a simple sex-chromosome mechanism: XO/XY. As to which of these two XO and XY came first is not evident. For heteropterans and other supposedly holokinetic groups, it is not clear the processes by which the multiple mechanisms are derived from the simpler forms.

In his analysis of Pentatomomorpha, Leston (1956, 1958) converted all multiple sex-elements to one, a simplification based on Troedsson (1944) and Schrader's (1947) postulate that multiple elements in a holokinetic system originated by simple fragmentation of the primitive sex-chromosome: XO. This suggests a pure line of sex-chromosome evolution different and removed from a pure line of autosomal-chromosome evolution. This certainly is not the case in monocentric chromosome systems of which Orthoptera is a vivid example. Holocentric chromosome systemsapparently are not simpler

than the former because there does not seem to be any obvious differences in the extent of karyotype variability in the two groups and Pentatomidae (Holokinetic) is a well known example (Halkka and Heinonen, 1966) of uniformity in chromosome numbers (White, 1969).

Also from the differences in the total sex-chromosome mass observed between different species in Harpactorinae's 24A + XXXY group and specifically within the genus Rhinocoris, (R. nitidulus and R. hutsebauti, standing out), and autosomal karyotype differences within the 24A unit (well illustrated in genus Phonoctonus) this does not seem to be the case.

It seems more likely that the new sex-mechanisms arose along related pathways as those of monocentric chromosomes with exchange of chromosomal material between autosomes and sex units of the karyotypes. Autosomal chromosome fragments surely play an important role in the modification of the number of sex-chromosomes. Duplication by non-disjunction also seems very possible. Simple fragmentation per se cannot account for the evolution of the Rhinocoris nitidulus sex karyotype from that

of the ancestral Rhinocoris stock represented by Rhinocoris hutsebauti, (24A + XY)

4.4.2 Karyotypes and relationships of Reduviidae to other groups of Heteroptera:

Discussing phylogenetic relationship in various families of Heteroptera, Manna (1958) and Banerjee (1958) concluded that the 2n-number 12A + XY represents the primitive karyotype in Heteroptera and that the evolution of Reduviidae from Lygaeoidea has been accompanied by an increase in the basic number of chromosomes and a change from a simple X to a multiple X condition. However heteropterists appear unanimous in their view that there is no evidence to support the evolution of Reduviidae from Lygaeoidea. The presence of similar karyotypes in these groups is probably a case of parallel evolution only.

Within Cicicomorphan series where reduviids clearly belong, Miridae as reported by Leston (1957), Kumar (1971), Akingbohungbe (1974) shows a modal 2n-number of 32A + XY within a 2n-number range of 14 to 80.

It is however intersting that Phylus melanocephalus belonging to the mirid subfamily Phylinae

(modal 2n-number for subfamily equals 32) has a diploid number of 16A + XY. Leston attributed this to a possible retention of a proto-mirid number. Nabidae which is thought to be the living group closest to this proto-mirid group (of generalized cimicids) have type 2n-number of 16A + XY (Leston 1957). China (1955) thinks Joppeicidae is a relic group representing an ancestral form of the Reduviidae. Carayon (1954, 1962) tried to show that Tingidae links Miridae and Reduviidae; and Drake & Slater (1957), Drake and Davis (1960)&Stys (1962) believe Thaumastocoridae has some reduvioid characters. Kumar (1964) argues against thaumastocorid - reduviid relationship. Unfortunately the karyotypes of Joppeicidae and Thaumastocoridae remain unknown. Tingidae (2 species known) exhibits 12A + XY and an a typical heretopteran meiosis: 1st division is reductional for both the sex-chromosomes and autosomes (Makino, 1951).

Unless we can explain away the current composition of the family Reduviidae by convergent evolution theory, the above suggestions tend to create a problem as regards the direction of

karyotype evolution. Morphological considerations (Davis; Kumar etc.) have established groups such as Tribelocephalinae, Holoptilinae, Phymatinae and Ectrichodinae as the ancestral, most primitive or least specialised of the family. Except for Holoptilinae on which no work has been reported yet, the other members of this group are characterized by high diploid numbers (23A + XY; 22A + XO). The association of the primitive sex-mechanisms XY/XO with these high autosomal units is noteworthy. Symmetry of karyotypes within Reduviidae seems to decrease with decreasing diploid number, making lower numbered karyotypes more assymmetrical. In his work on Ranunculaceae, Lewitsky (1931) pointed out the general prallelism of more symmetrical karyotypes with specialised forms. Further, other series of Heteroptera such primitive families as Belastomidae, Naucoridae, Nepidae, Notonectidae and Mesoveliidae also have high diploid numbers and usually an XY sex determining mechanism (Leston, 1958).

These trends are partially opposite to those suggested by Manna (1958) and Banerjee (1958). It appears more likely that reduviid subfamilies

arose from a 28A + XY stock by reductions of 2n-number. In this case, the presence within Harpactorinae of Polididus armatissimus with a diploid number 12A + XY and thought to be a relic of the ancestral stock (Jande 1960), could be due to unparallel cytological and phenotypical evolution; cytological changes being by sudden frangmentations, translocations, loss of autosomes etc., within this species. That means changes in external phenotype lagged behind karyotype changes. The posibility of such a situation is mentioned by Jackson (1971). In such a case it appears that only the autosomal elements evolved, unless the primitive sex-karyotype which appears to have persisted was re-developed, secondarily.

With this suggested direction of karyotype evolution within Reduviidae it appears that fragmentations, duplication, non-disjunctions, polysomy, fissions, fusions and losses all acting together or in various unit groups have played a part in the evolution of the Reduviid karyotype. The possibility of transient polyploidy and agmatoploidy in the distant evolutionary history of Heteropterans is not ruled out.

In the context of the above suggestions and the available cytological information, karyotype evolutionary order in Reduviidae seems to be Tribelocephalinae (most primitive), Ectrichodinae, Phymatinae, Rhaphidosominae, Harpactorinae Apiomerinae, Triatominae, Reduviinae, Stenopodinae and Emesinae apparently the most evolved (in this sequence).

The intermediate position, cytologically of the apparently most specialised groups of Reduviidae i.e. Harpactorinae and Rhaphidosominae is probably important to the solution of the problem.

Louis and Kumar (1972) established an order (external morphological) of increasing specialization among Reduviidae subfamilies: Tribelocephalinae, Ectrichodinae, Stenopodinae, Emesinae Salyavatinae, Piratinae, Reduviinae, Harpactorinae and Rhaphidosominae. In the absence of a good method of quantitative characterization and comparison of chromosomes of karyotypes, comparisons by DNA content determination will provide an interesting insight into the dynamics of genone material within the karyotypes. This might enlighten us on the questions of karyotype evolution and its direction in the Reduviidae.

