

in many species deviates but slightly from the supposed ancestral number. Among the more specialised forms, only one case of $n = 9$ is known (*Perithemis*, Libellulidae).

It seems most likely that the present numerical variation in odonate karyotypes has developed by the occurrence of breaks leading to haploid numbers 10 to 15 and by fusions leading to haploid numbers 3 to 7 in ancestral forms which had a chromosome number $n = 9$.

The high- n karyotypes are not homogenous by origin either. Fusion of two or a few elements gives rise to secondary high- n types ($14 \rightarrow 13 \rightarrow 12$ etc.). In many such cases the fusion can be traced because the fused chromosomes are significantly longer than the other chromosomes of the set. If only two chromosomes are fused, the sex chromosome is usually involved, and a neo-XX/XY sex determination mechanism replaces the usual XX/XO type. The fusion is not always found in all populations of the same species, nor does it always occur in all cells of one individual (*Aeshna grandis* (L.), etc.).

Figure 2 illustrates our hypothesis of karyotype evolution in dragonflies. It has the advantage of (1) being based on independently obtained evidence regarding phylogenetical position and karyotype; (2) being able to account for any chromosome number.

Nothing can be said at present regarding the nature of breaks and fusions. The diffuse nature of the centromere however, makes the survival of chromosome fragments possible.

It is interesting to note that low- n complements were found in tropical species only, whereas secondarily reduced high- n complements so far have been recorded only in dragonflies from the Temperate Region.

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Dagvlinder op licht. In 1967 zat omstreeks 1 uur op een nacht bij windstil weer een *Thecla betulae* L. bij de lamp.

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