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THE KARYOTYPE OF THE DAMSELFLY, *EPALLAGE FATIME* (CHARPENTIER, 1840) [1] (ODONATA, ZYGOPTERA: *EPALLAGIDAE*), WITH A NOTE ON THE CYTOTAXONOMIC AFFINITIES IN THE SUPERFAMILY CALOPTERYGOIDEA

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Epallage fatime (CHARP.) is the first member of the family studied cytologically. The chromosome number is: $2n$ ♂ = 25, n ♂ = 13. The sex element is the smallest of the set at all stages of the spermatogenetic cycle. It is usually negatively heterocyclic at spermatogonial metaphase, whereas it is positively heteropycnotic at primary spermatocyte prophase and diakinesis.

While the cytological similarities between *Epallagidae*, *Hetaerinidae* and *Calopterygidae* suggest their close mutual affinities, the three differ essentially from the *Polythoridae*. This view is only partly in agreement with the evidence on the structural and venational characters (cf. FRASER, 1954).

Contrary to FRASER's opinion (FRASER, 1957), the *Pseudolestidae* can not be regarded, on the basis of the cytological information available, as an annectent family to the Calopterygoidea, but stand well apart from all other cytologically known Zygoptera.

Introduction

The *Epallagidae* are the fourth hitherto cytologically studied family of the calopterygoidean branch of Zygoptera. The other three families are *Polythoridae*, *Hetaerinidae* and *Calopterygidae*. Cytological information is still lacking on the three primitive families of the group, viz. *Amphipterygidae*, *Chlorocyphidae* and *Heliochartidae*, whereas CUMMING (1964) reported on the chromosome number of one member of the annectent family *Pseudolestidae*.

The family is mainly Oriental in distribution, but extends as far westwards as Southeastern Europe, whereas it has no representatives

[1] In CHARPENTIER's original description (1840. *Lib. Eur.*, pp. 132–134, pl. 45, fig. 2) the specific name is spelled as *fatime* and not *fatima* as cited erroneously by FRASER (1934 pp. 76–78, figs. 22, 23 a, b). The spelling *fatima* by KIRBY (1890. *Cat. Odon.*, p. 108) is therefore wrong.

in Australia. So far ten living and five fossil genera (Jurassic, Eocene, Oligocene) were defined.

The genus *Epallage* CHARPENTIER has a Near East and East Mediterranean distribution and is the only representative of the family in Europe. It ranges from Northwestern India and Kashmir (FRASER, 1934) to Caucasus and Central Asia (Kopet-Dag) (POPOVA, 1953) and further into Macedonia, Bulgaria and Romania (BUCHHOLZ, 1967). If *E. alma* SELYS from Persia can indeed be regarded as a local race of *E. fatime* (CHARP.), as suggested by FRASER (1934), the genus is monotypic.

The larval stage of *E. fatime* was described by POPOVA (1953). It is rheophilic and bivoltine in the territory of the U.S.S.R.

The family is supposed to originate from an amphipterygid-like ancestor somewhere in Oceania. The genus *Epallage* is considered as one of the most primitive forms found in the family (FRASER, 1957).

Material and Method

The observations were carried out on three mature males collected on April 23rd, 1970 at Epta Piges Stream, Kolimbia, Island of Rhodos, Greece. Living insects were transported to the Netherlands in paper triangles. On their arrival to the laboratory, on April 28th, when the microscopic preparations were made, they were still alive, in relatively good condition and cytologically active. Though no preparations were made of females, it should be noted, that the latter tolerate transportation much better than males. On arrival at the laboratory no male was able to fly, whereas all females took on wings when released from the triangles.

For fixing and staining the lacto-acetic-orcein squash method was used. The 12 slides yielded 340 microphotographs. These were taken a few hours to two days after fixation, with a Zeiss photomicroscope (projective 3.2, optovar 1.25, 100 × oil immersion, green filter) on Agfa-Gevaert copex panchromatic film (magnification on negative 400 ×). Figures 2 and 3 are made without and the others with phase contrast optics. The positives were printed originally at 2250 × and are reduced in this paper to 1500×.