Further, a closer study of karyotypically interesting species like those that belong to one morphological group - subfamily, but show affinity by diploid number etc. to another group e.g. Thodelmus addahensis (a stenopodine showing a harpactorine 2n-number) might be of interest.

4.5 Holokinetic Theory:

The V-shape, with the apices of the Vs towards poles, of separating bivalents at anaphase I and especially anaphase II was evident in most squashes of Reduviinae and Stenopodinae species. This as Manna (1951) pointed out tends to suggest a monocentric nature of chromosomes and discredit the holokinetic theory. Also the greater similarities being shown in the directions of change for the two chromosome forms tends to suggest much closer structural forms in monocentric and supposedly holocentric chromosomes than under the current theories.

SUMMARY

1. 46 species of male tropical reduviids belonging to 6 subfamilies collected in Southern Ghana (i.e. between latitudes $5^{O}N$, $8^{O}N$ and longitudes $2^{O}W$, $1^{O}E$) were cytologically investigated.

2. Course of meiosis was found to be typically heteropteran in all species except Tetroxia nigrospinosa Villiers (Reduviinae) in which the path of meiosis is not clear. The spermatogonial chromosome numbers (2n) sex determining mechanism etc of all the species are discussed.

3. Pictures and tracings of karyotypes observed for each species are presented as plates along with the localities from which the insects were collected. Information gathered was pooled with the information in literature (giving a pool of 12 subfamilies), analyzed and discussed. An attempt was made to use quantitative methods to compare 2n-number distribution in the subfamilies.

4. Reduviinae was found to exhibit diploid numbers ranging from 18-30 of which the modal number is 23. A stable autosome range of 16A - 26A was found in the subfamily.

Sex chromosome mechanisms also range from XY - 4X + Y; 3X + Y was not recorded. 14 species from Reduviinae are now known cytologically, 12 of these being a contribution of this study. Most common autosome group was found to be 20A (35.7%) and XY as the most common sex-mechanism.

5. 12 species of Stenopodinae are known cytologically 7 being from this study. Sex chromosome mechanisms range from XXY - 4X + Y and autosomes from 20A - 24A. The modal 2n-number was calculated as 23 = 20A + XXY.

6. The subfamily Salyavatinae was investigated for the first time. 2n-number in 2 species, Lisarda vandenplasi and Petalocheirus rubiginosus were found be 23 + 20A + XXY and 22 = 20A + XY respectively.

7. Most common 2n-number for the 29 species of Triatominae investigated by Ueshima (1966) was 22 = 20A + XY within a range of 20-25.

8. All five (5) species of Piratinae investigated by Jande (1959) and Banerjee (1959) had 20 autosomes and differed only in sex chromosome mechanism which ranged from XY - XXY.

9. Karyotypes of 43 species of Harpactorinae are known cytologically 23 being from this study. Autosome numbers were found to be within the range 12-26 with 24A easily the commonest. The 2n-number range was found to be 14-30 with 28 = 24A + XXXY dominating.

10. Phymatinae and Ectrichodinae are represented by single species each with 2n-number 30 = 28A + XO in the males.

11. 2 species of Apiomerinae investigated by Payne (1912) and White (1951) all had 2n-number 24 = 22A + XY.

12. Emesiaae are represented by 2 species (Ueshima 1963). Barce fraferna (Baker) was found to be 20 = 18A + XY and Empicoris rubromaculatus (Blackburn) had 16=14A+XY.

13. Tribelocephalinae was investigated for the first time. The species Tribelocephala curticornis Villiers was found to have the 2n-number as 30 = 28A + XY.

14. 2 species of Rhaphidosominae are known cytologically. Lopodytes quadrispinosa reported by Louis and Kumar (1973) and Rhaphidosoma truncatum reported in this study were found to exhibit 2n-numbers of 27 =

24A + XXY and 26 = 24A + XY respectively.

15. An apparent rarity of differences in autosome number between related species emerged. From this it was concluded that cytological groupings based on autosome numbers rather than on conventional 2n-numbers were on firmer grounds at least in Reduviidae. Three (3) groups were recognised for the family Reduviidae. Within these, 2n-numbers appeared sufficiently restricted and consistent to be of definitive and systematic value.

16. The 3 autosome groups proposed, 20A, 24A and 28A were found to have a close parallelism to those morphological groups proposed earlier by Davis (1957, 1961, 1966, 1969) and Louis and Kumar (1973). On this ground it was suggested that a re-organization of the sub-families of Reduviidae be effected based on these groups. The ultimate aim of this to be achieving homogeneity (both morphological and cytological) at family level comparable to that of Pentatomidae.

17. 3 new families are suggested: PIRATIDAE including Piratinae, Salyavatinae, Reduviinae

Triatominae, Stenopodinae and probably Emesinae; HARPACTORIDAE with Harpactorinae, Rhaphidosominae; and probably Apiomerinae; and PHYMATIDAE grouping Phymatinae (Carayon et al, 1958), Tribelocephalinae and Ectrichodinae. Further work on other subfamilies of Reduviidae was recommended to help fit them into the proposed groupings.

18. It was suggested that reduviid subfamilies arose from a 28A + XY stock by reduction of diploid number. If one accepts this direction of karyotype evolution, the subfamilies can be put in the following order of evolution: Tribelocephalinae (most primitive), Ectrichodinae Phymatinae, Rhaphidosominae, Harpactorinae, Apiomerinae, Triatominae, Reduviinae, Stenopodinae and Emesinae apparently the most evolved (in this sequence).

19. A systematic DNA measurement and a closer study of karyotypically interesting species was recommended as it was considered important for determination of the dynamics of genome material within the family Reduviidae. A review of the Holokinetic theory was also advocated.

26. Louis (1974a & b) found that the three colour forms of Rhinocoris bicolor (Fab) do not interbreed. The genitalia morphology and the karyotypes of these colour forms were studied and it was concluded that they are really three (3) distinct species. The following names were proposed : R. bicolor (Fab) (white form); R. ghaurii n. sp.(red, orange form) and R. louisii n. sp. (yellow form).

REFERENCES

Akingbohungbe, A.E. 1974. Chromosome numbers of some North-American Mirids (Heteroptera : Miridae). Can. J. Genet. and Cytol. 16: 251-256.

Amyot, C.J.B. & Serville, A. 1843. Histoire Naturelle des Insectes, Hemipteres, Paris.

