Book review

ZUNINO, M., BELLÉS, X. & BLAS, M. Edit. 1992 (dated 1991). Advances in Coleopterology. 323 pp. Published by the European Association of Coleopterology, Silvestrelli & Cappelletto, Torino 1991. Available from: Asociación Española de Coleopterología, Departamento de Biología Animal, Facultad de Biología, Universidad de Barcelona, Diagonal 645, 08028 Barcelona, Spain. Price 7,000 Pesetas.

This book represents the proceedings of an International Symposium held in Barcelona in 1989 in which 38 contributors from 14 countries presented 20 papers. All contributions are in English, though the text often reflects the flavour of the original language of the authors, and, sometimes, the whims of the printers as well. The contributions span a wide range of subjects which may be grouped as follows: ecology (2 papers), behaviour (2 papers), morphology and biometry (3 papers), karyology (5 papers), evolution (8 papers). Papers within the latter category range from palaeontology to island biogeography through to a stimulating review on probable coevolution between several species of Cycadales (gymnosperms) and some Cucujoidea.

As long as evolution remains the "Leitmotiv" of modern biological research, I regard the numerical dominance of papers (and pages) devoted to this aspect of the research as one of the main qualities of the book. A problem with a number of evolutionary hypotheses, however, is that they are expressed in an informal way, making them difficult to test. But this is much less the case when evolution is synthetically expressed in the form of phylogenetic diagrams tracing its most probable course or the most probable pattern of a trait. Most (but not all) contributors concerned with this problem produced diagrams of this sort referring to a cladistic context or using the cladistic terminology. The results, nonetheless, appear convincing to various degrees, as I shall show by means of the following two examples:

SLIPINSKI & PAKALUK (pages 79 - 88) argue that the present classification of the cerylonid series of Cucujoidea may be erroneous since it implies 9 evolutionary steps for two critical characters they consider (i. e. number of adult spiracles and closed mesocoxal cavities). On this basis they offer "a parsimonious" partly resolved cladogram which needs only "five steps for both characters". In truth, these figures result from miscounting and the whole argument is based on a confusion related more to the number and to the definition of taxa to be included in the analysis than to parsimonious phylogenies. The crux of the problem lies with two initial difficulties: 1) the Cerylonidae, characterized by 5 abdominal spiracles in the adult, are traditionally considered to include the Euxestinae with 7 spiracles, and, 2) the Endomychidae (with closed mesocoxal cavities) currently include three subfamilies exhibiting the open condition. SLIPINSKI & PAKALUK concentrate their action on two different fronts: a) they propose separation of the non-homogeneous subfamilies from the family to which they were traditionally assigned (this decision is obviously destined to reduce the number of evolutionary

Table 1. Minimum number of steps in the evolution of the mesocoxal cavities and of the number of adult abdominal spiracles in a group of families of Cucujoidea according to different classificatory constraints and to different character evolution models.

	Character evolution	
	Unordered	Irreversible
Traditional classification (with Endomychidae and Cerylonidae polymorphic)	4	5
Traditional classification and phylogeny as given by SLIPINSKI & PAKALUK	4	6
Splitting Endomychidae and Cerylonidae into monomorphic taxa only	2	3
Splitting and rearranging Endomychidae and Cerylonidae as suggested by SLIPINSKI & PAKALUK	2	4

steps necessary to construct any conceivable phylogeny), and, b) they propose a new phylogenetic rearrangement of the taxa under discussion. As a matter of fact, their phylogeny is really (one of) the "best" possible ones in terms of parsimony if characters are allowed to evolve freely. In this phylo-

geny the minimum number of evolutionary steps needed by the new hypothesis is 2. Such a phylogenetic reconstruction implies that the open mesocoxal cavities of Alexiidae and Coccinellidae must be explained by a secondary loss. The proponents of the hypothesis, however, state that their phylogeny needs a minimum of 5 evolutionary steps and the reasons for it is that they assume irreversibility of character evolution. Under this assumption the minimum number of steps necessary to construct their phylogeny is 4 but an important set of several thousand possible different phylogenies respecting the same assumptions and needing only 3 evolutionary steps exist. I compare here (Table 1) these different hypotheses and assumptions in terms of parsimony (i. e. of the minimum number of evolutionary steps they need) but I don't think it necessary to describe any of them in detail since I am convinced that consideration of additional characters (mentioned in part but not used by SLIPINSKI & PAKALUK) should allow a much more reliable result.

On the other hand, HANNAPPEL & PAULUS (pages 89 -127) propose an interesting classification of some Australian and New Zealand Helodidae based on larval morphology only. The results are far from being definitive since four "genera" are designated by their locality name only, due to the lack of association with adults. These authors, in addition, succeeded in the difficult task of finding one of the 17 shortest possible cladograms on a data matrix of 11 taxa X 30 characters. The remaining 36 characters in their list of 66, in fact, are autapomorphic and, as such, cladistically uninformative. Five informative characters in their cladogram are defined as "questionable apomorphies". Excluding them from the cladistic analysis restricts the number of possible phylogenetic reconstructions to three, one of which still corresponds to the one proposed by HANNAPPEL & PAULUS. Less convincing is the discussion presented under the heading of "Phylogenetic relationships". In this section the authors question their correct interpretation of another two characters used to construct the previous phylogeny and propose an additional hypothetical cladogram meant as a possible alternative to the previous one in case character misinterpretation had occurred. Of course, suppression of both characters increases the number of possible phylogenetic trees from 3 to 6, but one of the latter trees still shows the same topology as the one originally proposed by HANNAPPEL & PAULUS. Deriving the cladogram of Fig. 42 (their alternative phylogeny) from the data matrix after exclusion of the last two doubtful characters needs five additional evolutionary steps. Re-coding these characters according to their alternative interpretation equally allows the construction of 6 (three steps longer) cladograms, one of which matches the first phylogeny proposed by the authors. Forcing their alternative phylogeny (Fig. 42) to fit the re-interpreted data matrix needs three additional evolutionary steps.

All my statements about the number of possible phylogenies and of minimum evolutionary steps are the result of computer-based parsimony analyses. I am not pretending that tracing phylogenies by hand is wrong in itself: this way of hypotheses testing may be preferred subjectively and it may be equivalent to *a priori* character weighting. Only, in this case, one should avoid referring to parsimony and clear up in advance the decision rules he intends to apply.

The editors state that their target was "to gather a series of ... stimulating contributions". In this respect I believe they accomplished their task and I would recommend the book not only to the students directly concerned with the topics of the different papers but to a broader audience of entomologists as well.

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