

Comparative biology and phylogeny of the cyclostome groups of Braconidae: the polyphyletic origin of endoparasitism. James B. Whitfield.

Evolution of life history strategies in the Aphelinidae. James. B. Woolley.

Forum

PROTECTING INSECT COLLECTIONS FROM PESTS WHAT IS THE BEST APPROACH?

by

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At the beginning of my job, there was no insect collection. Formerly, insects and mites intercepted in quarantine were mailed to a specialist who identified them but did not return the material, as this was not requested. From 1981 on, I gathered many specimens and I now have a small collection of about 5,000 specimens of grasshoppers, leafhoppers, bugs, moths, flies and beetles, and I plan to have it enriched with wasps. Maintaining the collection, however, is rather difficult in our subtropical climate, where either carpet-beetles or book-lice rapidly develop on any available organic matter, transforming it into a fine powder after two weeks or less. Small samples are being kept in a deep-freeze until they are identified, but prepared and labelled insects must be preserved with protecting chemicals. One of the most common methods was placing naphthalene crystals in the insect boxes. The advantage of this is well known and many old collections were saved through centuries using this chemical. However, there are also two unfavourable properties of naphthalene: first, this chemical contains small quantities of impurities, forming heterocyclic components of the so-called carcinogenic chemicals, and many of us spend a lifetime in the same room with our collections along with that eminent danger; and secondly, the cabinets where the collections are kept are filled with the odor of naphthalene, causing visitors to sneeze due to the allergy of its scent. During my visit to foreign institutions, I have looked for collection fumigants. There are usually three different methods: the classical way with naphthalene; a new one where no naphthalene is admitted but periodically the rooms are fumigated with toxic gases; and a third one, using a natural, estheric oil product, a plant extract, with a pleasant odor and with no allergic effects to human beings - but which have properties to repel harmful insects. I would like to hear the opinions and suggestions of others. I would like to know the names of non-carcinogenic substances that can be used to protect insect collections.

not

THE IMPORTANCE OF BEING A CLADIST

by

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Cladists are prevailing in the current discussion with antycladists (see Forum in Sphecos nos. 11 & 13), provoking me to enter on the side of the minority.

I have been following Willi Hennig's phylogenetic analysis methodology for two decades (my description of this method in: Rasnitsyn, A.P. 1969. Origin and evolution of the Lower Hymenoptera. Nauka Press, Moscow - was probably the first one in Russian), and I still know no better approach to the subject. During all that time I have been taking a sharply negative position concerning cladism, once again being, together with my co-author, possibly the first one to discuss the problem in my country (Ponomarenko, A.G., Rasnitsyn, A.P. 1971. On the phenetic and phylogenetic systems. Zool. Zhurnal, 50 (1):5-14). The reasons for so stable an "inconsistency" may be of some interest to Sphecos readers.

The most important thing is that phylogenetic analysis and cladism (phylogenetic systematics of Hennig) are independent methodologies with different aims and terminology. Syn-, aut-, apo- and plesiomorphies, as well as homoplasy, are the terms of phylogenetic analysis, while mono-, para-, holo-, and polyphyly are relevant only in the framework of cladism (and other theories of taxonomy). Equally, phylogenetic analysis pursues the aim of learning about the succession of the divergence events and all the processes and circumstances taking place during and between the divergences, while cladistics has another task, that is to construct a system closely reflecting genealogy. Cladists claim that their system reflects phylogeny, but they are wrong. Their system is destined to reflect only a cladogram, i.e. a full succession of events of the divergence, but this is genealogy, while phylogeny is a wider notion which includes additionally at least a scale of the differences acquired by the respective phyla during their history after their divergence.

Ignoring the latter half of the phylogeny, cladistics leaves space for alternative theories of taxonomy, and this space is not empty, of course. It is partially filled with phenetics which constructs its systems using only a scale of differences and ignoring the genealogy. The rest of the space between cladism and phenetics is filled with an ordinary, routine taxonomy called evolutionary systematics which tries to reflect both the genealogy and the scale of the differences acquired (naturally, at the expense of exactness in reflecting both of these aspects of phylogeny).