Banerjee, M.R. 1958. A study of the chromosomes during meiosis in twenty-eight species of Hemiptera (Heteroptera, Homoptera). Proc. Zool. Soc. Calcutta. 11 : 9 - 31.

Barth, R. 1956. Estudos anatomicos e histologicos sobre a subfamilia Triatominae (Heteroptera, Reduviidae). V. Anatomia do testiculo e espermio-citogenese do Triatoma infestans. Mem. Inst. Osw. Cruz 54 : 135 - 229.

Buck, R.C. 1967. Mitosis and meiosis in Rhodnius prolixus: The fine structure of the spindle and diffuse kinetochore. J. Ultrastruct. Res. 18 : 489 - 510.

Carayon, J. 1954. Organes assumant les fonctions de la spermatheque chez divers Heteroptères. Bull. Soc. Zool. France. 79: 189-197.

Carayon, J., Usinger, P.L. and Wygodzinsky, P. 1959. Notes on the higher classification of the Reduviidae with description of a new tribe of the Phymatidae (Hemiptera : Heteroptera). Rev. Zool. Bot. Afr. 57: 256 - 281.

Chandra, H.G.S. 1962. Inverted meiotic sequence in triploid females of the mealy bug Planococcus citri Ph.D. Thesis Univ. of Calif.

China, W.E. 1955. A reconsideration of the systematic position of the family Joppeicidae Reuter (Hemiptera-Heteroptera) with notes on the phylogeny of the suborder. Ann. Mag. Nat. Hist. 8 : 353-370.

China, W. & Miller, N. 1959. Check-list and keys to the families and subfamilies of the Hemiptera-Heteroptera. Bull. Brit. Museum (Nat. History),Entomology 8: 1 - 45.

Davis, N.T. 1957. Contributions to the morphology and phylogeny of the Reduvioidea (Hemiptera: Heteroptera). Part I. The morphology of the abdomen and genitalia of Phymatidae. Ann. Ent. Soc. Amer. 50: 432 - 443.

Davis, N.T. 1961. Contributions to the morphology and phylogeny of the Reduvioidea (Hemiptera: Heteroptera). Part II. Wing venation Ibid 54: 340 - 350.

Davis, N.T. 1966. Contributions to the morphology and phylogeny of the Reduvioidea (Hemiptera: Heteroptera). Part III. The male and female genitalia. Ibid 59: 911 - 923.

Davis, N.T. 1969. Contributions to the morphology and phylogeny of the Reduvioidea (Hemiptera: Heteroptera). Part IV, The harpactoroid complex. Ibid 62: 74 - 94.

Drake, C.J. and Davis, N.T. 1960. The morphology, phylogeny and higher classification of the family Tingidae, including the description of a new genus of the subfamily Vianaidinae. Ent. Aner. 39: 1 - 100.

Drake, C.J. and Slater, J.A. 1957. The phylogeny and systematics of the family Thaumastocoridae (Hemiptera: Heteroptera). Ann. Ent. Soc. Amer. 50: 353 - 370.

Halkka, O. & Heinonen, L. 1966. Chromosome numbers in 20 American or Sudanese leaf hoppers, with notes on the role of cytology in Homopteran taxonomy. Ann. Ent. Fennicae 32: 11 - 19.

Henning, W. 1966. Phylogenetic systematics. University of Illinois Press, Ubana.

Hewitt, G. and G. Schroeter, 1968. Population cytology of Oedaleonotus: The Karyotypic Facies of Oedaleonotus enigma (Scudder). Chromosoma (Berl.) 25: 212 - 140.

Hughes-Schrader, S. 1944. A primitive coccid chromosome cycle in Puto sp. Biol. Bull. 87: 167 - 176.

Hughes-Schrader, S. 1948. Cytology of coccids (Coccoidea-Homoptera) Adv. Genet. 2: 127-203.

Hughes-Schrader S. 1955. Chromosomes of the gaint scale Aspidoproctus maximus (Coccoidea-Margarodidae) with special reference to asynapsis and sperm formation. Chromosoma (Berl.) 7: 420 - 438.

Hughes-Schrader, S. & Schrader, F. 1961. The kinetochore of the Hemiptera. Chromosoma 12: 327 - 50.

Jackson, R. 1971. Karyotype in systematics. Ann. Rev. Ecol. Syst. 2: 327 - 368.

Jande, S.S. 1959a. An analysis of the chromosomes in the four species of the family Belastomatidae (Heteroptera, Cryptocerata). Res. Bull. Panj. Univ. 10: 25 - 34.

Jande, S.S. 1959b. Chromosome number and sex mechanism in twenty-seven species of Indian Heteroptera. Res. Bull. Panj. Univ. 10: 215 - 217.

Jande, S. 1960. Chromosome mechanism in Polididus armatissimus (Reduviidae : Heteroptera). Separatum Experientia 16: 440 - 441.

Ed: Jacobs, P.A., Price, W.H. & P. Law. Human population cytogenetics, Pfizer Medical Monograph 5, Edinburgh University Press, Edinburgh (1970).

Jeannel R. 1919. Voyage de Ch. Alluaud et R. Jeannel en Afrique Orientale. Insectes Hemipteres III.

John, B. & G.M. Hewitt, 1968. Patterns pathways and process of chromosome evolution in Orthoptera. Chromosoma (Berl.) 25: 40 - 74.

Kumar, R. 1962. Morpho-taxonomic studies on the genitalia and salivary glands of some Cimicomorpha (Rhynchota, Hemiptera). Tijdschrift Voor Entomologie 105: 1 - 23.

Kumar, R. 1971. Chromosomes of cocoa-capsids (Heteroptera: Miridae). Caryologia 24: 229 - 237.

La Cour, L.F. 1955. The Luzula systems analysed by X-rays, Heredity, Suppl. 6: 77 - 81.

Leston, D. 1957. Cytotaxonomy of Miridae and Nabidae (Hemiptera). Chromosoma (Bd) 8: 5609 - 616.

Leston, D. 1956 (58). Chromosome number and systematics of Pentatomomorpha (Hemiptera). Proceedings Tenth International Congress of Entomology, Montreal 2: 911-918.

Leston, D. 1970. Entomology of the cocoa farm. Ann. Rev. Ent. 15: 273 - 294.

Leston, D., Pendergrast and Southwood, T.R.E. 1954. Classification of the terrestrial Heteroptera (Geocorisae). Nature 174: 91-92.

Lewitsky, G. 1931. The karyotype in systematics. Bull. Applied Bot. Genet. Plant Breeding. 27: 220 - 40.