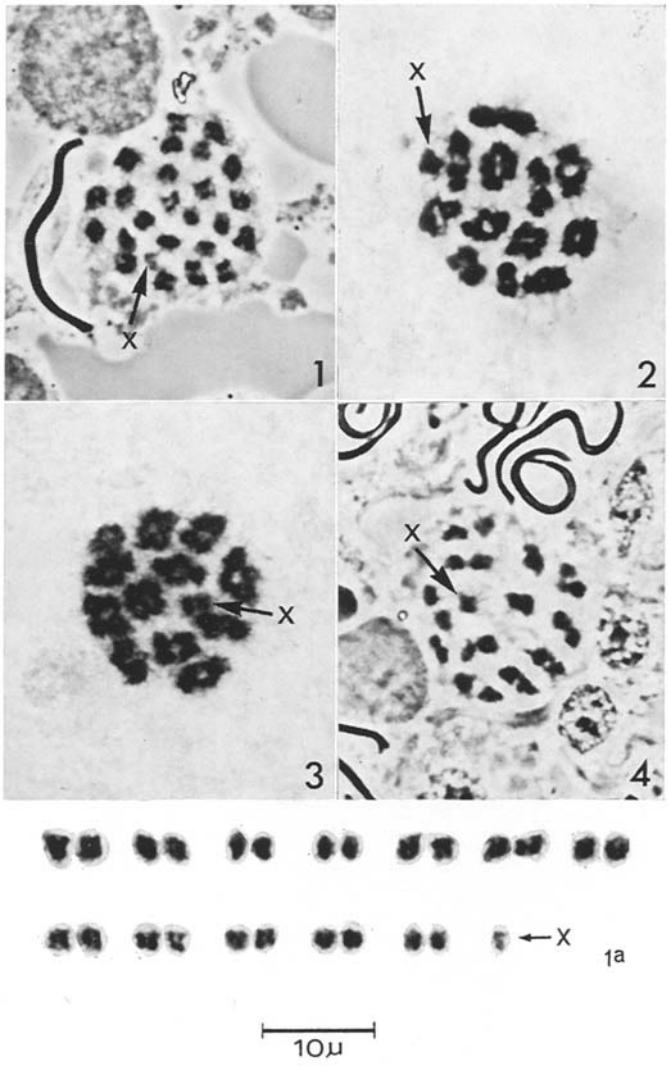

Plate 1. Figures 1–4. Chromosomes of *Epallage fatime* (CHARP.) (Rhodos, Greece) (1500 ×). The arrows indicate the sex element. 1 – Spermatogonial metaphase and karyogram. 2–3 – Primary spermatocyte metaphase (polar views). 4 – Secondary spermatocyte metaphase (polar view).

Observations and Discussion

THE CHROMOSOMES OF *Epallage fatime* (CHARP).

In spermatogonial metaphase there are 25 elements of gradually decreasing magnitude. In the polar views of this stage their length ranges between 2.4 and 1.8 μ approximately (Figure 1). In this way the spermatogonial chromosomes of *E. fatime* could be classified as medium sized among the zygopterous dragonflies.

There are no m-chromosomes and the X is the smallest of the set. It is approximately equal in length to the members of the smallest pair of autosomes. At primary spermatocyte metaphase the latter form a bivalent, which is clearly distinguishable from the other bivalents by its inferior size, though it is nearly twice as long as the X at this stage (Figures 2 and 3). The small autosomal element is recognizable also in the polar views of the secondary spermatocyte metaphase (Figure 4).

In the great majority of figures of the polar view of spermatogonial metaphase of all three specimens studied, the sex element is negatively heterocyclic (Figure 1). This feature is of particular interest and has so far never been recorded for the spermatogonial metaphase of a dragonfly. At primary spermatocyte metaphase, on the other hand, negatively heterocyclic X chromosomes have been occasionally observed in a few species (cf. KIAUTA, 1969a). In our *Epallage*-material however, the sex element is at this stage isocyclic without exception.

The 12 diakinetic bivalents have a single chiasma per bivalent, whereas the sex element follows the usual odonate pattern during the spermatocyte cycles (positive heteropycnosis up to diakinesis, heterokinesis at anaphase II).

A NOTE ON THE CYTOTAXONOMIC AFFINITIES IN THE CALOPTERYGOIDEAN FAMILIES

Though the cytological information on the calopterygoidean dragonflies is still greatly incomplete and covers, aside from a single member of the annectent family *Pseudolestidae*, only four of the seven families of the group, it seems useful to briefly discuss the phylogenetic affinities as they appear in the light of the cytotaxonomic evidence.

There are many shortcomings in FRASER's reclassification of the Order (FRASER, 1957), including several controversies between his text and his genealogical tree in the same publication, but no other phylogenetic treatment of the Order as a whole has lately been carried out. His views on the affinities and phylogenetic position of the cytologically studied calopterygoidean families, based on comparative studies of structural and venational characters, should be, therefore, compared with the results of cytological observations.