Which approach is better? Cladistics has an evident advantage when compared to ordinary taxonomy since it presents an explicit algorithm (description of the procedure) on how to construct the cladistic system: take a cladogram and let each of its clades become a taxon, with those more inclusive receiving a higher rank.

I have failed to find a comparable description of algorithm of the evolutionary system, but this does not seem to be a decisive disadvantage of the approach because such an algorithm can be constructed (it has been constructed, in fact, in the 1971 paper referred to above): the taxon as a monophyletic continuum. Monophyly covers both holo- and paraphyly here, while the continuum means an uninterrupted chain, irrespective of being simple, branched or looped, which is constructed from elements (OTU of phenetics) where the similarity within any pair of neighbouring elements is higher than the similarity of any element of the continuum to elements of other continua.

The definition is eclectic in the artificial conjunction of phenetic (continuum) and phylogenetic (monophyly) principles, isn't it? Not at all. Continuum is proposed here as a constructing principle, while monophyly as a controlling one: at first we construct the continuum and then we try to falsify its monophyly. Usually we fail, but if we manage to do it, the optimal strategy seems to gather as much additional information as possible in order to reconsider the case on the broadest basis. Typically this procedure has resulted in falsification of either the evidence of polyphyly of the continuum or the hypothesis of the continuum itself. In the first case we are left with a monophyletic continuum, in the second one with two (or several) continua which prove to be only superficially similar. I do not deny a possibility of the existence of a polyphyletic continuum. I only think that we should find a reliable example prior to deciding what we are going to do with it. Nevertheless, it is a disadvantage of the method, indeed. There is an additional advantage as well: a cladistic system cannot be substantiated better than the respective cladogram (genealogy) is, and the latter is usually much more difficult to elucidate comparing the level of similarity. In contrast, the evolutionary (trivial) system tries to use evidence from both the genealogy and from similarity and, thus, is usually supported much better.

All of the above arguments do not seem to me decisive, however. To reflect or not to reflect on the scale of the differences acquired - that is the question, and its solution depends on what function the system is destined to fulfill. Cladistic systems are being constructed to reflect the genealogy, only genealogy and nothing but genealogy. Isn't that enough? By the way, a simple picture of the cladogram fulfills this function much better, but this is not the question. To my mind, there are other important functions. I should indicate three leading ones: to store the relevant information (each of us knows how much information is associated with the name *Spheg*), to prognose the distribution of the characters (we characterize the order Hymenoptera as having a haploid-diploid genetic system and do not worry that ever some of its superfamilies have never been studied karyologically), and to serve as an interdisciplinary language, so that each name may be

meaningful (to denote a group of reasonable similarity) to the most diverse points of view, including that of, say, biochemists, behaviourists, farmers, and artists.

All three functions imply a priority of the similarity. It should be taken as evidence in favour of phenetics and contrary to the reflection of geneology in the system. This is not the case, however. In this context, the similarity means a level identified on the basis of all the characters including those not explored yet. This knowledge is not obtainable, of course, so we have to construct the system based on indirect evidence. The known similarity (evaluated on the basis of the studied characters) is such evidence, and geneology is evidence as well. Otherwise, if the known similarity were the only reliable evidence, well grounded (not easily falsified), polyphyletic continua would be an ordinary thing, which is not the case. And, on the contrary, if the geneology were the only reliable evidence, the paraphyletic taxa (such as Sphecidae not including bees, Reptilia not lumped with birds and mammals, Protozoa without Metazoa, etc.) all would be easily falsified as continua, which is not the case either. That is why it seems to me very important to be neither a cladist nor a phenetist.

CAN ALL SPECIES BE DEFINED BY AUTAPOMORPHIES?

Last year, while enjoying the wonders of Sequoia National Park in California, Woj Pulawski and I dabbled briefly in some armchair philosophizing while sipping a few gin and tonics. Woj told me that there seemed to be one inherent problem with the cladistic approach to classification, at least at the species level. He pointed out that you can find autapomorphies (or unique, specialized characters) for most taxa, but that ultimately you end up with one taxon that has no autapomorphies. In other words it is definable only by plesiomorphic traits - a cladistic no no. Being a novice in cladistic methodology, I could only conclude that what he was saying sounded logical to me. I told Woj, however, that upon my return to Washington I would consult with some of the more learned cladophiles in the Smithsonian to find out how they handle this seeming conundrum. The opinions and thoughts of Jim Carpenter, Mary Micevich, and Mike Schauff on this topic are offered below for your edification.