Louis, D. 1974a. Life Cycle of immature stages of the Reduviidae (Hemiptera: Heteroptera) of the cocoa farms of Ghana. J. Ent. Soc. Nigeria 13: 3 - 54.

Louis, D. 1974b. Biology of Reduviidae of the cocoa-farms in Ghana. Am. Nat. 91: 68 - 89.

Louis and Kumar, 1972. Morphology of the alimentary and reproductive organs in Reduviidae (Hemiptera: Heteroptera) with comments on interrelationships within the family. Ann. Ent. Soc. Amer. 66/3: 635 - 639.

Makino, S. 1951. An atlas of the chromosome numbers in animals. Iowa State College Press, Ames, Iowa.

Manna, G.K. 1950. Multiple sex-chromosome mechanism in a reduviid bug, Conorhinus rubrofasciatus (de Geer). Proc. Zool. Soc. Bengal 3: 155 - 161.

Manna, G.K. 1951. Chromosomes of Indian Heteroptera. A study of chromosomes during meiosis in 43 species. Proc. Zool. Soc. Bengal, 4: 1 - 116.

Manna, G.K. 1956 (1958). Cytology and inter-relationships between various groups of Heteroptera. Proceedings Tenth Int. Congress of Entomology, 2: 919 - 934.

Manna, G.K. 1962. A further evaluation of the cytology and inter-relationships between various groups of Heteroptera. Nucleus 5: 7 - 28.

Miller. N.C.E. 1955. The synonymy of Eupheno Gistel (Hemiptera-Heteroptera-Reduviidae-Reduviinae) and the description of a new subfamily. Ann. Mag. Nat. Hist. (12) 8: 449-452.

Miller, N.C.E. 1956. A new subfamily of Reduviidae from the Solomon Islands. Ann. Mag. Nat. Hist. (12) 9: 587 - 590.

Mittwoch, U. 1967. Sex chromosomes. Academic Press, London and New York.

Montgomery, T.H. 1901. A study of the chromosomes of the germ cells of the metazoa. Trans. Amer. Phil. Soc. 20: 154 - 236.

Montgomery, T.H. 1902. A study of the chromosomes of the germ cells of Metazoa. Tr. Amer. Phil. Soc. 20: 154 - 230.

Montgomery, T.H. 1906. Chromosomes in the spermatogenesis of the Hemiptera-Heteroptera. Ibid. 21: 97 - 173.

Montgomery, T.H. 1910. On the dimegalous sperm and chromosomal variation of Fuschistus with reference to chromosomal continuity. Arch. Zellforschg Leipzig 5: 120 - 145.

Nordenskjold, H. 1961. Tetrad analysis and the course of meiosis in three hybrids of Luzula campestris. Hereditas (Lund). 47: 203 - 238.

Parshad, R. 1957a. Cytological studies in Heteroptera; III. A comparative study of chromosomes in the male germ-cells of eleven species of the sub-family Pentatominae. Research Bulletin, Panjab University 122: 401 - 420.

Parshad, R. 1957b. Cytological studies in Heteroptera: Chromosome Complement and meiosis in 26 species of Pentatomoidea, Lygaeoidea Coreoidea with considerations of cytological bearing on the status of these superfamilies. Research Bulletin, Panjab University No. 133: 521 - 559.

Payne, F. 1909. Some new types of chromosome distribution and their relation to Sex. Biol. Bull. Woods Hole. 16: 119 - 166.

Payne, F. 1910. The chromosomes of Acholla multispinosa. Biol. Bull. Woods Holt. 18: 174 - 179.

Payne, F. 1912. A further study of the chromosomes of Reduviidae. II. The nucleolus in the young oocytes and the origin of the ova in Gelastocoris. J. Morph. 23: 331-347.

Ris, H. 1942. A cytological and experimental analysis of the meiotic behaviour of the univalent X. chromosome in the bearberry aphid Tamalia (=Phyllaphis) coweni. J. exp. Zool. 90: 267 - 326.

Ryckman, R.E. 1962. Biosystematics and hosts of the Triatoma protracta complex (Hemiptera: Reduviidae) (Rodentia: Cricetidae). Univ. Calif. Publ. Ent. 27: 93 - 240.

Schrader, F. 1947. The role of kinetochore in the chromosomal evolution of the Hemiptera and Homoptera. Evolution 1: 134 - 142.

Schraeder, F. and Hughes-Schraeder, S. 1956. Polyploidy and fragmentation in the chromosomal evolution of various species of Thyanta (Hemiptera). Chromosoma 7: 469 - 496.

Schreiber, G., J. Pellegrino, 1950. Eteropicnosi do autosomi come possible mechanismo di speciazione (Ricerche citologiche su alcumi Emitteri neotropici). Sci. Genet. 3: 215 - 226.

Smith, S.G. 1943. Techniques for study of insect chromosomes. Canadian Entomologist 2: 21 - 34.

Stride, G.O. (1954). On the specific status of Phonoctonus subimpictus Stål. Rev. Zool. Bot. Afr. I, 1 & 2: 13 - 17.

Stys, P. 1962. Venation of metathoracic wings and notes on the relationships of Microphysidae (Heteroptera) Acta. Soc. Ent. Czechoslov. 59: 234 - 239.

Troeddson, P. 1944. The behaviour of the compound sex chromosomes in the females of certain Hemiptera, Heteroptera. J. Morph. 75: 103 - 147.

Ueshima, N. 1963a. Chromosome behaviour of the Cimex pilosellus complex (Cimicidae: Hemiptera). Chromosoma (Berl.) 14: 511-521.

Ueshima, N. 1963b. New techniques in cytotaxonomy. Chromosome Information Service 4: 17 - 18.

Ueshima, N. 1966. Cytotaxonomy of the Triatominae (Reduviidae: Hemiptera). Chromosoma (Berl.) 18: 97 - 122.

Ueshima, N. 1967. Supernumerary chromosomes in the human Bed Bug Cimex lectularius Linn. (Cimicidae: Hemiptera). Chromosoma (Berl.) 20: 311 - 331.

Usinger, R.L. 1943. A revised classification of the Reduvioidea with a new subfamily from South America. Ann. Ent. Soc. Amer. 36: 602 - 618.

Usinger, R.L. 1944. The Triatominae of North and Central America and the West Indies and their public health significance Publ. Hlth. Bull., 288: 1 - 83.

Villiers, F. 1948. Faune de l'Empire Francais IX. Hemipteres Reduviides de l'Afrique Noire. Paris Office de la Recherche Scientifique Coloniale.

Warren et al*

White, M.J.D. 1940. The origin and evolution of Multiple Sex-Chromosome mechanisms. J. Genet. 40: 303 - 336.