The following are the main points of FRASER's view on the phylogenetic affinities of the cytologically studied calopterygoidean families:

(1) The *Amphipterygidae*-like forms are considered as direct ancestors of all other calopterygoidean families;
(2) *Epallagidae* are placed in the direct phyletic line leading from *Amphipterygidae* towards the higher Calopterygoidea;
(3) From the *Epallagidae*-like ancestors have developed *Hetaerinidae* on one side, and the *Polythoridae-Calopterygidae* complex on the other;
(4) *Polythoridae* and *Calopterygidae* have a common ancestor, they have developed along different, but parallel lines and are considered to have reached the same level of advancement; they are thought to be the most advanced families of the group and among the most advanced Zygoptera in general;
(5) *Pseudolestidae* (with *Megapodagrionidae*) represent a primitive side branch below the lestinoidean stock. Because of the mixture of coenagrionidean, megapodagrionidan and amphipterygidan characters met with in the representatives of the family, they are considered, in the system, as annectent between the Coenagrionidea and Calopterygoidea.

The main cytological features of the families concerned are given in Table 1.

The information presented in Table 1 shows clearly, that the karyotype of *Epallage fatime* is remarkably similar to those prevailing in the families *Hetaerinidae* and *Calopterygidae* (save for the lack of an m-chromosome in our species), whereas it deviates from *Polythoridae* and is essentially different from that of the only cytologically studied member of the family *Pseudolestidae*.

If the cytotaxonomic characters of the families concerned are

TABLE 1

REVIEW OF THE MAIN CYTOTAXONOMIC FEATURES OF THE CALOPTERYGOIDEA AND THE ANNECTENTS[1])

Family	Genera (and number of species) studied cytologically	Chromosome number (n)				Remarks	General occurence of m-chromosome
		Type number	Range	Number of species with deviant number	Origin of variation		
POLYTHORIDAE	*Cora* SEL. (1), *Polythore* CALV. (1)	12	—	none	—	—	present
EPALLAGIDAE	*Epallage* CHARP. (1)	13	—	—	—	—	lacking
HETAERINIDAE	*Hetaerina* SEL. (7)	13	13, 14	1	autosomal fragmentation (?)	—	present in all $n = 13$ species
CALOPTERYGIDAE	*Anaciagrion* KENN. (1), *Calopteryx* BURM. (5), *Matrona* SEL. (1), *Mnais* SEL. (2)	13	see Remarks			in two of the four studied geographic races of one species (*Calopyterx*) fragmentation of certain autosome(s) in some cells of the same individual, while not in others ($n = 14$–17)	present; pronounced variation in relative size among geographic populations of the same species (*Calopteryx*)
PSEUDOLESTIDAE	*Hypolestes* GUNDL. (1)	9(?)	—	—	—	—	lacking

[1]) For references Cf. KIAUTA (1970).

combined with the general trend in the karyotypic evolution of Odonata (cf. KIAUTA, 1967; 1968; 1969a; 1969b) the following suggestions can be drawn:

(1) The karyotypes of *Epallagidae*, *Hetaerinidae* and *Calopterygidae* have reached a similar evolutionary level;

(2) *Polythoridae* do not appear to have reached the same phylogenetic level as *Calopterygidae*. They are more primitive than the latter family and it is perhaps not unlikely, in view of the distribution of the chromosome numbers in Zygoptera, that they represent a less advanced side branch on the calopterygoidean stem;

(3) *Hetaerinidae*, on the other hand, seem to have developed along parallel lines to *Calopterygidae* (the idea has been expressed already by FRASER, 1957, though he did not follow it up in his genealogical tree). The family should be given at least the same, if not perhaps even a higher, phylogenetic level as *Calopterygidae*. For the highest evolutionary level of *Hetaerinidae* pleads the discovery of an $n = 14$ species in the family (CUMMING, 1964). This number is characteristic of the most advanced dragonfly families and makes the case of *Hetaerinidae* unique in the superfamily;

(4) *Pseudolestidae*, as far as it can be judged on the basis of a single representative of the subfamily *Pseudolestinae* hitherto studied cytologically, can not be regarded as an annectent family either to Calopterygoidea or to Coenagrionidea, but stand well apart from all other cytologically known Zygoptera. A phylogenetically primitive position of the family is certainly in agreement with the cytological evidence. (In our opinion, aside from cytotaxonomic considerations, FRASER's creation of this family seems most unfortunate. It is made up of seven living and two fossil genera, divided into three subfamilies, two of which are greatly aberrant and composed of but a single genus. There are hardly any structural characters common to the whole family).

Cytological criteria are certainly an insufficient basis for the indication of phylogenetic relationships between the higher taxa, but so is any separate character. The above evidence suggests that different characters lead to different conclusions. Therefore other than venational and macrostructural features should certainly also be taken into consideration when the next attempt at the reclassification of the Order will be made.

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