

The uniquely derived character concept and its application to the Delphacidae

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The taxonomist has two tasks, which are only partially separable. The first is to recognize species and to devise keys so that others can recognize them. The second is to group together species into groups which one believes to bear a closer relationship to each other than to other organisms, preferably by descent from a common ancestor.

Ever since the Linnaean genera, the animal kingdom has been divided and subdivided, and various entomologists have tried to draw trees showing the natural relationships. In fact, every taxon above the species level implies a hope of having split off a monophyletic group.

The wide diversity in classification and trees, based on different authors' ideas as to which were the characters giving the correct clues to ancestry have led various workers in the past twenty years to search for more objective methods of choice. Hennig wrote a book based on the idea that the sharing of derived characters ('synapomorphy') was more significant than the sharing of ancestral characters ('symplesiomorphy'). Camin and Sokal and later Fitch looked for the tree in which the total number of changes in character-state over the whole data-matrix was minimized and the Fitch method has the advantage that no decision is necessary as to which is the ancestral character-state and which the derived—not always an obvious choice! These methods have been called 'parsimony methods'.

I published an alternative method about twelve years ago based on the fact that what the taxonomist is looking for is a set of uniquely derived char-

acters — *i.e.* those that only evolved once in one direction within the history of the group under study. If two independent characters, each with two states, are both uniquely derived, there will be not more than three out of the four possible combinations among the species studied.

So by taking characters two at a time, we can pick out the pairs of characters where one or both cannot be uniquely derived. Again assumptions similar to those of the parsimony methods I referred to earlier will suggest trees that fit the data most simply. Methods are described in detail in papers which I published in 1969 and 1972 and both Fortran and Basic programs can be supplied to anyone interested.

A group of Auchenorrhyncha that has caused much uncertainty in classification is the family Delphacidae. In a paper published in 1964, W. Wagner divided this family into 9 subfamilies and split the old *Calligypona* genus (which I had mistakenly called *Delphacodes* earlier) into about 20 fragments! His subfamily classification particularly worried me, as I felt that many of his groups were less distinct than the tribes in the Deltocephalinae, as separated by Emelyanov.

Wagner's concept of a group appears to be based on a philosophy that it is characterized by a successive development in a certain direction. However, if one believes that species evolve by isolation, as expounded by Mayr, peculiar local circumstances can cause regression of some characters and advancement of others!

In the case of *Asiraca*, it can be split off from the rest of the European Delphacids on the basis of four different characters, i.e.

- 1) The form of the spur at the apex of the hind tibiae
- 2) The number of spines on the hind tibiae
- 3) The pattern of spines on the apex of the hind first tibial segment
- 4) The form of the aedeagus.

Here we have four independent characters all telling the same story — "compatible" is the accepted word — and on that basis I am happy to regard the Asiracinae as forming a good subfamily.

However, older authors took the view that the genera *Criomorphus*, *Stiroma*, *Ditropis* and *Eurybregma*, with two frontal keels throughout, were closely related, and I put them together in a single genus in my 1960 Handbook. However, Wagner felt that the weak development of the keels in the three latter genera brought them closer to *Eurysa*, which has a single obsolescent keel, and has made a subfamily allocation accordingly. In other words, he has regarded the obsolescence of the keels to be a uniquely derived character and the doubling of the keel not to be so!

When I saw Vilbaste's valuable paper on classification of the nymphs, I hoped that this would provide further useful characters, mainly in the numbers and positions of the sensory pits. However, his key to the *Javesella* nymphs shows that, if this genus is uniquely derived (of which I have little real doubt!), many of these characters are not, being present in both states both within and outside the genus. There is one character, however, that appears to divide the genera into three groups, without cutting across

accepted generic groupings, and this is the arrangement of the sensory pits on the sixth and seventh abdominal tergites. There was one exception, in fact, which caused Vilbaste to erect a new genus.

In fact, should the latter be regarded as a uniquely derived character, the four genera *Criomorphus*, *Stiroma*, *Ditropis* and *Eurybregma* fall into one group, together with *Eurysula lurida*, and *Eurysa* (*sensu stricto*) in another. Of course, Wagner may have picked the really uniquely derived character, but it seems a shaky foundation on which to found a subfamily.

One word that is frequent in Wagner's keys is 'Tendenz' — for instance, the subfamily Delphacinae, as defined by him, is based on a tendency to broadening or lengthening of the basal antennal segment, leading to his inclusion of *Conomelus*, *Euides* and *Delphax*. In the case of the first genus, the character is not easily appreciated and, I feel, weak grounds for separation from *Euconomelus* at subfamily level. Again, this grouping is incompatible with Vilbaste's character of the sensory pits of the sixth and seventh abdominal tergites.

I have started trying to draw up a data-matrix so as to try out numerical methods. However, the more I look at the data, the less hopeful am I that it will produce any conclusive classification. I have not yet studied in detail Ossiannilsson's genital scale. However, I feel that we need good new characters, possibly of a chemotaxonomic nature or based on electron microscope studies.

In the meanwhile, I suggest that the uniquely derived character concept is worth bearing in mind not only for numerical studies, but in establishing any higher classification.