White, M.J.D. 1951. Structural heterozygosity in natural populations of the grasshopper Trimerotropis sparsa. Evolution 5: 376-394.

White, M.J.D. 1951. A cytological survey of wild populations of Trinerotropis and Circotettix (Orthoptera, Acrididae). II. Racial differentiation in T. sparsa. Genetics 36: 31 - 53.

White M.J.D. 1954. Animal cytology and evolution '2nd ed. Cambridge University Press, London and New York.

White, M.J.D. 1956. Cytogenetics and Systematic Entomology. Ann. Rev. Ent. 2: 71 - 90.

White, M.J.D. 1969. Chromosomal rearrangement and speciation in animals. Ann. Rev. Genet. 3: 75 - 98.

Wigglesworth, V.B. 1936. The function of the corpus allatum in the growth and reproduction of Rhodnius prolixus (Hemiptera) Quart. J. micr. Sci., London 79: 91 - 122.

William, G. 1954. Field observations on the cocoa mirids Sahlbergella singularis Hagl. and and Distantiella theobroma (Dist.) in the Gold Coast. Part III. Population Fluctuations. Bull. Ent. Res. 45: 723-744.

Wilson, E.B. 1911. Studies on chromosomes VII. A review of the chromosomes of Nezara; with some more general considerations. J. Morph. 22: 71 - 110.

Wygodzinsky, P. 1951. Contribucion al concocimiento del genero Metapterus Costa, 1860 de las Americas y de Juan Fernandez (Hemiptera Reduviidae). Rev. chil. Ent. 1: 113 - 138.

Wygodzinsky, P. 1966. A monograph of the Emesinae (Reduviidae: Hemiptera). Bull. Am. Mus. Nat. Hist. 133: 1 - 614.

Xavier, A.C.M. 1945. Caryologia comparada de alguns Hemipteros Heteroptros (Pentatomideos e Coreideos). Mem. Est. Mus. Zool. Univ. Coimbra, 163: 1 - 105.

* Warren, E.M., Gassner, G. and Breland, O.P. 1960 Somatic chromosomes of praying mantids as shown by the squash technique. Texas Reports on Biology and Medicine. 18 : 674 - 679.

APPENDIX TABLE I: Chromosome complements of male Reduviidae in literature.

Species	Chromosome Formula 2n number	Author
SUBFAMILY: EMESINAE		
Barce fraferna (Baker)	18A+XY	Ueshima, 1963 b
Empicoris rubromaculatus (Blackburn)	14A+XY	Ueshima, 1963 b
SUBFAMILY: STENOPODINAE		
Oncocephalus impudicus Reuter	20A+XXY	Jande, 1959 a
Oncocephalus sp. A	20A+XXY	Jande, 1959 a
Oncocephalus sp. B	20A+XXXY	Jande, 1959 a
Prirontis modesta (Banks)	20A+XXXXY	Payne, 1912
Pygolampis foeda Stål	22A+XXY	Jande, 1959 a
SUBFAMILY: REDUVIINAE		
Pasiropsis sp.	24A+XXXXY	Jande, 1959 b
Reduvius personatus (L)	20A+XY	Payne, 1912
SUBFAMILY: TRIATOMINAE		
Dipetalogaster maximus (Uhler)	20A+XY	Ueshima, 1966
Ponstrogylus lesseri (Wygodzinsky)	20A+XXY	Ueshima, 1966
Ponstrogylus megistus (Busmeister)	18A+XY	Schreiber & Pellegrino 1950
Paratriatonea hirsuta Barber	18A+XXY	Barth, 1957

Psammolestes coreodes Bergroth	20A+XY	Ueshima, 1966
Rhodnius oneglectus Lent	10A+XY	Schreiber & Pellegrino, 1950
Rhodnius prolixus (Stål)	20A+XY	Barth, 1957; Ueshima, 1966 Ryckman 1962
Triatoma barberi Usinger	20A+XY	Ueshima 1966
Triatoma brasiliensis Neiva	20A+XY	Schreiber & Pellegrino, 1950
Triatoma delpontei Roman & Abalos	20A+XY	Ueshima, 1966
Triatoma dimidiata (Latreille)	20A+XY	Schreiber & Pellegrino, 1950
Triatoma eratyrusiforme Del Pente	20A+XXXY	Ueshima, 1966
Triatoma gersbaeckeri (Stål)	20A+XXY	Ueshima, 1966
Triatoma infestans (Klug)	20A+XY	Barth, 1957,1959
Triatoma maculata (Erichson)	20A+XY	Ueshima, 1966
Triatoma nitida Usinger	20A+XY	Schreiber,& Pellegrino, 1957
Triatoma patagonica Del Ponte	18A+XY	Schreiber & Pellegrino, 1957
Triatoma penninsularis Usinger	20A+XXY	Ueshima, 1966
Triatoma phyllosoma pallidopennis (Stål)	20A+XXY	Ueshima, 1966
Triatoma platensis Neiva	20A+XY	Schreiber & Pellegrino, 1950
Triatoma protracta Uhler	20A+XXY	Ueshima 1966
Triatoma rubida Uhler	20A+XXY	Ueshima, 1966
Triatoma rubrofasciata (De Geer)	22A+XXY	Manna, 1950

Triatoma rubrovaria (Blanchand)	20A+XY	Schreiber & Pellegrino, 1950
Triatoma sanguisuga (Leconte)	20A+XXY	Payne, 1909,1912
Triatoma sinaleensis Ryckman	20A+XXY	Ueshima, 1966
Triatoma sordida (Stål)	20A+XY	Barth, 1956, Ueshima, 1966
Triatoma vetticeps (Stål)	20A+XXXY	Barth, 1957
SUBFAMILY: APIOMERINAE		
Apiomeris crassipes (Fab.)	22A+XY	Payne, 1912
Apiomeris spinnipes	22A+XY	White, 1951
SUBFAMILY: PIRATINAE		
Androclus pictus (Herrich-Schaeffer)	20A+XY	Jande, 1959 b
Ectomocoris atrox Stål)	20A+XY	Banerjee, 1959
Ectomocoris cordiger Stål	20A+XXY	Banerjee, 1959
Ectomocoris ochropterus Stål	20A+XXY	Banerjee, 1959
Sirthenea sp.	20A+XY	Jande, 1959 b
SUBFAMILY: RHAPHIDOSOMINAE		
Lopodytes quadrispinosus Villiers	24A+XXY	Kumar & Louis 1972
SUBFAMILY: HARPACTORINAE		
Acholla multispinosa (De Geer)	20A+XXXXXY	Troeddson. 1944 Montgomery 1901, 1906, 1910, Payne, 1910
Arilus cristatus (Linnaeus)	24A+XXXY	Troeddson, 1944
Coranus fuscipennis Reut	24A+XXY	Banerjee, 1959