A. S. Menke

Jim Carpenter (Museum of Comparative Zoology, Harvard University, Cambridge, Mass.): "About Pulawski's point, both theoretically and most of the time it doesn't arise as a problem. This is because most taxa have undergone mosaic evolution, and so are a mixture of both primitive and derived characters. Since they're all different mosaics, it's generally possible to find something unique to each taxon. But there are situations where you can't. At higher taxonomic levels, this usually occurs when you don't study enough characters, although you may study quite a few (I encountered this problem in my nearctic eumenine genera paper). But with species, you just may not be able to find autapomorphies because there just aren't enough characters (unless I suppose you do DNA sequencing or something fancy). I have this problem in Ancistrocerus - not all of the species can be so defined. In the case of this problem at the generic level and above I would say one should keep plugging away. But at the lowest levels, i.e., species, this is probably impractical. In Ancistroceris, I'm only worrying about defining species groups with apomorphies - the species seem to simply reshuffle the same characters. I guess that's about as well as I can do - maybe someone else will do better with morphology later, or else everything will someday be DNA sequenced (ha, ha)."

Mary Micevich (Systematic Entomology Lab., USDA, Washington DC; and Depts. of Entomology, Univ. of Maryland and Smithsonian Inst.) has this to say: "First, let me begin by reviewing the definitions for plesiomorphy and apomorphy as I use them. Plesiomorphies are character conditions or states which are considered to be ancestral or primitive and which define the ground plan for an entire set of terminal taxa (in Arnold's case, the species being studied). Apomorphies are differences in these ancestral character states which divide the terminal taxa into subsets and offer evidence for uniting these subsets into less inclusive monophyletic groups. Apomorphies can be of two kinds, synapomorphies and autapomorphies. Synapomorphies are

SPHECOS

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NUMBER 14, JULY, 1987

Editor's Musings

Too much time has passed since Sphecos last appeared but your old editor has been too swamped by other work to do anything about it. As a reward for your patience, Terry Nuhn and I have produced another double issue. Terry, as usual, did the lion's share of the typing, probably 97% of it for the two issues.

Most of the research news in this number is derived from those questionnaires that most of you filled out (er, that is, completed, Mick) last year. Because of the long delay some of this information may now be out of date, but at least everyone can see what others are doing research and otherwise.

The production of a new Sphecos Directory based on those questionnaires is not in the near future. I'm sorry, but there are only so many hours in the day and Terry works for me only two months out of the year. If anyone out there has access to a computer and would like to volunteer to enter information from the questionnaires and produce a new directory please contact me. Ron McGinley has a beautiful d-Base III software program that he had developed for the Melissa Directory that can be used very effectively for this chore and which I can probably make available to a volunteer with an IBM clone.

If any of you still have not returned the questionnaire to me, please do so NOW. Also, many of you completed the form in long hand and some of you use hen scratching that is literally unreadable!! If your information gets mangled in our attempts to decipher your scribbling, don't blame anyone but yourself! If you don't have a typewriter - please PRINT! Completed questionnaires are not supposed to look like a doctor's prescription handwriting!!

Research News

R. T. Simon Thomas (Mythsteelaan 32, 8072 PZ Nunspeet, Holland) is preparing a petition for submission to the International Comm. on Zoological Nomenclature in which conservation of the sphecid name Philanthus triangulum is requested.

R. J. Paxton (Dept. of Zoology, University College, P.O. Box 78, Cardiff CF1 1XL, U.K.) has been working on sex ratios in Mellinus arvensis.

David McCorquodale (Dept. of Zoology, Australian National University, Canberra, ACT, 2601 Australia) says: "I am now completing my Ph.D. thesis on communal nesting in Cerceris antipod with emphasis on behaviour of individual females, the role of nest defence in promoting comm