Fitihia spinulesa (Stål)	24A+XXY	Payne, 1909
Harpacto fuscipes (Fab.)	24A+XXXY	Manna, 1951
Harpactor marginatus	24A+XXXY	Banerjee, 1959
Hediocoris tibialis (Stål)	24A+XXXY	Jande, 1960
Sinea diadema (Fab.)	24A+XXXXXY	Montgomery, 1901, 1906, 1910
Sinea rileyi	24A+XXXXXY	Payne, 1912
Sinea spinipes	24A+XXXY	Payne, 1909,1912
Sphedanolestes (Aula) leucocephalus (Fab)	24A+XXXY	Kumar & Louis 1972
Syncanus collaris Fab	24A+XXXY	Banerjee, 1959
Staliastes rufus De Castelnau	24A+XY	Jande, 1959
Syncanus sp.	24A+XXXY	Manna, 1951
Velinus nodipes Uhler	24A+XXXY	Toshioka, 1933
Zelus exsangius (Stål)	24A+XY	Payne, 1909
Polididus armatisssamus	10A+XY	Toshioka, 1936
	12A+XY	Jande, 1960
Pselliopus cinctus (Fab.)	24A+XXXY	Payne, 1912
Rhinocoris rapax (Stål)	26A+XXY	Kumar & Louis, 1972
Rocconata annulicornis (Steil)	24A+XXY	Payne, 1909
Sinea confusa	24A+XXXY	Payne, 1909
Sinea complexa	24A+XXXY	Payne, 1909,1912

SUBFAMILY: ECTRICHODINAE		
Ectrichodes dispar Reuter	28A+XO	Manna, 1951
SUBFAMILY: PHYMATINAE*		
Phymata wolffi	28A+XO	Montgomery, 1906, 1907

*The systematic arrangement is based on Carayon et al (1958).

APPENDIX TABLE II: Dimensions of Rhinocoris bicolor (Fab) colour-forms (Males, 10 individuals per sample).

	ORANGE/RED (mm)	WHITE(mm)	YELLOW (mm)
Body Length	14.60 -18.60	12.60 - 15.00	11.40-15.60
	m 15.80±2.00	m 14.00±1.20	m 13.34±2.10
Head Length	2.80 - 3.10	2.50 - 3.00	2.65 - 2.95
	m 2.87±.15	m 2.79±.25	M 2.80±.15
Head Width	1.45 - 1.65	1.35 - 1.55	1.40 - 1.55
	m 1.53±1.00	m 1.48±.10	m 1.47±0.7
Eye Length	0.60 - 0.75	0.65 - 0.80	0.65 - 0.70
	m 0.68±0.8	m 0.73±.07	m 0.68±.03
Eye Width	0.30 - 0.35	0.30 - 0.40	0.30 - 0.40
	m 0.34±.03	M 0.36±.05	m 0.35±.05
Inter-ocular	0.80 - 1.00	0.75 - 0.85	0.75 - 0.85
(Width)	m 0.90±.10	m 0.83±.05	m 0.84±.05
Pronotum	1.05 - 1.45	1.10 - 1.25	1.00 - 1.25
(Length)	m 1.23±.20	m 1.16+.07	m 1.11±.12
Mesonotum	1.85 - 2.35	1.55 - 2.00	1.65 - 2.10
(Length)	m 2.09+.25	m 1.82±.22	m 1.844±.22
Scutellum	0.75 - 1.45	0.70 - 1.10	0.65 - 1.40
(Length)	m 1.11±.35	m 0.90±.20	m 0.98±.37
Pronotum	1.90 - 2.60	1.75 - 2.25	1.70 - 2.35
(Width)	m 2.18+.35	m 1.99±.25	m 2.00±.33

Mesonotum		3.55 - 4.55	3.10 - 3.80	3.25 - 4.05
(Width)		m 3.95±.50	m 3.54±.40	m 3.58±.40
Rostrum	a	1.25 - 1.60	1.10 - 1.50	1.25 - 1.30
		m 1.31±.15	m 1.27±.20	m 1.27±.03
	b	1.40 - 1.90	1.35 - 1.60	1.25 - 1.50
		m 1.61±.25	m 1.48±.13	m 1.39±.13
	c	0.50 - 0.65	0.50 - 0.55	0.45 - 0.50
		m 0.56±.07	m 0.52±.03	m 0.48±.03
Antennal	a	3.25 - 3.85	3.60 - 4.05	3.60 - 4.00
Segments		m 3.68±.30	m 3.85±.22	m 3.87±.20
	b	1.25 - 1.50	1.20 - 1.35	1.20 - 1.25
		m 1.35±.13	m 1.26±.07	m 1.23±.03
	c	2.20 - 2.27	1.90 - 2.05	2.10 - 2.50
		m 2.53±.27	m 1.98±.07	m 2.33±.20
	d	3.10 - 5.00	3.75 - 4.60	4.60 - 4.75
		m 4.07±.45	m 4.21±.42	m 4.68½.07
Forelegs	a	4.70 - 4.85	4.55 - 4.70	4.25 - 5.05
		m 4.79±.07	m 4.63±.07	m 4.60±.40
	b	4.95 - 5.25	4.80 - 5.13	4.45 - 5.50
		m 5.04±.15	m 4.90±.16	m 4.87±.03
	c	0.40 - 0.70	0.45 - 0.50	0.45 - 0.50
		m 0.54±.15	m 0.46±.03	m 0.47±03

	d	0.50 - 0.65	0.60 - 0.65	0.55 - 0.70
		m 0.57±.07	m 0.63±.03	m 0.63±.07
Midlegs	a	3.60 - 4.90	3.65 - 3.75	3.35 - 5.00
		m 4.36±.75	m 3.68±.05	m 3.97±.80
	b	4.10 - 5.15	4.30 - 4.95	3.75 - 5.40
		m 4.53±.50	m 4.12±.33	m.37±.80
	c	0.40 - 0.45	0.40 - 0.35	0.38 - 0.50
		m 0.42±.03	m 0.38±.03	m 0.44±.06
	d	0.50 - 0.65	0.55 - 0.65	0.60 - 0.65
		m 0.58±.07	m 0.60±.05	m 0.63±.03
Hindlegs	a	4.95 - 5.70	5.00 - 5.25	4.15 - 4.85
		m 5.40±.33	m 5.08±.13	m 4.57±.35
	b	6.35 - 7.15	6.05 - 6.40	4.65 - 5.90
		m 6.81±.40	m 6.23±.17	m5.47±.33
	c	0.45 - 0.55	0.40 - 0.50	0.40 - 0.45
		m 0.49±.05	m 0.45±.05	m 0.42±.03
	d	0.55 - 0.75	0.60 - 0.65	0.55 - 0.70
		m 0.63±0.10	m 0.62±.03	m 0.62±.07

APPENDIX TABLE III DISTRIBUTION OF 2N-NUMBERS

2n.n FREQ	14	16	18	20	21	22	23	24	25	26	27	28	29	30	SAMPLE SIZE	$\bar{X}$	SOURCE OF DATA
	1	1	-	3	1	17	14	4	2	4	3	10	3	2	66	24.07	REDUVIIDAE LITERATURE
	-	-	1	-	-	2	9	3	1	6	3	17	2	2	46	26.02	REDUVIIDAE KPORDUGBE IN THIS STUDY
	-	-	1	-	-	2	4	2	-	2	-	-	2	1	14	24.43	REDUVIINAE LITERATURE AND KPORDUGBE
	1	-	-	-	-	-	-	-	-	7	5	27	2	2	44	27.39	HARPACTORINAE LITERATURE AND KPORDIGBE'
	-	-	-	-	-	-	6	2	3	-	1	-	-	-	12	24.00	STENOPODINAE LITERATURE AND KPORDUGBE'
	-	-	-	1	1	15	9	2	1	-	-	-	-	-	29	22.45	TRIATOMINAE UESHIMA (1966)

APPENDIX TABLE IV: Mean and variance of 2n-numbers published before this study (LITERATURE SAMPLE)

X_1	X_1^2	f_1	$X_1 f_1$	$X_1^2 f_1$
14	196	1	14	196
16	256	1	16	256
18	324	0	0	0
20	400	3	60	1200
21	441	1	21	441
22	484	17	374	8228
23	529	14	322	7406
24	576	5	120	2880
25	625	2	50	1250
26	676	4	104	2704
27	729	3	81	2187
28	784	10	280	7840
29	841	3	87	2523
30	900	2	60	1800

$f_1 = \underline{66}$; $X_1 f_1 = \underline{1589}$; $X_1^2 f_1 = \underline{3899}$;

Mean: $\bar{X}1 = \frac{f1X1}{f_1} = 24.07$ where $f = n$

Variance: $S_1^2 = \frac{f_1 X_1^2 - n\bar{x}_1^2}{n - 1} = \frac{38911 - 66 \times 579.64}{66 - 1}$

$= \frac{654.8}{65} = \underline{10.07}$

APPENDIX TABLE V: Mean and variance of 2n-numbers from this study.

X_2	X_2^2	f_2	X_2f_2	$X_2^2f_2$
14	196	0	0	0
16	256	0	0	0
18	324	1	18	324
20	400	0	0	0
21	441	0	0	0
22	484	2	44	968
23	529	9	207	4761
24	576	3	72	1728
25	625	1	25	625
26	676	6	156	4056
27	729	3	81	2187
28	784	17	476	13328
29	841	2	58	1682
30	900	2	60	1800

$f_2 = X_2f_2 = 1197 \quad X_2^2f_2 = 31459$

Mean: $\bar{X}_2 = \frac{1197}{46} = \underline{26.02}$

Variance: $S_2^2 = \frac{f_2 X_2^2 - n\bar{x}_2^2}{n - 1} = \frac{31,459 - 46 \times 677.13}{46 - 1}$

$= \frac{31459 - 31148}{45}$

$= \frac{311}{45} = \underline{6.91}$

APPENDIX TABLE VI : REDUVIINAE; Mean and variance of 2n-numbers for the subfamily

X_1	X_1^2	f_1	$X_1 f_1$	$X_1^2 f_1$
14	-	-	-	-
15	-		-	-
16	-	-		-
17	-	-		-
18	324	1	18	324
19	-	-	-	-
20	-	-	-	-
21	-	-	-	-
22	484	2	44	968
23	529	4	92	2116
24	576	2	48	1152
25	-	-	-	-
26	676	2	52	1352
27	-	-	-	-
28	-	-	-	-
29	841	2	58	1682
30	900	1	30	900
		14	342	8494

Mean: $\overline{X}_1 = \frac{342}{14} = 24.429$

Variance: $S_1^2 = \frac{8494.0 - (14 \times 596.8)}{14 - 1}$

$= \frac{8494.0 - 8354.6}{13}$

$= 139.4 = 10.7$

APPENDIX TABLE VII: HARPACTORINAE: Mean and variance of 2n-numbers for the subfamily

X_2	X^2	f_2	$X_2 f_2$	$X_2^2 f_2$
14	196	1	14	196
15	-	-	-	-
16	-	-	-	-
17	-	-	-	-
18	-	-	-	-
19	-	-	-	-
20	-	-	-	-
21	-	-	-	-
22	-	-	-	-
23	-	-	-	-
24	-	-	-	-
25	-	-	-	-
26	676	7	182	4732
27	729	5	135	3645
28	784	27	756	21168
29	841	2	58	1682
30	900	2	60	1800
		44	1205	33223

Mean: $\overline{X_2} = \frac{1205}{44} = 27.386$

Variance: $S_2^2 = \frac{33223.0 - (44 \times 750.012)}{44 - 1}$

$= \frac{33223.0 - 33000.6}{43}$

$= \frac{222.4}{43} = 5.17$

APPENDIX TABLE VIII: STENOPODINAE: Mean and variance of 2n-numbers for the subfamily

X_3	X_3	f_3	$X_3 f_3$	$X_3^2 f_3$
14	-	-	-	-
15	-	-	-	-
16	-	-	-	-
17	-	-	-	-
18	-	-	-	-
19	-	-	-	-
20	-	-	-	-
21	-	-	-	-
22	-	-	-	-
23	529	6	138	3174
24	576	2	48	1152
25	625	3	75	1875
26	-	-	-	-
27	729	1	27	729
28	-	-	-	-
29	-	-	-	-
30	-	-	-	-
		12	288	6930

Mean: $\overline{X_3} = \frac{288}{12} = 24.00$

Variance $S_3^2 = \frac{6930 - (12 \times 576.00)}{12 - 1}$

$= \frac{6930 - (12 \times 576)}{11} = \frac{6930}{11}$

$= \frac{18}{11} = 1.64$

APPENDIX TABLE IX : TRIATOMINAE : Mean and variance of 2n-numbers for the subfamily

$2n/X_t$	X_t^2	ft	$X_t f_t$	$X_t^2 f_t$
14	-	-	-	-
15	-	-	-	-
16	-	-	-	-
17	-	-	-	-
18	-	-	-	-
19	-	-	-	-
20	400	1	20	400
21	441	1	21	441
22	484	15	330	7260
23	529	9	207	4761
24	576	2	48	1152
25	625	1	25	625
26	-	-	-	-
27	-	-	-	-
28	-	-	-	-
29	-	-	-	-
30	-	-	-	-
		f_t 29	$X_t f_t$ 651	$X_t^2 f_t$ 14639

Mean: $\overline{X_t} = \frac{651}{29} = 22.45$

Variance : $S_t^2 = \frac{14639 - 29 \times 504.00}{29 - 1}$

$S_t^2 = \frac{14639 - 14616}{28}$

$S_t^2 = \frac{23}{28} = 0.82$

Appendix Test I : Comparison of the distribution of published Reduviid diploid numbers (Literature sample) with those determined in this study (Appendix Table III, IV and V).

Variance ratio, $F = F_{65,45}$

$$= \frac{10.07}{6.91} = \underline{1.46}$$

Student t

$$= \frac{\bar{X}_2 - \bar{X}_1}{\sqrt{S^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

$$= \frac{26.02 - 24.07}{\sqrt{8.78 \left(\frac{1}{66} + \frac{1}{46}\right)}}$$

$$= \frac{1.95}{\sqrt{8.79(0.015+0.022)}} \qquad = \frac{1.95}{0.57}$$

$$= 3.42$$

Tabulated t value at 95% confidence level = 1.66

$3.42 > 1.66$

Therefore significant difference between 2 samples.

$\bar{X}_1 = 24.07$ = mean 2n-numbers for literature sample
$\bar{X}_2 = 26.02$ = mean 2n numbers for Kpordugbe's sample
Combined variance, $S^2 = \dfrac{f_1 x^2, - n x^2, + f_2 x \frac{2}{2} - n \bar{x} \frac{2}{2}}{n, + n_2 - 2}$

$$= \frac{654.8 + 311.0}{(66 + 46) - 2} \qquad = \underline{8.78}$$

Appendix Test II: Comparison of the distribution of Reduviinae diploid numbers with those of Harpactorinae (Appendix Tables III, VI, VII and Appendix Test I).

Variance ratio $F_{13,43} = \frac{10.70}{5.17} = \underline{2.07}$

Student's t

$$= \frac{27.37 - 24.43}{\sqrt{6.46\left(\frac{1}{14} + \frac{1}{44}\right)}}$$

$$= \frac{2.96}{\sqrt{6.46 \times 0.094}}$$

$$= \underline{3.79}$$

Tabulated t value at 95% confidence level = 1.67

$$3.79 > 1.67$$

Therefore, significant difference exists between the 2 samples.

Combined variance $S^2 = \frac{222.4 + 139.4}{(14 + 44) - 2} = \underline{6.46}$

$\overline{X}_1 = 24.43$ = mean 2n-numbers for subfamily Reduviinae

$\overline{X}_2 = 27.39$ = mean 2n-numbers for subfamily Harpactorinae

Appendix Test III: Comparison of the distribution of Reduviinae diploid numbers with those of stenopodinae (Appendix Tables III, VI, VII and Appendix Test I).

Variance ratio $F_{13,11} = \frac{10.70}{1.64} = \underline{6.52}$

Student's $t = \frac{24.43 - 24.00}{\sqrt{6.56\left(\frac{1}{I4} + \frac{1}{I2}\right)}} = \underline{0.43}$

Tabulated t value at 5% confidence level = 1.71

$0.43 < 1.71$

Therefore the is no evidence of a significant difference between the two samples.

Combined variance $S^2 = \frac{139.4 + 18.00}{(12 + 14) - 2} = 6.56$

$\overline{X_3} = 24.00$ = Mean 2n-numbers for subfamily Stenopodinae.

Appendix Test IV : Comparison of the distribution of Harpactorinae diploid numbers with those of Stenopodinae (Appendix Tables III, VII, VIII and Appendix Test I).

Variance ratio $F_{43,11} = \frac{5.17}{1.64} = \underline{3.15}$

Student's t $= \frac{27.39 - 24.00}{\sqrt{4.45\left(\frac{1}{12} + \frac{1}{44}\right)}} = 4.91$

Tabulated t value at 95% confidence level = 1.67

$4.91 > 1.67$

Therefore there is a significant difference between the two samples.

Combined variance $S^2 = \frac{222.4 + 18.00}{(12+44) - 2} = \underline{4.45}$

Appendix Test V: Comparison of the distribution of Triatominae diploid numbers with those of Stenopodinae (Appendix Tables III, VIII, IX and Appendix Test I).

Variance ratio $F_{11,28} = \frac{1.64}{0.82} = \underline{2.00}$

Student's t $= \frac{24.00 - 22.45}{\sqrt{1.05\left(\frac{1}{29} + \frac{1}{12}\right)}} = \underline{\underline{4.56}}$

Tabulated t value at 95% C.L. = 1.68

$4.56 > 1.68$

Therefore significant difference between two samples

$S^2 = \frac{23+18}{(29+12)-2} = 1.05$

$X_t = 22.45$ = mean 2n-numbers for subfamily Triatominae.

Appendix Test VI : Comparison of the distribution of Triatominae diploid numbers with those of Reduviinae (Appendix Tables III, VI, IX and Appendix Test I).

Variance ratio $F_{13,28} = \frac{10.70}{0.82} = \underline{13.05}$

Student's $t = \frac{24.43 - 22.45}{\sqrt{3.96\left(\frac{1}{14} + \frac{1}{29}\right)}} = \underline{3.14}$

Tabulated t value at 5% C.L. = 1.68

$3.14 > 1.68$

Therefore significant difference exists between two samples.

$S^2 = \frac{23 + 139.4}{(29+14)-2} = \underline{3.96}$

Appendix Test VII; Comparison of the distribution of Triatominae diploid numbers with those of Harpactorinae (Appendix Tables III, VII, IX & Appendix Test I).

Variance ratio $F_{43,28} = \frac{5.17}{0.82} = 6.30$

Student's $t = \frac{27.39 - 22.45}{\sqrt{3.46\left(\frac{1}{44} + \frac{1}{29}\right)}} = 11.76$

Tabulate t value at 95% C.L. = 1.67; $11.76 > 1.67$

Therefore very significant difference exists between the two samples.

$S^2 = \frac{23+222.40}{(29+44)-2}$ 3.46